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Abstracts

Huitu, O., Kuusela, S., Laaksonen, T. & Ruotsalainen A.L. (eds.)



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PLENARY PRESENTATIONS

Population scale drivers of individual variation and demography in migratory birds

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Individual variation in fitness drives both evolutionary and demographic changes in populations. Environmental heterogeneity is a major driver of individual variation and operates at various spatial and temporal scales, often in complex compositions. Migratory birds show an extreme example of space use among animals. They spend most of their time locally but use widely separated and often strongly contrasting habitats during the annual cycle. Habitat quality at either end of the migratory range influences fitness and conditions experienced in one season often carry-over to following seasons. In a model system where range expansion has been mapped both in winter and summer, individuals have been tracked across seasons and generations, throughout the annual cycle. During the range expansion, the population colonised a gradient of habitat quality. This variation in habitat shapes demographic patterns at different scales and interacts with both intrinsic and extrinsic factors in shaping individual variation and population processes. This system displays the inherent connectivity of events in the annual cycle of migratory birds and shows how population processes are driven by an interaction between individuals and their environment at various scales.

The influence of paleohistory on present-day patterns in biodiversity and ecosystems

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In this talk, I will provide a macroecological perspective on the role of long-term historical factors - supplementing and interacting with contemporary factors - in shaping current diversity and ecosystem patterns across spatial scales. Earth's climate has varied dramatically across geological time. Global and continental-scale studies of species distributions as well as of diversity - covering not just species richness and species composition, but also phylogenetic diversity- show strong imprints Quaternary glacial-interglacial climate oscillations as well as long-term cross-Cenozoic dynamics in climate. At smaller regional scales, there are also clear imprints on the Pleistocene glaciations in contemporary diversity patterns, reflecting strong impacts of these cold, dry climatic episodes. Importantly, these effects are not just seen at high latitudes, but also even in the tropics. There are also important non-climatic historical effects on distribution and diversity patterns, resulting from factors such as idiosyncratic patterns in lineage evolution and migration as well as prehistoric human impacts. In line with the species pool hypothesis, these large-scale historical dynamics can also shape the structure of local communities, supplementing the effects of local assembly processes. Furthermore, while much less investigated, there is emerging evidence that these historical dynamics also affect functional diversity and ecosystem functioning. Finally, I will discuss the implications of historical legacies in diversity and ecosystem patterns for ecological responses to future global change.

Evolutionary consequences of the transition from outcrossing to self-fertilization in plants

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The transition from outcrossing to selfing is one of the most frequent and well-studied mating system shifts in flowering plants. While theory predicts that self-fertilization should be associated with a reduced efficacy of natural selection, it remains unclear how rapidly these effects can be detected, and whether they are important for the long-term demise of selfing lineages. Furthermore, the transition from outcrossing to selfing is often associated with convergent evolution of a suite of reproductive traits that together characterize “the selfing syndrome”. Although the selfing syndrome is very common, little is known about the genetic and regulatory changes involved. The crucifer genus *Capsella* offers an opportunity to address these questions using genetic and genomic methods. Here, I will present some of our work on addressing the impact of the transition to selfing on the efficacy of natural selection, as well as the regulatory changes associated with the evolution of the selfing syndrome in the recently derived selfer *Capsella rubella*. Finally, I will discuss the implications of these findings for our understanding of the evolutionary consequences of this frequent mating system shift.

1. AQUATIC ECOLOGY

Recovery of lake vegetation following reduced eutrophication and acidification

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In recent decades, many aquatic ecosystems in Europe and North America have experienced reduced input of nutrients and acidifying substances because of improved sewage treatment and reduced emission of sulfur oxides. I will present an evaluation the consequences of these efforts to changes of water chemistry, species richness and composition of aquatic macrophytes in Danish lakes from 1990 to 2010. Reduction of eutrophication was strongest in, previously heavily impacted, hypereutrophic lakes. Water clarity however, improved the most in less impacted eutrophic lakes. Oligo- and mesotrophic lakes did not change significantly. Alkalinity and pH increased significantly in low-alkaline lakes, while well-buffered high-alkaline lakes did not show any change. Species richness per lake increased, on average, by 12% during the period. The increase was strongest in eutrophic lakes and among eutrophic species and could be directly attributed to reduction in phytoplankton biomass. The mean similarity among lakes in species composition increased during the study period. This was closely related to higher average species richness and caused by recolonization of lakes recovering from past eutrophication by predominantly commoner species. Higher pH in low-alkaline lakes was accompanied by a shift from acid-tolerant to more acid-sensitive species. The results demonstrate that societal investment in pollution control has been successful in terms of dramatically improving water quality of lakes and, with a time lag, species richness of macrophytes. Although relatively common species have spread across lakes and homogenized communities, continued pollution reductions could ensure survival of rare specialist species and perhaps even increase their future abundance.

The effect of heating up a stream on insect emergence

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A cold stream (IS7) in Hengill volcano 20 km east of Reykjavík was heated up by leading the stream water through a pipe into a heat exchanger in a nearby warm stream (IS8) and back to the lower reaches of the original stream. Emergence traps were placed in the unheated (7–10°C) and heated reaches (10–18°C) of the stream and in a warm stream (IS8) (19–22°C). This leads to changes in numbers of emerging insects, with a significant increase in total number of insects emerging from the heated stream and the warm stream. Of the total number of insects, Chironomidae were proportionally more numerous in the unheated reach compared with the heated reach, but blackflies (Simuliidae) and the predatory *Limnophora riparia* (Diptera) were both totally and proportionally more numerous in the heated reach. The fauna of the heated reach became more similar to the warm stream IS8. Heating up natural stream water by 3 to 8°C, similar temperature increase that is expected at high latitudes in the next century, will result in increased diversity and density of aquatic insects, higher production and increased density of predatory insects, to a lengthening of food chains and thus the height of the trophic network as a whole.

Spread of water-borne herbivore resistance in natural marine environment

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Several laboratory-scale studies have demonstrated that marine macroalgae can respond to water-borne grazing cues by increasing their resistance to herbivory. The functioning and relevance of this in natural populations is, however, yet unexplored. We present a manipulative field experiment testing whether water-borne cues of grazing in the brown alga *Fucus vesiculosus* L. induce resistance in the non-grazed conspecifics. By rearing recipient algae in the vicinity of the grazed emitter algae we explored over which distances cues could work, and whether the induction varies spatially or among algal genotypes. We further measured grazing damage, induced resistance and phlorotannins of the emitter algae to see whether these would affect the spread of resistance. Resistance induction via water-borne cues occurred in field conditions, but was spatially variable. In two of our four experimental blocks, undamaged neighbours within half and two meters from the emitter had increased resistance against further herbivory. Also, all the 26 genotypes responded similarly with induced resistance. In the other two blocks, there was no induction via water-borne cues. Spatial variation in the spread of resistance was not explained by the amount of grazing. Our results show that water-borne cues from grazing can be used by undamaged conspecifics to trigger their defences prior to actual grazing damage in natural macroalgal community. Further, in marine littoral environment the spreading of water-borne induction might depend more on environmental conditions such as wind-driven currents than on the amount of grazing.

Enriched rearing environment can enhance survival and disease resistance of aquaculture fishes

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The importance and volume of aquaculture is increasing worldwide. One major threat to this development is the vulnerability of intensive farming units to parasitic infections. Tanks typically used in large-scale fish production provide simplified, low-stimulus environments compared to natural conditions, which may influence several aspects of fish physiology and life expectancy. In the method of enriched rearing, tanks are supplied with structures and water dynamics to mimic variation found in natural conditions. We investigated the effects of enriched rearing on the occurrence of parasitic diseases in production-scale experiments comparing mortality, parasite abundance and disease resistance of salmonid fishes of wild and hatchery origin under enriched vs. standard rearing conditions during parasite epidemics. The results showed that fish from enriched rearing conditions and to some extent also those of wild background, had lower mortality, parasite abundance and higher resistance, during most epidemics compared to fish in standard rearing and of hatchery background. However, the effects of enriched rearing and parent background were not similar in all diseases, which may be due to ecology of each pathogen as well as depend on the species and age of the fish. Overall, the results suggest that fairly simple enrichment of the rearing environment can significantly decrease the harmfulness of some of the key pathogens found in aquaculture worldwide. These results may have important implications for ecologically and economically sustainable parasite prevention strategies in aquaculture.

No evidence for adaptive thermal transgenerational plasticity in metabolism of an ectotherm (*Daphnia pulex*), when minimizing the potential for confounding effects

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Environmental change may cause phenotypic changes that are inherited across generations in the absence of changes in DNA sequences through transgenerational plasticity (TGP). As for within-generation phenotypic plasticity, TGP may be an active response that has evolved to provide fitness benefits, or a passive response. Thus, to understand the ecological role of TGP it is not sufficient to demonstrate its presence; one also needs to evaluate whether it confers fitness benefits. Here we simultaneously test for TGP responses to thermal environments in metabolic rate and somatic growth rate in a zooplankton (*Daphnia pulex*), where the latter trait is closely related to population growth rate, and hence fitness. After transfer of ovulated eggs to a novel temperature, adjustments of metabolic rate occurred during their lifetime (i.e. within-generation plasticity). The observed direction of adjustment (upregulation at colder temperature) was consistent with the cold-adaptation hypothesis. However, no further change was observed during the subsequent two generations. Thus, the full possible extent of such adaptation was obtained through acclimation occurring during post-ovulation egg development and/or the juvenile stage, and no further changes could be ascribed to TGP. Consistent with this, we observed no tendency for increased somatic growth over the three generations when reared at novel temperatures, suggesting an absence of thermal TGP responses in traits other than metabolic rate that would provide fitness benefits. These results are inconsistent with existing studies of thermal TGP responses, and we discuss how previous experimental designs may have confounded TGP responses with within-generation plasticity and selective mortality.

2. ANIMAL ECOLOGY

Environmental stress and the flight of the butterfly

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Variation in environmental conditions can have drastic effects on natural populations. To successfully predict such effects, we need to understand how species respond to stressful conditions. We have used the resource allocation framework to study the mechanistic basis of fitness variation in butterflies. Insect flight is energetically very expensive, yet it is essential for fitness. By manipulating energy expenditure by increasing flight and by changing the availability of resources at different life-history stages, we have examined effects on energetics, reproductive output and lifespan. Butterflies conserve their flight capacity during dietary restriction, which highlights the importance of flight. Fecundity, on the other hand, drops significantly in nectar-feeders that rely on varying levels of adult food-derived resources. Interestingly, increased flight appears to alter the temporal patterns of reproduction as it leads to increased early-life fecundity. Examining the energetics of animals can also reveal dynamics that are not reflected in typically measured life-history traits, and thus give us insight into processes occurring under the surface. For example, flight increases food intake when resources are available and thus allows compensating for energetic costs. At the same time, increased metabolic rate may lead to other biochemical costs. Butterflies show clear responses to environmental variation and serve therefore as useful indicators of environmental change. Effects can however be species-specific due to different life-history strategies, which should be taken into account when predicting future changes at the population level.

Sick birds delay migration – Immune function influences migration phenology

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Most migrating birds make a number of stopovers during migration, and most energy and time of a migratory journey is spent during stopovers rather than on flight bouts. Among individuals a huge variation in the duration of stopovers exists. Some of this variation can be explained by weather conditions or fat stores. However, a considerable part of the variation remains unexplained. We explored whether the health status of a bird influences stopover duration and individual timing of migration. We caught long-distance migrants (LDM) and short-distance migrants (SDM) during autumn migration in Falsterbo, Sweden. We applied radio-transmitters to quantify individual stopover durations and experimentally immune-challenged half of the birds. We compared stopover duration between control and experimental birds and within and among SDM and LDM. We show that immune challenged birds prolong their stopover duration by almost 80% when undergoing an immune response. We also related baseline immune function to stopover duration and show that haptoglobin concentrations, a marker of inflammation, are positively related to stopover duration. Moreover, baseline immune function was related to individual timing of migration. Among LDM, early migrating individuals had lower levels of baseline immune function than late migrating individuals, while this pattern was reversed in SDM. Our data support the hypothesis that LDM are more time constrained than SDM. Moreover, our data suggest that in LDM high quality individuals leave first, while in SDM high quality individuals migrate later. Overall, our data provide evidence that immune function helps to explain individual variation in migration patterns.

What is ecological stoichiometry and how it can be used in studying the effects of nutrient loading in host-parasite interactions?

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Human induced changes in nutrient loading in the environment have been connected to increases in many parasitic and infectious diseases. Prediction of uniform global patterns in nutrient-driven changes in disease is, however, difficult. One potential framework for reviewing host-parasite interactions under varying nutrient ratios is ecological stoichiometry. This framework explores the balance of organismal requirements of chemical substances, most importantly carbon, nitrogen and phosphorus (C:N:P), and how it is reflected into the ecological interactions and processes. For example, increased P-loading is likely to favour organisms that are able to allocate a lot of P to ribosomal RNA needed for protein synthesis and growth, with a potential to modify species interactions at different trophic levels. Depending on the level of organismal hierarchy, changes in environmental nutrients can impinge on host-parasite interactions via 1) altered host resistance and parasite virulence through host stoichiometry at individual host level, 2) changed encounter/contact rates at population level, 3) changed host community structure. In our recent review (Aalto, Decaestecker & Pulkkinen 2015, Trends in Parasitology 31: 333-340) we suggest that the outcome of infection could depend on the differences in the elemental requirements and level of homeostasis of the hosts, and on the overlap in stoichiometric requirements of the host and the parasite.

Predation of *Neodiprion sertifer* cocoons by small mammals in relation to forest heterogeneity

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Forests are subjected to a certain level of damage by defoliator insects. This damage is usually not severe and trees will easily recover from these levels of herbivory. However periodically, herbivore numbers rapidly increase, causing high levels of defoliation. It is thought that forest structure and habitat heterogeneity can affect herbivorous insect performance. Heterogeneity can contribute indirectly to the stability of herbivore populations, providing a more attractive micro-habitat to natural enemies that potentially leading to reduce population fluctuations. Small mammals are important predators of insect cocoons, therefore we wanted to test whether a) Cocoon predation is higher in stands with high tree species diversity b) The presence of deadwood increases the predation on cocoons by small mammals. To test these hypotheses, we performed two experiments investigating the effect of forest heterogeneity on the predation of cocoons of the European pine sawfly, *Neodiprion sertifer* (Hymenoptera: Diprionidae). In our first experiment, groups of cocoons were placed below the soil litter close to selected pines in stands representing either monoculture of *Pinus sylvestris* or mixed forests. In the second experiment, we placed the cocoons in a similar matter but now the quantity of deadwood around the trees was manipulated to range from low to high deadwood cover. In both experiments cocoons were collected and counted after two weeks, missing or opened ones were considered predated. Our results suggest that forest heterogeneity can be important for cocoon predation by small mammals through increase in tree diversity and variation in the amount of deadwood.

Habitat-linked fine-scale genetic structure, foraging behaviour and demographic responses to land-use changes in the Eurasian kestrel

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Food availability is a major factor driving the reproductive output and survival of wild predator populations. However, few studies have investigated the interplay between land-use change, limitation in food resources triggering subsequent dietary shifts and spatial variation in fitness parameters. Here we predict that recent land-use change in northern landscapes might trigger a mismatch between individual and habitat quality during low food abundance years with negative consequences in terms of reproductive performance. In this project we used a 3-year dataset of Eurasian kestrels (*Falco tinnunculus*) breeding in western Finland, combining main prey abundance (highly cyclical vole populations) diet choice using stable isotopes as a new and powerful tool to investigate how trophic ecology relates to demography, fitness parameters (individual quality indices including i) genetic heterozygosity: n=453 individuals, 17 polymorphic microsatellites; ii) morphometric measurements; and, iii) breeding parameters) and landscape genetic methods (least cost paths). Specifically we investigated mismatches between individual quality, reproductive performance and landscape composition (intensive agricultural areas vs. heterogeneous habitats, i.e., mix of forest, clear-cuts and fields) under fluctuating food conditions. Stable isotope analyse showed that passerines and lizards are both important alternative prey during low vole abundance years. We found higher individual genetic heterozygosity together with earlier egg-laying dates in intensive agricultural areas compared to more heterogeneous habitats. These individuals had lower breeding success than birds breeding in heterogeneous habitats suggesting that more diverse landscape features offer more alternative prey in low vole abundance years. Our results have important implications for biodiversity conservation in Finnish agricultural landscapes.

3. EVOLUTIONARY ECOLOGY

Sex-dependent dominance at a single locus maintains variation in age at maturity in Atlantic salmon: a resolution for intra-locus sexual conflict?

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Sea age at maturity in Atlantic salmon is a life history trait closely linked to fitness, and displays remarkable, temporally stable, variation among populations. Using high-density single nucleotide polymorphism data across 57 wild populations and whole genome re-sequencing, we find that the variation around the an adiposity regulator gene, vestigial-like family member 3 (VGLL3), explained 39 % of phenotypic variation in age at maturity, an unexpectedly large proportion for what is usually considered a highly polygenic trait. Such large effects are predicted under balancing selection from either sexually antagonistic or spatially varying selection. Furthermore, the locus exhibits sex-dependent dominance, promoting earlier and later maturation in males and females, respectively. Our results provide the first empirical example of dominance reversal allowing greater optimization of phenotypes within each sex, contributing to the resolution of sexual conflict in a major and widespread evolutionary trade-off between age and size at maturity. They also provide key empirical evidence for how variation in reproductive strategies can be maintained over large geographical scales. We anticipate these findings will have a substantial impact on population management in a range of harvested species where trends towards earlier maturation have been observed.

Truth and lies – honest signalling and automimicry in an aposematic insect

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Aposematism is the combination of a conspicuous primary signal with a secondary defence. In order for aposematism to be successful, predators must learn to associate the aposematic signal with unpalatability or toxicity. However, the level of defence may not be uniform across all members of a species. Automimicry occurs when some individuals possess lower levels of defence, but retain the same aposematic signal. This is especially likely to develop if the defence is costly. The levels of automimicry in a population may dramatically affect predator learning and avoidance. It is thought that without some selection against automimics, keeping signals "honest", cheaters may invade the population and break down the relationship between signal and defence. Here we investigate variation in chemical defence in an aposematic insect, the wood tiger moth. This species represents an interesting case study as it displays both within and between-sex variation in colour. Female colouration varies continuously from yellow to red, with red providing the stronger anti-predator signal. We show that the level of chemical defence in this species varies considerably between individuals, despite not being sequestered from diet, and is highly heritable. Additionally, our data suggest that honest signalling is operating within male moths, and potentially also across the sexes, as females appear to have both the strongest primary signal and chemical defence. Despite this, variation in female colour was not correlated with defence level. This has important implications for the maintenance of aposematic signalling, and the occurrence of signal polymorphism, in aposematic species.

Evolvability of plastic responses to temperature in life history traits of a population of *Daphnia*

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Understanding how life history traits change as a consequence of changing temperatures is crucial for predicting populations' response to climate change. We exposed 10 genotypes from a Norwegian population of *Daphnia magna* to 8 different temperatures (range 12– 28 degrees) and estimated the plastic response of three life history traits: somatic growth rate, age at maturation and size at maturation. We decomposed the phenotypic variance of each trait into genetic, environmental, gene-by-environment (GxE) and residual variances. Clonal variances in trait mean and reaction norms were expressed on the scale of evolvability (variance / mean square). Somatic growth rate and age at maturation are highly affected by temperature and show evolvability of both trait mean and reaction norm. In contrast size at maturation is environmentally canalized, but still displays an important evolvability of trait mean. This study, which is the first to estimate evolvability of phenotypic plasticity, suggests that the studied population has the potential to respond to climate change by changing its plastic response to temperature in several life history traits. Finally, we speculate that the environmental canalization of size at maturation result from strong stabilizing selection in the wild. This would suggest that this trait is the most correlated with fitness in this population.

4. THEORETICAL ECOLOGY

Oh, how we pick and choose: on theoretical constructs in subfields of ecology

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Ecology consists of a large number of theoretical constructs, empirical patterns and methods; a pool from which applied ecology can draw ideas when exploring practical problems. Subfields of applied ecology - including pest control, conservation, and wildlife management - deal with the management of biological populations, and should therefore rest on the same ecological foundations. But is this really the case? We study this issue by analyzing recent citation rates (2010–2014) to more than 130 highly cited, classic publications, covering a wide range of topics. Using ordination methods, we find a clear clustering of journals, where conservation occupies another part of the ordination space than pest control. Classifying papers into broad topics reveals that the ordination patterns are driven by striking differences in how often ecological concepts are used in different subfields. While some patterns are easy to understand, e.g. the use of biodiversity concepts in conservation, others are left unexplained. For instance, the lack of spatial concepts and competition in pest control, predation in conservation journals, and foodweb ideas in wildlife journals are harder to understand. Microbial ecology also appears devoid of large parts of ecological theory. These patterns imply distinct divides within ecology, where subfields selectively use certain parts of ecological theory. Therefore, we argue that work in applied ecology would benefit from broader theoretical perspectives. Collaboration and inspiration across sub-disciplines could be one way to achieve this, perhaps inspiring novel research directions.

Ecological processes drive the epidemiology of environmental pathogens

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Pathogens arising from environmental microbiota form an important threat to wildlife, food production, and human health. Good examples of environmental, opportunistic pathogens include *Cholera* (human), anthrax (cattle and wild life), *Flavobacterium* (salmonid fish) and white nose syndrome (North American bats). The epidemiology of such pathogens cannot be understood with traditional models that ignore the ecological and evolutionary processes—such as biotic interactions and fluctuations in environmental conditions—affecting the free-living stage of these organisms. By combining a host model (transition between susceptible, infected, and recovered individuals) to an ecological model, including a pathogen as a member of a species community, we have shown that loss of diversity in the outside-host community can lead to a catastrophic emergence of pathogen outbreaks. When the system is subjected to environmental variation, the severity and temporal predictability of fluctuations has an important effect on epidemiology; depending on the conditions, either persistent infections or outbreaks can arise in situations where infections do not occur under a stable environment. An important assumption is that the infection process is dose-dependent, which can be derived from a mechanistic model. We have also shown that such a model provides a good fit experimental data. Environmental pathogens cannot be eradicated by treating hosts, as the environment provides an endless pathogen reservoir. Our results provide important insight for understanding the epidemiology of these pathogens, which can be utilized for devising experiments and developing policies for mitigating and preventing pathogen outbreaks.

Optimizing boreal forest management to reduce trade-offs between timber, carbon storage and biodiversity

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The boreal biome, representing approximately one third of remaining global forests, provides many crucial ecosystem services. A particular challenge in the boreal biome is to reconcile demand for increased timber production with provision of other ecosystem services and biodiversity. However, there is still little knowledge about how forest management can help to resolve this challenge. In our study, we applied seven alternative forest management regimes using a forest growth simulator in a large boreal forest production landscape. First, we estimated the potential of the landscape to provide harvest revenues, store carbon and maintain biodiversity across a 50-year time period. Then, we applied multiobjective optimization to identify trade-offs between these three objectives, and to identify the optimal combination of forest management regimes to achieve these objectives. We found that the achievable levels of biodiversity and carbon storage as well as the trade-off between them were strongly dependent on the level of timber revenue we want to achieve. It was not possible to achieve high levels of either biodiversity or carbon storage if the objective of forest management was to maximize timber harvest. As compared with the recommended forest management regime in Fennoscandia, reducing intermediate thinnings, extending stand rotations, and increasing the amount of area set aside from forestry may be necessary to safeguard biodiversity and non-timber ecosystem services. We conclude that it is possible to reduce the trade-offs between different objectives by applying diversified forest management planning at the landscape-level.

5. EVOLUTIONARY ECOLOGY

Trans-generational immune priming in honeybees

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Insects lack antibodies, the carriers of immunological memory that vertebrate mothers can transfer to their offspring. Yet, it has been shown that an insect mother facing pathogens can prime her offspring's immune system. To date, it has remained enigmatic how insects achieve specific trans-generational immune priming despite the absence of antibody-based immunity. Here, we show for the first time, how this is made possible in honeybees via an egg-yolk protein binding to immune elicitors that are then carried to eggs. This yolk protein, called vitellogenin, is able to bind to different bacteria and pathogen specific molecules. We use *E. coli* fragments as markers to show how vitellogenin is necessary for the carrying of immune elicitors to eggs. Our findings are not only revealing a new function of vitellogenin, but also demonstrate how very high specificity of immune priming can be achieved without antibodies. These findings help to revolutionize our understanding of how organisms fight pathogens. Furthermore it is essential for designing tools for protection of ecologically and economically important insects, such as the honeybees.

Sub-inhibitory antibiotic concentrations can radically alter the eco-evolutionary consumer-resource dynamics in microbial communities

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Modern medicine relies heavily on the effective use of antibiotics. However, antibiotic resistant pathogens are on the rise. This problem has been often studied in simplified single species setting, but in natural environments bacteria reside in multispecies communities where they interact with other microbes. Yet, virtually nothing is known about community aspects, such as how predation affects the emergence and spread of antibiotic resistance. Furthermore, recent evidence highlights the importance of sub-inhibitory concentrations of antibiotics on bacteria. In addition to the fact that these low concentrations can alter the bacterial gene expression, communication, and select for antibiotic resistant genotypes, an important question is whether this modifies the community level dynamics. By using experimental evolution methods with a microbial model system consisting of bacterial prey, *Pseudomonas fluorescens* SBW25, parasitic phages and protozoan predators, we found that subinhibitory concentrations of antibiotic streptomycin can radically alter the eco-evolutionary community dynamics. Moreover, the community structure determined the emergence of antibiotic resistant genotypes in the bacterial population. In addition to the phenotypic data, also a massive sequencing of the experimental *Pseudomonas* populations is underway. Our results highlight the importance of understanding the eco-evolutionary community aspects when fighting the antibiotic resistance problem.

The interplay between ecology and evolution at small spatial scales: insight from Arctic charr in lava caves in Iceland

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A key question in evolutionary biology is to understand which factors shape biological diversity. This is especially true at the intra-specific level, where evolutionary and ecological processes interact to shape the phenotypic and genetic structure of natural populations. Long-term monitoring studies on highly replicated wild populations are particularly powerful to study divergence in space and time. We have studied phenotypic and genetic diversity of Arctic charr (*Salvelinus alpinus*) across four years and twenty lava caves around Lake Mývatn, NE. Iceland. Mark-recapture studies, combined with population genetics, show that these caves are inhabited by small local populations of charr with very low connectivity across caves. Individual tagging, combined with measurements of growth and morphology, further show phenotypic divergence at small spatial scales. Additionally local ecological factors seem to affect phenotypic traits in these populations. These results strongly indicate that both evolution and ecological factors play a role in shaping genetic and phenotypic structure of wild populations at contemporary times.

Divergent natural selection on the ability to reproduce facilitates ecological speciation

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The distributions of species are not only determined by where they can survive - they must also be able to successfully reproduce. For animals with external fertilisation, the environment can exercise strong selection pressures not only on the soma of individuals, but also on their gametes and other reproductive traits. This can reduce the reproductive success of immigrants in novel environments and thus hamper gene flow. We conducted a series of aquarium experiments on the sand goby (*Pomatoschistus minutus*) from marine and brackish environments in order to understand how local adaptation of reproduction affects reproductive success. We found that males spawning as immigrants in non-native salinities have significantly lower hatching success and proportion of moving spermatozoa compared to resident males. All males of brackish origin failed to hatch a clutch of eggs in marine water. Growth and condition of adults were, however, not affected by non-native salinity. We interpret these results as evidence for local adaptation of sperm and possibly also components of paternal care, resulting in a "reproductive inability by immigrants" that in all essentiality corresponds to "immigrant inviability". The marine and brackish environment differs in a diverse set of abiotic and biotic environmental factors and selection will be multifarious. We suggest that such reproductive inability by immigrants has the potential to hamper gene flow and under a "feedback loop" view of speciation facilitate further divergence and reproductive isolation.

Evolutionary transitions in agricultural performance related to crop domestication by fungus-farming ants

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The ant farmers (Tribe: Attini) provide fascinating parallels with human farmers, having domesticated their fungal crops for improved nutritional and metabolic efficiency over millions of years. Specialized fungal cultivar adaptations were likely important factors driving the evolution of larger and more complex farming societies, although links between fungal physiology and farming performance remain poorly understood. We tested for transitions in how ant farmers use nutritional compost to produce their fungus crops in diverse farming systems spanning the attine phylogeny. We found that a basal attine growing a non-domesticated fungal crop avoids the high-carbohydrate, low-protein substrate that maximizes fungus growth (edible hyphae), apparently to avoid reproductive conflicts (inedible mushrooms). In contrast, an advanced industrial-scale leafcutter ant growing a specialized domesticated crop appears to avoid such production tradeoffs because it harvests a single nutritional blend to simultaneously maximize crop quality and quantity. These results, and their associated performance consequences, suggest that while early ant farmers faced constraints on farming productivity stemming from divergent evolutionary interests of symbiotic partners, these differences were largely resolved through crop domestication. Such production benefits may explain the rise of leafcutter ants as ecologically dominant herbivores across neotropical ecosystems.

6. ARCTIC ECOLOGY

What drives patterns of herbivore diversity in the Arctic?

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Vertebrate herbivores exert a strong trophic influence in terrestrial Arctic ecosystems and their diversity is expected to influence the outcomes of plant-herbivore interactions. Several hypotheses have been put forward to explain patterns of species diversity at the global scale, but drivers seem to be region- and guild-specific. Despite recent efforts to document biodiversity in the Arctic, no study has systematically evaluated the relative role of different drivers in shaping broad diversity patterns of herbivores. The aim of this study was to identify patterns of species richness of vertebrate herbivores and their drivers in the Arctic. We compiled information on the distribution of vertebrate (bird and mammal) herbivores in the Arctic scale, and used eight variables representing the most relevant hypotheses to explain patterns of species richness. Overall, herbivore species richness in the Arctic was positively related to plant productivity (as assessed with the Normalized Difference Vegetation Index) and to the species richness of predators. To a lesser extent, patterns of species richness of herbivores were also related to mean annual temperature and distance to the coast (bird richness peaking near the coast and mammal richness inland). Our results suggest that biotic interactions, with either higher or lower trophic levels or both, can shape patterns of species richness of herbivores at a biome-wide scale. Changes in primary productivity and predator communities linked to ongoing environmental changes in the Arctic are likely to affect the distribution of herbivore diversity.

Climate change effects on phenology in alpine plant communities

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Phenology in plants is sensitive to changes in temperature and generally trends towards earlier spring phenology have been observed in the Northern Hemisphere. However, changes in precipitation patterns can be important at high elevation, because increased snowfall during winter can shorten the growing season. Accelerated flowering after late snowmelt indicate plastic phenological responses, but the timing of flowering is to some extent genetically determined since there is strong selection in plants from cold sites to flower early to complete the life cycle within a growing season. To study phenological responses in alpine plant communities to warmer and wetter conditions, a climate grid combining a temperature and a precipitation gradient was used to assess the independent and joint impacts of both variables. Phenology was assessed for 40 plant species on vegetation turfs that have been transplanted to warmer, wetter and both warmer & wetter conditions. We explicitly asked, to what extent differences in phenological responses are plastic or genetically determined. Plant communities showed both plastic and genetic responses with earlier flowering communities transplanted to warmer and warmer & wetter climate and later flowering in wetter climate. Understanding to what extent species will respond to future climate change by phenotypic plasticity or adaptation is important, because it could affect their ability to persist.

Relative contribution of plant functional attributes, abiotic and biotic environments to tundra heath communities structuring

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In the general context of ongoing tundra shrubification, the heterogeneity of locally observed patterns suggests some variation in the relative importance of the multiple drivers structuring tundra communities. Beyond the evidence of the contribution to community dynamics and functioning of biotic interactions, relative plant functional strategies and environmental severity, how they interact and jointly shape the community in harsh environments still remain poorly understood. Here we report an experimental test of growth and survivorship of several dwarf shrubs across an environmental harshness gradient. The design consisted of the transplants of target species that differed in stature and leafing strategy along hillock-depression meso-topographic gradients. Environmental conditions ranged from severe winter abrasive winds and spring drought on the uppermost level to relatively snow protected conditions and shorter growing season at the lowermost level. The coverage of target neighbouring vegetation was used as a proxy for biotic interactions intensity. Target plant performances were primarily more affected by winter damage on the hillock than by shorter growing season in the depression. But the sensitivity to exposure was also strongly species-dependent and no general response linked to leafing strategy or stature emerged. Eventually, positive response to the density of neighbouring vegetation was detected in the exposed habitat. Our results deepen our understanding of the local structure of plant communities in the heterogeneous meso-topography of the subarctic tundra. The plant community structure as well as tundra response to environmental changes is shaped by a complex and variable interplay between abiotic conditions, biotic interactions and plant attributes.

Interaction strength between plants and small rodents differs between population peaks

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Variability in the strength of trophic relationships is an integral, but often neglected, part of food web functioning. The temporal consistence of such variation is particularly poorly known, as empirical validation of biotic interaction models is rare. One important general attribute of herbivore population cycles is that cycle amplitude (i.e. peak phase density) vary in both space and time. Here we tested the hypothesis that plants, in their functions as food and shelter, determine peak phase density. We combined fine-resolution data on the two interacting trophic levels with a large-scale study design encompassing three watersheds of subarctic tundra extending over two rodent population peaks. We first modelled the effect of food and shelter plants on rodent density during one population peak and then assessed whether these models could predict the density of the three rodent species present in this ecosystem during the next peak. Both food and shelter biomass were related to rodent density during the first peak. Yet, the predictions from the statistical plant-rodent models parameterized based on spatial data from the first peak matched poorly the observations during the next population peak when plants and rodents were little correlated. Hence, the strength of relationship between vegetation and rodents is temporally variable and vegetation alone cannot explain the variability in rodent population peak phase density. Such heterogeneity in the strength of a key food web interaction demonstrates that temporal replication is necessary in order to generalize conclusions on trophic interaction strength.

Coping with fast climate change in northern ecosystems: mechanisms underlying the population-level response of a specialist avian predator

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Northern ecosystems are facing unprecedented climate modifications, which pose a major threat for arctic species. Climate can influence fitness parameters of specialist predators either through reduced reproduction or survival following increasing adverse weather conditions or via changes in the population dynamics of their main prey. Here, we combined three overlapping long-term datasets on the breeding density and parameters of a rodent-specialist predator, the rough-legged buzzard *Buteo lagopus*, its main prey population dynamics and climate variables, collected in subarctic areas of Finland and Norway, to assess the impact of changing climate on the predator reproductive response. Rough-legged buzzards responded to ongoing climate change by advancing their laying date as a consequence of earlier snowmelt. However, we documented for the same period a decrease in breeding success, which principally resulted from an indirect effect of changes in the dynamics of their main prey, i.e. grey-sided voles *Microtus oeconomus*, and not from the expected negative effect of unfavourable weather conditions during the brood-rearing period on nestling survival. Additionally, we showed the striking impact of autumn and winter weather conditions on vole population growth rates, with a strong positive correlation between mean snow depth in autumn and winter and both winter and summer population growth rates. Our results highlighted that, in northern ecosystems, ongoing climate change has the potential to impact specialist predator species through two mechanistic linkages, which may in the long-run, threaten the viability of their populations, and lead to severe cascading trophic effects at the ecosystem level.

7. BEHAVIORAL ECOLOGY

Senescence of personality in a wild bird

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Despite a growing body of literature reporting developmental changes in personality, few studies have adopted a lifetime perspective to study age-related changes in personality traits. Since most personality traits are heritable and linked with fitness, ontogenetic changes can have important evolutionary implications. In this paper, we explore age-related changes in two behavioural responses to handling, both of which are heritable and associated with fitness, in wild blue tits. We find that one of these responses (handling aggression), which is positively correlated with fitness, declines with age. We show that this age-related decline is not due to selective disappearance, but occurs also within individuals. To our knowledge, this study is the first to demonstrate a senescent decline in a personality trait in the wild. We further find that individuals differ significantly in their rate of ageing, but find no statistical support for the presence of genotype-age interactions on personality. Future research on personality would benefit from a more explicit lifetime perspective.

How does lifetime reproductive success in the Siberian flying squirrel relate to availability of food and good quality habitats?

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A major threat to population viability of many species worldwide is habitat loss. Especially species living in boreal forests, such as the Siberian flying squirrel (*Pteromys volans*), have experienced steady population declines as forest structure and composition has changed dramatically due to modern forestry. The Siberian flying squirrel is an old-growth forest species that prefer mature spruce dominated forest with access to deciduous trees for forage and large European aspens as sites for natural nesting cavities. Although extensive effort has documented how the occurrence of the species relates to the availability of crucial forest types, little effort has been put in determining how the availability of high quality habitat patches affects the lifetime reproductive success (LRS) of this species. LRS is commonly decomposed into four components, survival until first reproduction, reproductive longevity, offspring production and offspring survival. Effects of habitat quality and food availability can affect any of these components. Here we use a 20 year longitudinal dataset on adult Siberian flying squirrel females from western Finland to assess whether LRS is affected by availability of high quality habitats (mature spruce dominated forest) and food availability (annual production of birch catkins and aspen pollen production). More specifically, we investigated the relationship of the proportion of optimal habitat and food availability with lifetime production of offspring and reproductive longevity. Preliminary analyses indicate that there is a non-linear relationship between the proportion optimal habitat around the nest site and LRS.

Mixed diets - insects know how to stay healthy

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Under natural conditions insects are exposed to high abundance variation in parasite pressure. The defence against infections involves both innate immune system, but also various behavioral adaptations. The latter one includes the usage of active compounds, which can be sequestered from their food. Diet is one of the major factors influencing insect's life history and is thus important for development and survival. The ability to actively change the diet and ingest biologically active compounds after encountering an infection is called self-medication. Self-medication is characterized by four criteria: I) deliberate contact, II) increase of host fitness, III) detrimental for the parasite and IV) harmful for non-infected hosts. Although suspected in many cases, true self-medication has been hard to prove in natural systems. Many herbivorous insects are polyphagous and thus are able to use different host plants as a food source. However, we still lack the understanding of how the diet preferences are changing depending on the developmental stage and infection risk. Here we use the polyphagous wood tiger moth *Parasemia plantaginis*, bacterial pathogen *Serratia marcescens* as well as two different plant species, *Taraxacum officinale* and *Plantago major*. Our results show that insect's ability to survive an infection is increasing when ingesting a mixed diet of both plants, but it is specifically dependent on the temporary composition of the diet. Furthermore trade-offs between immune response and the different diets could be shown and the true occurrence of self-medication was examined.

Can insectivorous birds anticipate the future? Insect egg deposition makes pines attractive to birds

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Insectivorous birds can eat sawfly eggs, but a tree with insect eggs could also indicate "future food" (i.e. hatching larvae). Earlier studies have shown attraction of insectivorous birds to herbivore-damaged trees without the birds actually seeing or smelling the larvae. For the first time we show with great tits (*Parus major*), blue tits (*Cyanistes caeruleus*), pine sawflies (*Diprion pini*) and Scots pines (*Pinus sylvestris*) a similar attraction to egg-induced trees. Adult sawflies were placed on the lower part of a branch for egg-deposition. After three days the lower egg-laden part of the branch was cut off, and the upper, systemically egg-induced branch (without eggs) was transferred to a bird experiment aviary together with an egg-free control branch. Each bird's behaviour was followed for 10 minutes. The birds of both species significantly more often visited first the branch induced by egg-deposition than the control branch. They also visited it more times during the first two minutes. We found that birds could have recognized the egg-induced branches by olfaction since the pine branches emitted numerous terpenoid volatile organic compounds, of which (*E*)- β -farnesene was released in higher quantities from the egg-induced branches. On the other hand, visual cues might be relevant too, since control branches reflected light significantly more than egg-induced ones.

Host manipulation by a tropically transmitted eye fluke parasite

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Parasite manipulation hypothesis predicts that enhancement of host predation risk is advantageous for fully developed parasite larvae, but the opposite (predation suppression) for immature larvae. While the enhancement of predation risk by fully developed parasites is well supported empirically, there is still little evidence of predation suppression manipulation by non-infective parasite stages. We used the trematode eye fluke *Diplostomum pseudospathaceum* and juvenile rainbow trout *Oncorhynchus mykiss* to study the parasite manipulation hypothesis. Definitive host of *D. pseudospathaceum* is fish-eating bird, to which the parasite is transmitted via predation of the fish host by bird. In the first experiment, the young, not yet infective parasite larvae decreased aggressiveness of juvenile rainbow trout. By the time when larvae were fully infective (30 d), the aggressiveness increased and exceeded that of control fish. However, despite the increased aggressiveness, the experimentally infected fish lost contests for a territory against the control fish, which should expose them to predation. In the second experiment - designed especially to test the predation suppression idea - the immature, not yet infective parasite larvae decreased vulnerability of host fish to simulated predation (dip-net catch) and decreased activity (horizontal move) of the host fish when compared with the control fish harbouring no larvae. These results support the view that tropically transmitted parasites can induce such behaviours in their host that increase likelihood of host predation when the parasite is fully developed, but decrease host predation risk until the parasite has reached infectivity - both traits being beneficial for the parasite.

8. PLANT ECOLOGY

Epiphytic metapopulation dynamics in a managed forest landscape

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Understanding the relative importance of the metapopulation dynamic of the species is crucial for predicting future metapopulation size and persistence. For instance, the extent to which sessile organisms are dispersal vs establishment limited is key information for understanding and projecting metapopulation dynamics in the landscape. Here we present a pair of studies, one observational and one experimental intended to estimate the relative importance of dispersal and establishment limitation on the colonization of the epiphytic lichen *Lobaria pulmonaria* in a managed boreal forest landscape. We first estimated the rate of colonization-extinction based on a re-survey in 2008 of the species originally sampled in 1999. Second, we estimated the establishment probability of the species by evaluating recruitment in 2014 after propagules being experimentally transplanted on non-occupied but presumably suitable trees in the study area in 2004. Finally, we quantified the relative importance of dispersal, establishment, and dynamics of host trees in the future persistence of the species with simulated scenarios over 100 years. Among the 2033 trees mapped in the first survey, we recorded six *L. pulmonaria* colonisations in the second survey in 2008. Eight deterministic extinction events were observed among 138 occupied trees. On the other hand, ten years after sowing experiments, *L. pulmonaria* had established on 8 % of 99 experimental trees, but no establishments were recorded in clear cut or dry forests. Simulations of the future dynamics underlined the strong influence of propagule availability, connectivity to occupied trees and tree rotation time on the future metapopulation size of the species.

Small-scale spatial distribution of plant species in an agricultural landscape

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Species distribution modelling is often targeting single species and correlations in spatial patterns and environmental responses across species are usually not included in the models. This may be about to change as new methods for joint species distribution modelling are being developed. In this presentation, I will explore some of these possibilities using data on small-scale distribution in common plant species in an agricultural landscape. In a study area of 5 x 6 km in central Norway, presence-absence data on eight plant species characteristic for semi-natural grasslands were recorded on 930 plots of 10 x 10 meters. The distribution of these species was then examined using a probit regression model in which the joint probabilities of occurrence could be estimated using the correlation matrix of a multivariate normal distribution. The approach was first developed by Pollock et al. (2014) and makes it possible to separate correlation in occurrence between species due to environmental variables from residual correlation. In general, the correlation in occurrence among the studied species was high and similarities in environmental responses were the main cause of this. Finally, the outcome of the joint distribution model is compared with results from logistic regression models developed for each species and some of the differences between these approaches are highlighted.

Climate-driven changes in biotic interactions affect seedling recruitment and species richness in semi-natural grasslands

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Biotic interactions are important determinants of plant community structure and function. Shifts in these interactions due to global climate change, mediated through disproportional increases of certain species or functional groups, may therefore have strong effects on plant community properties. Still, we lack knowledge of community-level effects of climate-driven alterations of biotic interactions. In this study we examined how a dominant functional group affected seedling recruitment and community properties of subordinate plant species by experimentally removing graminoids in semi-natural grasslands in southern Norway. To test whether the effect of graminoids varied with climate, the removal experiment was replicated along broad-scale temperature and precipitation gradients. Competition from graminoids predominantly limited seedling recruitment and species richness of the non-graminoid plant community across the climate gradients. The relative importance of competition also increased with increasing temperature: while interactions with graminoids varied from competition to facilitation along the precipitation gradient under cold climates, only competition was found under warm climates. These findings partly correspond with the results of a previous population-level study, indicating that increased relative importance of competition may be a common response to climate warming across organizational levels of plant communities. Our study suggests that competitive interactions with graminoids may further limit non-graminoid seedling recruitment and species richness in semi-natural grasslands in a warmer future climate, thereby reducing biodiversity of these often highly diverse ecosystems.

Winner takes it all in mycorrhizal networks

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Mycorrhizal fungi connect plants to their immediate neighbours. These connections may transfer information and resources between individuals of the same and different species. Within plant species, the potential connectivity of networks is high. We tested the effect of symbiont fungal identity and diversity on net network effect within species under controlled conditions in greenhouse. In parallel experiments under field conditions in an arctic meadow, we explored the net network effects on subordinate individuals. Field experiments revealed that network connections changed the source of nitrogen subordinate individuals acquired. The subordinate plant growth was suppressed by mycorrhizal network in the field. In greenhouse, mycorrhizal fungal species translocated different amounts of nitrogen to subordinate individuals. More diverse symbiont networks were not beneficial to the subordinate individuals, but the effect depended on the species identity. The results support the view that mycorrhizal networks result in highly asymmetric competition where the dominant plants take more than their share of soil resources. The asymmetric benefit in mycorrhizal networks is interesting in evolutionary ecology perspective.

Modelling survival of plants with unobservable stages - consequences of assumptions about prolonged dormancy for population model predictions

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Matrix population models are used to study the viability of endangered plant species, and model parameters, such as survival, are estimated from the monitoring data. Some plant species have unobservable life stages, prolonged dormancy, when individuals stay belowground for one or several years. If such a plant never reappears, its true fate (dead or dormant) may remain unknown. Therefore, researchers have made assumptions about survival during dormancy. These assumptions have direct consequences for survival estimates, but the effects on population model predictions have not been studied earlier. We defined two common assumptions about survival during dormancy. First, plants might die during the first year belowground and those survived will re-emerge with constant rate (Instant death). Second, plants could die during any given year belowground and re-emerge conditioned on survival (Slow death). Using a theoretical life history of two stages we tested how these assumptions affect predictions from the deterministic matrix population model. We applied the same analysis to the long-term data of two endangered species, *Isotria medeoloides* and *Epipactis atrorubens*. Our results show that, if we are interested in the overall viability of a population, either Instant or Slow death assumption can be used, since population growth rate did not vary between assumptions. However, there were differences in reproductive values, life expectancies, and sensitivity and elasticity of population growth rate on survival depending on model assumptions. Therefore, if the aim of a study is to formulate a management plan, the consequences of assumptions for model predictions should be carefully evaluated.

9. COMMUNITY ECOLOGY

Ecosystem services from grasslands: more important than you might think

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Extensively managed grasslands are globally recognized for their high biodiversity as well as their socioeconomic and cultural values. However, their full capacity to deliver ecosystem services as parts of agricultural systems and their multifunctional role is surprisingly understudied compared to other production ecosystems. Based on case studies from North Europe and South Africa, we make a comprehensive overview of ecosystem services generated in natural and semi-natural grasslands. In addition to livestock production (fodder and meat), these grasslands can supply many other ecosystem services under high demand from society, e.g., water supply and flow regulation, carbon storage, erosion control, climate mitigation, cultural values, pollination and biological control of agricultural pests. We identify bundles of ecosystem services, trade-offs and synergies among the services and discuss how these may inform management practices. We argue that grasslands, which cover twice the area suitable for crop production, can play a larger role for global food security. Ruminant grazers are efficient converters of non-edible plant biomass such as grass into human-edible energy and nutrients, without competing with humans for use of crops. Furthermore, grassland dairy and meat production systems may not necessarily have the large climate effects that intensified meat production based on cropland has. Thus, grazing on grasslands can be used to replace meat production based on arable crop feeds. By integrating grasslands into agricultural production systems and land use decisions locally and regionally, their contribution to functional landscapes, biodiversity conservation, ecosystem services, to food security and sustainable livelihoods can be greatly enhanced.

Can ecospace predict variation in biodiversity?

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Understanding patterns in biodiversity is a key to ecology. While important progress have been achieved in topics such as community species richness, species pool build-up, ecosystem function and conservation, bottom line is a lack of conceptual unification. A framework for understanding variation in biodiversity between communities within landscapes is badly missing. Such a framework should be able to encompass more than a single taxonomic group and - especially - the megadiverse groups of insects and fungi. The concept of ecospace is proposed as a template for uniting gradient-based community ecology with niche and assembly theory at the scale of the biotope. It is further proposed that biotope ecospace may be extended in space and time to incorporate evolutionary, historical and biogeographical determinants of biodiversity. Finally, the term metaspaces is suggested to transcend ecospace, acknowledging that although the variation between biotopes, communities and ecosystems may not per se sustain life, it definitely adds to biodiversity by the principle of complementarity. The ecospace framework will probably be a helpful indicator in management for conservation.

Using citizen science data and a range of modelling approaches to predict the impacts of forest management and climate change

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Understanding how species' distributions are likely to change into the future in response to forest management and climate change is an important conservation goal. Species distribution models (SDMs) are widely applied to tackle such questions. SDMs require spatially extensive species' observation datasets, and as such, citizen science recording schemes provide an excellent resource. However, such datasets are accompanied by problems of geographic and environmental bias introduced through recorder behaviour. A range of modelling approaches has therefore been developed to deal with such biased data. I will present the results of applying several such methods to model the distribution of species of polyporous fungi in Sweden. I will present projections of the impacts of forest management and climate change scenarios on the distribution of polypore species, showing how predictions made using different SDMs agree and differ. Such an approach allows inferences to be made about the most appropriate forest management strategies for species conservation while simultaneously acknowledging uncertainties. It also allows potential interactive effects of forest management and climate change on the distributions of dead-wood dependent fungi to be identified.

The role of biotic interactions in spatial models of biodiversity

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Spatial modelling is a widely used method to examine and predict biological responses in space and time. The method is based on statistical relationships between spatially explicit biological and environmental data. As the detected relationships in such models, and thus possible predictions, are directly related to the predictor variables used, their selection should be ecologically justified. Theory and experimental studies postulate that sessile species are not only affected by their abiotic environment, but also by other species, i.e. biotic interactions, the impacts of which can be context-dependent. Here, we study the influence of biotic interactions, and examine if their effect varies among guilds and environmental gradients (*sensu* stress gradient hypothesis = SGH), and subsequently across landscapes. The models are built exploiting fine-scale data on arctic-alpine vascular plant, bryophyte and lichen communities. Models including biotic interactions were compared to the models based on abiotic data only. Including plant-plant interactions consistently lowered bias in species richness predictions. Further, the magnitude and outcome of biotic interactions varied between species and guilds, with distinctly different effects on competitive and stress-tolerant vascular plants, and on bryophytes and lichens. In addition, support was found for the SGH, with the community-level impacts of biotic interactions varying across landscapes. To conclude, biotic interactions are typically neglected in spatial models of biodiversity, despite having a critical role in structuring ecosystems, as demonstrated here. Spatial predictions of biodiversity trends under global environmental change could therefore critically benefit from accounting for biotic interactions and their context-dependency.

Measuring and predicting the influence of traits on the assembly processes of wood-inhabiting fungi

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Functional traits determine the responses of species to biotic and abiotic variation and thus influence the ability of organisms to adapt to particular environmental characteristics. The identification of traits influencing the responses of species and individuals to changes in environmental conditions can provide functional, mechanistic and predictive perspectives on processes shaping the assembly and dynamics of ecological communities. In spite of several recent studies that have attempted to understand the relationships between fungal traits and morphological and functional diversity, only little is still known about which traits significantly influence the occurrences of fungi under different environmental conditions. Furthermore, also interspecific interactions play an important role, and their directions and strengths have been documented to be non-randomly distributed across species, but their distribution across traits remains uninvestigated. We aim to examine how much variation in occurrence patterns can be related to traits that have been hypothesized to be of functional importance by using an extensive dataset that involves major variation in fungal taxonomical groups, as well as in environmental characteristics, and applying a trait-based joint species distribution model to relate variation in species occurrence to environmental characteristics. Specifically, we measure how much of the responses of the species to their environment can be attributed to traits, assess which traits influence the link from environmental conditions to species occurrence, predict how communities inhabiting different kinds of habitat scenarios vary in their trait composition, and assess whether interactive associations are (non-)randomly distributed across traits.

Conflicting objectives in production forests pose a challenge for forest management

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Conflicts between ecosystem services have been shown to be common and their severity to be affected by management interventions. In order to improve the sustainability of natural resource use, the occurrence of these conflicts and the effects that management actions have on them need to be understood. We studied the conflicts among ecosystem services and the potential to solve them by management choices in boreal production forests. Our study area consisted of nearly 30,000 forest stands which were simulated for 50 years into the future under alternative management scenarios. The study included four ecosystem services – timber production, bilberry production, carbon storage, and pest regulation – and one biodiversity conservation objective defined as availability of dead wood resources. We 1) measured the conflicts among each pair of objectives, and 2) identified a compromise solution for each pairwise conflict defined as one which simultaneously minimizes the losses for both objectives. We found the conflicts between timber production and the other four objectives to be by far the most severe. They were also the most challenging to solve by choice of management regime, whereas the mild conflicts among the other objectives could be efficiently solved. Our results show that conflicts between timber production and other objectives are typical and severe, while non-extractive benefits including biodiversity conservation can be more easily reconciled with each other. To mitigate the most severe conflicts in boreal forests increased diversity in the adopted management regimes and care in the application of management activities is required.

10. MOLECULAR ECOLOGY

Predictable allele frequency changes due to habitat fragmentation in the Glanville fritillary butterfly

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Describing the evolutionary dynamics of populations that have gone extinct is challenging, as their genetic composition prior to extinction is generally unknown. The Glanville fritillary butterfly (*Melitaea cinxia*) has a large extant metapopulation in the Åland Islands, but declined to extinction in the nearby fragmented SW Finnish archipelago during the 20th century. We genotyped museum samples for 222 SNPs across the genome including SNPs selected from candidate genes and neutral regions. SW Finnish populations had significantly reduced genetic diversity before their extinction, and their allele frequencies gradually diverged from those in contemporary Åland populations over 80 years. We identified 14 outlier loci among the candidate SNPs, mostly related to flight, in which allele frequencies have changed more than expected based on changes in the neutral SNPs. A comparison of outlier allele frequencies in three independent datasets of contemporary samples, where detailed demographic and ecological information was available, showed consistent allele frequency shifts in extinct populations with populations with high rates of population turnover and populations occupying fragmented landscapes. This indicates that extinct populations had an increase in alleles associated with good colonisation capacity before their extinction. Whilst the evolutionary response to habitat fragmentation may have enhanced the viability of the populations, it did not save the species from regional extinction in the face of severe habitat fragmentation. These results highlight a potentially common situation in changing environments: evolutionary changes are not strong enough to fully compensate for the direct adverse effects of environmental change and thereby rescue populations from extinction.

Spatial subsidies in spider diets vary with shoreline structure: Evidence from molecular diet analysis and stable isotopes.

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Predators living on shorelines often benefit greatly from feeding on organisms coming from the marine or aquatic environment. One predator group that is particularly abundant on marine shorelines is spiders that consume both detritivores feeding on marine detritus, and on species (such as chironomids) that live as larvae in the marine system and come ashore as adults. However, elucidating the food web structure in spider systems is difficult due to the external digestion of spiders. The most common method is stable isotope analysis, but this method gives a very coarse description. An alternative today is using molecular tools, and to sequence the contents of the spider guts, a method that is in strong development. In this study, we combined stable isotopes and molecular tools to examine how spider dependence on marine inflow varies with spider species and shoreline structure. We are able to identify specific prey species through sequencing and then match these with stable isotope compositions of the spiders. The analyses show that *Pardosa amentata* is more dependent on marine subsidies than *P. prativaga*, but also that the marine dependence is larger on open shores compared to vegetated shores. The use of two different tools allows us to make conclusions on the utility of gut sequencing and stable isotope analysis, suggesting the pros and cons of the two methods.

The molecular mechanisms and reversibility of fisheries-induced evolution

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Large shifts in phenotypic traits have been observed in exploited fish populations, which have not always fully recovered despite fishing has been ceased. Fisheries-induced evolution (FIE) can explain these potentially slowly reversible changes. However, detecting signals of FIE and its potential reversibility has proven difficult. We study the molecular mechanisms of FIE by sequencing the transcriptome of experimental fish (wild-origin zebrafish, *Danio rerio*) that have been harvested size selectively for five generations and then maintained under no-selection for six generations. We studied 1) what are the molecular mechanisms underlying FIE, 2) does intensive size-selective harvesting affect gene expression variation and genetic diversity, and 3) whether the genetic changes caused by size-selective harvesting are reversible. Our results show that five generations of size selection induced substantial changes in gene expression. We further show that harvesting generally reduced gene expression variation and genetic diversity. Harvest-induced changes in gene expression were eroded to some extent after cessation of size-selective harvesting but there was no clear sign of full genetic recovery. Similarly, gene expression variation and genetic diversity did not rebound back to the pre-harvesting levels among the size-selectively harvested fish.

Ecological speciation in salmonids

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Speciation is a fundamental evolutionary process continuously creating the diversity of life. Knowledge about the mechanisms and conditions required for species to evolve by adapting to surrounding environments is of paramount importance for predicting future responses to climatically (or anthropogenically) induced environmental change. Salmonid fishes are excellent model species for studying fundamental issues relating to genomic adaptation and speciation in the wild due to their iconic and diverse set of life-histories. I present insights from two case-studies in Pacific salmon. In the first study we find candidate genes of importance for responding to ecologically divergent selection between eco-morphs of sockeye salmon (*Oncorhynchus nerka*) over very short geographic distances. In another study we compared temporally isolated populations of pink salmon (*O. gorbuscha*) that remain sympatric through sharing of spawning habitats in alternate years - yet, these lineages exhibit different adaptabilities to novel environments. Here, our results point to an important role of the standing pool of genetic variation for a population's ability to adapt to environmental change. In conclusion, the results increase our knowledge about the interplay of genetic variation and ecological selection in driving early stages of speciation. Further, identification of adaptive genetic variation is expected to improve the genetically informed management of these precious resources.

Contribution of epigenetic mechanisms to phenotypic plasticity in the filamentous fungus *Neurospora crassa*

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Environment never stays constant throughout an organism's life. Physiological homeostasis must be maintained on the face of changing environments; many developmental transitions must be timed correctly using environmental cues. This phenomenon is called phenotypic plasticity. While we have made some progress in unraveling the genetic basis of phenotypic plasticity, much still remains unknown. The role of epigenetic mechanisms, or chromatin modifications, in particular is poorly known. We used the filamentous fungus *Neurospora crassa* to investigate the contribution of epigenetic mechanisms to phenotypic plasticity. We measured reaction norms of mutants that are deficient in different epigenetic mechanisms, such as DNA methylation, histone methylation, histone deacetylation, or RNA interference. We asked how do epigenetic mechanisms affect the shape of the reaction norms, are the effects specific to certain environments, and which epigenetic mechanisms are involved. We find that epigenetic mechanisms do affect phenotypic plasticity and these effects are mechanism and environment specific. In particular Histone 3 lysine 36 methylation is required for response to high temperatures, and histone 3 lysine 4 trimethylation is required for response to low pH. Temperature response is also affected by a histone demethylase and the RNA interference pathway. Shapes of the reaction norms are affected in several cases. Furthermore, have begun investigating whether transgenerational effects are present in *Neurospora* and whether epigenetics could be a mechanism that mediates those effects.

A joint estimate of sexual, asexual and gamete dispersal range of an epiphytic lichen

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Dispersal is a vital population process for the long-term persistence of populations, as it is necessary for finding suitable habitats and breeding partners. In sessile species, dispersal is restricted to the reproductive phase. Most epiphytic lichen species can reproduce either sexually or asexually, but most of our knowledge concerning their dispersal capacity is derived from studies which do not separate between these modes. Since there is a different dispersal range in sexual and asexual diaspores, the relative contribution of these determines gene flow within and between populations. Using *Lobaria pulmonaria* as a model species, we estimate the dispersal distance of both reproductive modes and the spermatia (gametes) which have a function similar to pollen. To our knowledge, this is the first joint estimate of these three separate dispersal processes. By use of parentage analysis, we estimated the distance between clonal offspring and their parents, sexually produced offspring and their mothers as well as the distance between the fathers and mothers in the case of sexual reproduction. Our results show that clonal dispersal is very short (about 100 meters), while the distance between sexually produced offspring and their mothers could be several thousand meters. Spermatia dispersal is intermediate, over several hundred meters. Long distance dispersal occurs mainly through sexual reproduction, and the dispersal capacity of spermatia has a vital role in ensuring successful sexual reproduction. Population- and habitat density will therefore influence the likelihood of long distance dispersal by determining if enough individuals are within reach of each other for mating.

ALL POSTERS

P001 *Flavobacterium columnare* in Finnish lakes

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Columnaris disease, a bacterial disease caused by *Flavobacterium columnare*, is a serious problem for freshwater fish farming worldwide. In Finland, outbreaks of this bacterium have become serious cause for losses in salmonid aquaculture, especially in fry and fingerling cultivation. However, the sources of *F. columnare* infections at fish farms have remained largely unknown. The bacteria might come to fish farms with incoming water at the onset of each outbreak, or prevail at the fish farm and start to multiply in favorable conditions. The objectives of this study were i) to screen the frequency of occurrence for *F. columnare* in lake water and littoral biofilms at different geographical distances to fish farms, ii) to collect data on the physical and chemical properties of sampling sites, and iii) to compare the genetic and phenotypic characteristics of *F. columnare* isolates from the natural environment to those originating from fish farm. The genotypes of the isolates were determined using the previously described ARISA method, where genetic grouping of the isolates is based on variation in the 16S-23S intergenic spacer region (ISR). By comparing the virulence of the isolates and the physical and chemical properties of sampling sites we aim to clarify the factors affecting the survival and growth of *F. columnare* in the outside-host environment. By comparing the genetic and phenotypic characteristics between isolates originating from nature and fish farm, we aim to clarify the mechanisms contributing to the occurrence of columnaris outbreaks at fish farms.

P002 The importance of including both local and landscape variables when explaining plant species richness and composition.

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The well-established species-area relationship is considered to be one of the most fundamental relationships in ecology. However, spatial configuration of habitats in the landscape and how it affects plant species richness (number of species) and composition (species identity), have become more in focus. Structural connectivity describes how well connected habitat patches are in a landscape and the probability that species exchange between patches will occur. In this study from the Swedish archipelago, we focus on different spatial measures (i.e. island area, height of island (relative age), distance to mainland, and structural connectivity) and how it explains plant species richness compared to composition. Plant species were inventoried on 112 islands in 12 different landscapes. Area, and height which is correlated to area, and distance to mainland were not surprisingly important for both richness and composition. However, structural connectivity was also important for composition. Even if the most common and rare species are excluded, area still is important both for richness and composition, but structural connectivity influence species composition too. I developed the structural connectivity measure in this study to include species-area relationship and degree of fragmentation. The importance of structural connectivity illustrates the effect of the surrounding landscape on species ability to disperse in the landscape, indicating the importance to adopt a wider context when investigating plant species presence or absence in a habitat.

P003 GWAS in brown trout for the resistance and tolerance to the proliferative kidney disease

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The myxozoan parasite *Tetracapsuloides bryosalmonae* infects many fish of the family salmonidae, such as trout and salmon, and is responsible for the proliferative kidney disease (PKD). The infected fish experience a strong inflammatory response, anemia and kidney hypertrophy. In several brown trout (*Salmo trutta*) populations, variation in resistance traits reflecting (parasite load) and tolerance (disease severity for given parasite load) has been observed among infected individuals. However, the genetic bases of variation for both resistance and tolerance remain unknown. Genome wide association studies (GWAS) are often used to reveal the genomic loci that are responsible for the observed trait variation. To investigate the extent and nature of genetic variation underlying the trait variation, we performed a GWAS using 265 infected fish samples from a natural river population. The DNA samples were taken from the kidneys of infected fish and genotyped using double restriction associated DNA (dRAD) sequencing approach. So far, we built the reference sequences by clustering and thousands of SNPs were generated using already available tools. We hope to present further results such as on the association between SNPs and traits during the Oikos-2016 meeting.

P004 Subarctic soil fungal communities vary in different reindeer grazing pressures

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We studied soil fungal communities in Reisadalen field, northern Norway. Study area is divided by a reindeer fence, the two sides differing with reindeer grazing pressure. Different grazing intensities has lasted for decades resulting in different plant communities in the area, lightly grazed side having a high shrub cover and heavily grazed side being dominated by herbs and grasses. We set study plots for each side of the fence with four treatments: control, fertilizing, warming and fertilizing + warming, aiming to test the possible effects of global warming. We collected soil samples from the plots and analysed fungal communities using Ion Torrent sequencing. Distinct changes in soil fungal communities were found between the treatments. Fungal communities differed most between the two sides of the fence, apparently due to different vegetation cover on light and heavily grazed areas.

P005 Factors affecting the distribution of the native Eurasian beaver and the invasive North American beaver in Finland

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Two beaver species occur at present in Finland: the native Eurasian beaver (*Castor fiber*) which is classified as near threatened in Finland, and the invasive North American beaver (*Castor canadensis*). The original Eurasian beaver was hunted to extinction in the 19th century and beavers were reintroduced to Finland in the 1930s with individuals from Norway and North America. At present, the Eurasian beaver occurs only in western Finland, whereas the North American beaver is abundant in southeastern and eastern Finland. Recently it has dispersed towards the Eurasian beaver's range. This raises concern that the two species may become sympatric in near future and compete for the same resources. In the worst case the alien species may exclude the native beaver. In order to protect the Eurasian beaver and to control the North American beaver population, knowledge about the factors affecting their distribution in Finland is essential. Beaver monitoring counts have been organized in Finland every three years with the aid of local hunters who report the number and location of beaver lodges. Data on regional beaver lodge abundance in 1995–2013 was utilized to model population dynamics and species distribution. In addition, habitat selection was studied with data on beaver lodge locations in 2013.

P006 The effects of climate change on carbon dynamics in alpine ecosystems

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Alpine ecosystems provide important ecosystem functions, services and holds significant carbon pools. Climate change is projected to have direct and system-wide impacts on alpine biodiversity and these ecosystem functions and services. Interactive effects of temperature and precipitation along with compositional and functional variation pose considerable challenges in assessing alpine carbon pools. Our project makes use of a climate grid consisting of 12 experimental sites combining four levels of annual precipitation with three levels of mean summer temperature to separate effects of precipitation and temperature. In each site three major plant functional groups, graminoids, forbs and bryophytes, are removed in all possible combinations to determine their role in ecosystem functioning. Ecosystem CO₂ fluxes are measured to estimate Reco, GPP, and NEE across the grid. Ecosystem carbon stocks are measured both above- and belowground and decomposition rates are measured using the Tea Bag Index. The results of this project will contribute to our understanding of carbon dynamics in alpine ecosystems under changing environmental conditions and the feedbacks they have on climate.

P007 Effects of Climate on the Black-legged Kittiwake (*Rissa tridactyla*)

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Seabirds are declining worldwide as a result of anthropogenic influences, primarily through climate change affecting the food availability. One of the declining species is the black-legged kittiwake (*Rissa tridactyla*), whose breeding populations in Norway have declined by 60-80 % since the 1980's. Chick growth is a good indicator of the environmental conditions as it reflects food availability during the rearing period, and affects post-fledging survival and population recruitment. The present study investigated the impact of various climatic variables on the growth rate of kittiwake chicks. This was done by using data on individual chick growth rates obtained during the breeding seasons of 2007 through 2015 from the island Anda, in northern Norway. The growth of 179 kittiwake chicks was assessed against the North Atlantic Oscillation winter index (NAOw), sea-surface temperatures of the pre-breeding and breeding season, precipitation, wind, and air temperature using a non-linear mixed effects model. Precipitation and NAOw were both shown to negatively affect the growth rate of the chicks. Precipitation presumably affects chick growth rates directly through increasing their energy budgets. The NAOw is assumed to affect chick growth through food availability, although no significant results were found between diets and the NAOw index. As chick growth is likely to affect post-fledging survival, increased knowledge on which climatic parameters affect the growth, and to what extent, is useful for distinguishing the effects of climate from other factors influencing the populations. This is important in order to direct management efforts towards all factors influencing the population development.

P008 Environmental variation generates opportunist pathogen outbreaks

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Many socio-economically important pathogens persist and grow in the outside host environment and opportunistically invade host individuals. Some notable examples of such pathogens are cholera in humans, anthrax in wildlife and columnaris disease in commercial fisheries. Environmental conditions affect heavily the free-living state of these pathogens and subsequently the transmission and probability of pathogen outbreaks. Using a modelling approach combining a traditional SIRS model to environmental opportunist pathogen dynamics, we have shown that epidemiological dynamics are profoundly driven by the quality of environmental variability. Moreover, the effects of variability depend on which part of the underlying system is affected. The frequency and severity of outbreaks is heavily influenced by formation of immunity and demographic turnover. Assuming that a successive infection formation often requires a certain infective dose of pathogens, establishment of novel emerging environmental pathogens is unlikely without environmental variation. Uncovering these issues helps in understanding and controlling diseases caused by environmental pathogens.

P009 Broadness of thermal tolerance is linked to decreased virulence in fish pathogen - Does climate change alter disease epidemics?

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Longer summers associated with climate change are expected to lengthen the period of environmentally borne disease outbreaks. By changing the thermal tolerance of naturally occurring opportunistic pathogens climate change could also alter the virulence of the pathogens. Here, using a multi-locus sequence analysis, temperature dependent growth experiment and virulence experiment, we show that the fish pathogen *Flavobacterium columnare* trades off virulence with thermal tolerance breadth. High virulence was associated with reduced ability to tolerate a wide range of temperatures. Moreover, ca. 80 clones sampled over ten years across Finnish fish farms seem to be derived from two ancestral lineages and have semi-clonal and epidemic population structure. However, genotypes were independent from the geographic origin and year of analysed isolates. Thermal tolerance data showed no relationship based on geography but genotypes explained thermal tolerance differences in *F. columnare* isolates. Our results suggest that the link between thermal tolerance and virulence in *F. columnare* can effectively lead in to the changes of the virulence and disease outbreaks when climate warming proceeds.

P010 Ecological studies in the northernmost birch forests in Norway

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The northernmost birch forests in the world are found along the coast in Finnmark (Norway). These forests at the northern edge of the boreal biome form a transition between the boreal and alpine biome. The current study focuses on the study of ground vegetation, estimating age of the stand and ecological conditions within 28 selected forest stands. Important objective of this study is to identify whether these forests are climatically limited. The soil temperature was measured at depths between 5 and 10 cm below top soil layer and air temperatures were extrapolated from meteorology stations. In addition, the soil samples and tree cores were collected at each site. The results of TWINSpan analysis indicated ground vegetation to be dominated by heaths or herb grass vegetation type. From the tree-cores, the age of the forests was estimated to be 40–80 years. These results suggested that the current position of forests is not an outcome of recent movement. From our findings, we could find a decreasing pH levels in soil, with increasing distance from coastline. The soil nutrients (Ca, Mg, K, and P) did not show any specific trends with increasing oceanity or altitude. The growing season soil and air temperature was $9.4\text{ }^{\circ}\text{C} \pm 0.6$ and $9.5\text{ }^{\circ}\text{C} \pm 0.5$ respectively. Our results indicate that the northernmost birch forests are not limited by the air and soil temperature conditions, as they lie far south of $10\text{ }^{\circ}\text{C}$ isotherm.

P011 Impact of different size herbivores on plant biomass in Yamal (Russia)

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Herbivores, together with climate, change plant biomass. We investigate to what extent the biomass of four functional groups of plants (N-fixing forbs, N-non-fixing forbs, erect willow shrubs (*Salix* sp) and dwarf birch (*Betula nana*)) is reduced by herbivores of different sizes and ask whether their effect is cumulative or complementary. In order to answer that question, we conducted an enclosure experiment in southern Yamal (Russia). The study was carried in three habitats: forb tundra, willow meadows and mesic tundra. Enclosures were designed to exclude 1) all herbivores, i.e. small rodents (voles and lemmings), ptarmigans, hares and reindeers, 2) medium sized herbivores, and 3) reindeers only. In addition control plots were chosen. Biomass was measured using the point intercept method. In this paper we analyse the data from the first year of this ten-year long study. Preliminary results showed that the exclusion of all herbivores could have a positive impact on *Betula nana*. For the N-fixing forbs and *Salix*, we expected an increase in biomass in plots where herbivores were excluded, but the preliminary results were not conclusive. This is likely due to the fact that this study was too recent and the changes were not large enough to be significant. The conclusions of this study will be important to understand how increasing numbers of semi-domestic reindeers interact with other species in shaping the low arctic tundra vegetation.

P012 The current status of life history of the American mink is the result of its overadaptations

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Does any environmental change shift an individual's optimal life history strategy always, or there are species whose strategy to optimize survival and reproduction in face of the ecological changes imposed by the environment remains stable? Long-term (1978-2015) study of the American mink in the Russian Far East, Northwest Russia and the Urals, semi-desert showed that this species survives and thrives excellently throughout the space under consideration. Why American mink is successful in colonizing new ecosystems? It is known that species inherit a huge quantity of structural elements that are formed based on "outdated" information, and among them with high probability may be present and those that are able to improve individual fitness with respect to the new state of the environment and even contain elements of 'overadaptations' or anticipatory adaptation. 'In periods of rapid changes in the environment ... the importance of such structural features may be comparable with the value of mutations, but unlike the latter, which mostly are lethal, they are the products of the long biological selection and therefore they do not disturb the harmonious epistatic gene interaction. The current status of life history of the American mink is the result of its overadaptations. Analysis of the causes of this phenomenon shows that the overadaptations are characteristic species that are widespread and have formed under a wide range of environmental parameters. These are usually species of high latitudes and altitude.

P013 Egg size mediated developmental plasticity in divergent Arctic charr populations

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Phenotypic diversity occurs at multiple levels: among and within species, populations and siblings. Understanding the determinants of phenotypic variation and its consequences for the performance of individuals and diversification of natural populations remains a challenge for evolutionary biology. A putative, but rarely investigated, facilitator of adaptive diversification includes maternally mediated developmental plasticity such as egg size. Egg size has diverse consequences for organismal performance, such as modulating the rate of early development in ectotherms. For example, egg size has been shown to affect developmental rate and behaviour in Arctic char (*Salvelinus alpinus*). Our early findings indicate that expression levels of genes related to development are higher in embryos from smaller eggs in comparison to their larger conspecifics. These results are amongst the first to demonstrate the importance of egg size in influencing developmental trajectories in relation to the evolution of rapid diversification.

P014 Habitat selection of freshwater fish - mechanistic studies as a basis for understanding community dynamics

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Habitat use is influenced by abiotic factors, affecting individual processes such as foraging, movement and metabolism, and by biotic interactions resulting from these processes. However, to clarify mechanisms governing habitat use, individual-based processes need to be broken down into more detail. In particular, the environment-dependence needs to be accounted for in the trade-off between the potential profits of using a habitat and the risk of mortality therein. Moreover, physiological and ecological processes scale with body size. Changes in any of these processes may lead to shifts in habitat use. Such shifts will, in turn, cause feedbacks from size-based interactions among individuals, to population and community dynamics. Yet, the mechanisms of how environment- and size-dependent species interactions shape habitat use have not been explicitly studied. To better understand mechanisms governing habitat use, we experimentally tested the vulnerability of two competing zooplanktivores, vendace (*Coregonus albula*) and roach (*Rutilus rutilus*), to predation by perch (*Perca fluviatilis*). In a second experiment, we used different temperature and light conditions to measure environment-dependent foraging capacities and energetic costs of vendace and roach. We used these rates together with empirical data from lakes to calculate energy intake and costs, and estimate predation risk, based on measured densities and sizes of prey and predators, and abiotic conditions. Our results exemplify how habitat use of co-existing species can be better understood by including individual-level physiological processes and their environment-dependence. We emphasize the importance of including habitat selection in ecological studies aiming to predict community responses in a changing climate.

P015 Effects of atmospheric nitrogen deposition on biodiversity and ecosystem function in grasslands

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The deposition of atmospheric nitrogen is a major threat to terrestrial and limnic ecosystems today, resulting in the loss of biodiversity and changes in ecosystem function. Many densely-populated regions have experienced high N deposition levels for decades and here the negative effects are already evident. In other regions, such as Norway, the deposition levels have so far been lower, and it can be hard to separate the effects of N deposition from other global change drivers such as climate and land-use change. Also, airborne N comes in different forms, reduced N (ammonia; from agriculture and other local sources) and oxidized N (NO_x; from industry and other long-distance sources), and the effects of the two forms might differ. The BEGIN project aims to quantify relative effects of N deposition on the biodiversity and productivity of grasslands. Our field experiment combines N deposition and biomass removal (cutting). We are seeing effects of N addition, and of different N forms, on the local ecosystem diversity and productivity. We find that increased N leads to a decrease in species richness regardless of cutting regime. Under increasing N, no-cut treatment leads to an increase in the relative proportion of graminoid biomass. One-cut treatment makes the relative proportion of graminoid biomass go down. We also see hints for a critical load of N deposition in relation to species richness. Nitrogen deposition and eutrophication are major threats to biodiversity and ecosystem function in (semi-)natural ecosystems, and the results will be of relevance for nature conservation and restoration.

P016 Spatial variation in the presence of endosymbionts in leaf-mining and gall-forming insects on pedunculate oak (*Quercus robur*)

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This study investigates the presence of endosymbiotic bacteria in leaf-mining and gall-forming insects on the pedunculate oak, a tree known for its diverse insect community. Endosymbiotic bacteria, found in a wide range of insects, have been shown to affect various herbivore traits, including parasitoid resistance, food digestion and the manipulation of plant physiology. There may be strong differences among insect species, among locations and among individuals in the presence and identity of these endosymbionts. In order to investigate spatial variation in the endosymbiont community, we collected leaf-miners and galls from oaks at three spatial scales: within a landscape, among regions, and among countries. At the moment, the samples are being tested for the presence of several endosymbiotic taxa as well as different strains of the known endosymbiont *Wolbachia*. Interestingly, preliminary analyses suggest that: i) *Wolbachia* is commonly present in some of our focal species, but entirely absent from others; ii) intraspecific variation in the presence of endosymbionts is common; and iii) *Wolbachia* strains are highly diverse. It is our aim to shed more light on the distribution of endosymbionts across the food web, and to see if the observed patterns can be explained by insect phylogeny, differences between feeding guilds, seasonal differences, and horizontal transmission by shared parasitoids. In summary, this project will provide insight into the spatial ecology and functional role of endosymbionts in a herbivore food web on oak.

P017 The relative importance of cryptochromes, phototropins and UVR8 photoreceptors in the control of plant responses to spectral quality changes in simulated under-canopy light.

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Plant canopies significantly alter the spectral composition of sunlight, for instance blue light is depleted under plant canopies but UV radiation can be relatively enriched. These qualitative changes are perceived by under-canopy plants that use the information obtained about their surroundings to produce photomorphogenic responses and acclimation in leaf pigments. While the functions of cryptochromes (cry), phototropins (phot), and UVR8 have been well described for individual wavebands of light, their role in the phenology of plants that live in shade is yet to be well defined. We examined Arabidopsis mutants deficient in these three classes of photoreceptors in controlled conditions under artificial spectra using combinations differing in blue and UV radiation to simulate canopy shade. Our objective was to identify the redundancy, overlap, and differentiation of response in each photoreceptor mutant through the blue and UV portions of the spectrum. Beyond the known cry and phot responses to blue light and of UVR8 to UV radiation, we report large interactive effects of blue and UV treatments indicating that both cry and UVR8 are required for fully-functional flavonoid photoprotective responses to short-wave radiation. In contrast, only the UVR8-deficient mutants produced more anthocyanins instead of flavonoids under UV treatments. Describing the mechanisms of these responses shows how photoreceptors coordinate plant acclimation to dynamic light conditions, such as those found under plant canopies. The wavelength range of these photoreceptor responses has implications for under-canopy plants since blue and UV are differently affected by springtime canopy closure by broadleaved trees.

P018 How does an opportunistic pathogen adapt to a changing world?

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Organisms evolving in fluctuating conditions are expected to be selected for broader tolerance and can be pre-adapted to novel environments. In particular, the evolution of opportunistic pathogens in a changing environment can lead to increased virulence once inside the host. Both genetic and epigenetic mechanisms can be involved, and while genetic changes occurring in bacterial strains evolving under constant conditions have been well documented previously, much less is known about the genetic and epigenetic changes involved in adaptation to fluctuating conditions. We used *Serratia marcescens* in an experimental evolution setup to determine how an environmental, opportunistic pathogen evolves under fluctuating temperatures compared to constant ones, and how this might affect its performance in novel conditions. We characterised the genomes and epigenomes of evolved strains with Single Molecule, Real-Time (SMRT) sequencing to determine the relative roles of genetic and epigenetic changes in adaptation to fluctuating vs constant conditions. Strains evolved in fluctuating temperatures out-performed strains evolved in constant condition at all measurement temperatures and in novel environments containing chemical or biotic stressors. Genetic changes were correlated with phenotypic measurements. Surprisingly, the dominant adaptive trajectory in the fluctuating environment seemed to be the parallel acquisition of phage resistance mechanisms, which might be explained by the potential activation of prophages during stressful exposure to changing conditions. Epigenetic data are currently under analysis. Our results show that evolution under fluctuating conditions might lead to unexpected evolutionary trajectories, making it harder to predict the effect of increased temperature fluctuations on environmental pathogens.

P019 Biotic and abiotic drivers of earthworm distributions in Finland

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Earthworms are ecosystem engineers which change the physical and chemical structure of soil by burrowing, modifying, and turning over soil. These effects can lead to a cascading series of changes on ecosystem functioning and other taxa. However, the current distributions of earthworms in natural habitats across Finland are poorly understood, as previous research has been concentrated in south-central Finland or has focused on agricultural land. Earthworms were surveyed at 60 locations in spruce and birch/mixed forests along a north-south gradient across Finland. We tested competing hypotheses about the factors driving earthworm distributions, including effects of forest type, distance to the nearest agricultural area, distance to water, latitude, longitude, and soil moisture. Latitude was the strongest predictor of earthworm occurrence, abundance, and richness, with fewer earthworms and fewer species of earthworms occurring farther north. Earthworms may have restricted distributions in the north due to climate constraints (i.e., niche limits) or dispersal limitations. We plan to test this experimentally and are also developing a citizen science program to obtain broader information on earthworm distributions in Finland. An understanding of current distributions of earthworms is critical given their substantial impacts on other species and ecosystem functioning, and it will also allow predictions of future earthworm distributions under climate change.

P020 Habitat use of *Saguinus* spp. inferred from the presence of ferns and lycophytes

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Studies in Western Amazonia have found that the distributions of many groups of plants are highly correlated with soil properties, and that ferns and lycophytes are good indicators of this kind of general patterns. It has also been suggested that such habitat differences may affect the occurrences of animals. This study aims to produce a habitat map based on fern and lycophyte data in order to help interpret the results of long-term primate studies that have been carried out in the Quebrada Blanco Biological Station (EBQB) in North-Eastern Peru. Data on the habitat use of monkeys (mainly *Saguinus mystax* and *Saguinus nigrifrons*) have been collected along a permanent trail system during a number of studies on their behaviour and ecology. Now we have systematically registered the abundances of all ferns and lycophytes along 11 transects established adjacent to the trails used for monkey surveys. The most common fern species in the study area are indicators of relatively poor soils, but indicators of more productive soils are present in two areas. Preliminary results for a single survey year show that monkey ranges are smaller in the areas inferred to have richer soils. Further analyses will be carried out to test if this result holds for all ten years of monkey survey data.

P021 The physics of ecological interactions

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Ecological interactions do not happen in a vacuum but take place on very tangible, physical stages. This truism is very much acknowledged by field ecologists, who ponder daily about the effects of the physical dimensions of the habitat on their study objects. Also, the biophysical study of single organisms has a long and rich tradition in ecology. But the effects of physical factors on ecological interactions have rarely been considered in their own rights. As a result, ecological interaction networks, not least among them food webs, have been abstracted from the physical medium in which the interacting organisms struggle for life. Here, I will present a primer on recent theoretical investigations we have started that aim to uncover the effects of classical mechanical forces on trophic interactions in aquatic and terrestrial habitats.

P022 Packed like sardines: transient dynamics in guppy rapid evolution.

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Density dependent selection and life-history evolution are tightly intertwined, constituting an evo-evolutionary feedback. Population density is determined by demography, which emerges from the sum of individual life-histories. At the same time, different life-histories can be affected differently by density; for instance slow growing individuals, that produce fewer and bigger offspring, can perform better at high density, when resources are limited. As life-history evolves, demography changes, affecting density conditions and, ultimately, density dependent selection. The Trinidadian guppy (*Poecilia reticulata*) is an optimal model system to study this eco-evolutionary dynamic. When translocated from high predation (HP) to low predation (LP) environments, guppies show rapid evolution. At equilibrium, guppies in LP environments have slower life-histories and higher population densities compared to guppies in HP environments. Density dependent selection has been proposed to drive this rapid evolution. Nonetheless, empirical studies considering equilibrium phenotypes found no significant advantage of the LP phenotype at high densities. We propose that these studies are missing an important transient dynamic, necessary to explain the rapid evolution. In our study we explore two non-mutually exclusive hypotheses of transient dynamics. We propose that a transient state of extreme density, caused by the fast life-history typical of the introduced HP phenotype, is necessary for the LP phenotype to evolve. We also propose that seasonality can affect density conditions, either magnifying or reducing the resource limitation. We conduct these studies using an individual based dataset following four introduced guppy populations across seven consecutive years.

P023 Importance of plasticity for divergence of threespine stickleback (*Gasterosteus aculeatus*) in the dynamic Lake Mývatn, Iceland

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Lake Mývatn is one of the best studied ecosystems in Iceland showing strong environmental gradients (e.g. in temperature, depth, substrate) and spatial and temporal differences in invertebrate composition. Many invertebrates, in particular chironomid midges and benthic cladocerans, are important prey for threespine stickleback (*Gasterosteus aculeatus*). As adaptive divergence in response to natural selection is frequently related to diet and/or habitat use, the spatial and temporal variation in prey type and abundance in lake Mývatn may facilitate resource mediated diversification. Along this line, lake Mývatn stickleback show phenotypic differences in i) feeding morphology and ii) body size, likely mediated by responses to prey and temperature. However, it is not known to date whether these phenotypic differences are due to genetic or plastic responses. We performed a laboratory common garden rearing experiment to test for the relative contribution of plastic and genetic effects on key phenotypic traits in stickleback from two habitats in the lake (mined and warm). Full-sib offspring from artificial crosses were raised at a combination of two different diets (midge vs. artificial pellets) and temperatures (13 and 23C) up to nine months. We found consistent differences between the two habitat types in gill raker morphology, body size and age at sexual maturation, but also strong plastic responses and genotype x environment interactions. Our results strongly indicate a mixture of genetic divergence and phenotypic plasticity and support the existence of two morphs in the lake. Our study indicates an interplay between plastic and genetic responses in diversification.

P024 Fecundity and female size - Bigger is not always better.

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It is generally found that larger females have a higher reproductive output. This is also the case for freshwater crayfish, where positive relationships between female size and number of eggs have been found for many species. Large females are thus expected to be more important for recruitment and population growth rate compared to small females, by producing more offspring. We investigated this in signal crayfish (*Pacifastacus leniusculus*) populations in two lakes in eastern Sweden. Females were collected in autumn prior to mating and ovarian egg number was counted. In late spring females were again collected and pleopodal egg number was counted. As expected, and found earlier, there was a positive linear relationship between ovarian egg count and female size in autumn. In contrast to expectations there was however almost no relationship between female size and pleopodal egg number in the spring, just prior to hatching. The largest signal crayfish females did not contribute more offspring to the next generation. The usual management advice to save the larger females to promote population growth was thus not applicable in this case.

P025 Towards a framework for predicting arctic food web response to climate change

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Predator-prey interactions are a key force in shaping animal communities. Across latitudes, arthropods outnumber other animal groups in terms of both species diversity and biomass. Yet, predation among arthropods has been poorly explored, much due to methodological obstacles. Species-poor systems, such as the terrestrial Arctic, have been proposed to be particularly affected by the trophic dynamics of predacious animals, resulting in top-down regulation of lower trophic levels. Both, the species and their interactions in the Arctic are currently affected by climate change, changing our perspective on food web connectivity and stability. Top predators such as wolf spiders may particularly be impacted, as with shifts in the abundance of functionally important prey taxa, they may shift their preferences to prey involved in other ecological functions. Spiders may therefore serve as model organisms to study the functional effects of shifts in prey choice towards alternative sources and consequently altered food web structure. In this project, we study feeding ecologies of wolf spider *Pardosa glacialis* in the high arctic region of Zackenberg, NE-Greenland. In July 2015, we collected spiders and their prey along an altitudinal gradient representing different microclimates. Our first results indicate large spatial variation in prey availability, both in abundance and diversity. In the next step we will screen spider gut contents for prey DNA using next generation sequencing, then analyse the dynamics of feeding interactions through functional response experiments. This combined approach will help us establish the type and intensity of trophic interactions under changing climatic conditions.

P026 Landscape-scale gradients and temporal changes in prey species of the white-tailed eagle (*Haliaeetus albicilla*)

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The return of apex predators re-shapes population densities of their prey species, creating conflicts and challenges for the conservation and management of both predator and prey populations. The population of white-tailed eagles (*Haliaeetus albicilla*) in the Baltic Sea has grown rapidly since the 1980's after a previous population crash, causing growing predation pressure on its prey species. The aim of this study was to provide detailed information about the diet of the white-tailed eagle along landscape-scaled gradients and about temporal changes in their diet over 25 years. To analyse the diet, we used an extensive dataset with 7 700 identified prey remains collected during the breeding season from the Åland Islands (Finland) 1985–2010. The diet consisted mainly of birds (69.6 %) and fish (27.3 %) and to a smaller extent of mammals. There was, however, a strong gradient in diet depending on the landscape of the territory (at 2 km radii around the nests). The smaller the proportion of land in the territory was (in outer archipelago), the higher the proportion of birds, and the larger the proportion of land (inner archipelago), the higher the proportion of fish. During the study period the proportion of birds in the diet grew and the proportion of fish declined, except for the areas with most land where the situation was the reverse. These results support the view of the white-tailed eagle as an opportunistic hunter, preying on the most available prey and switching to other prey when the availability changes.

P027 Untargeted metabolomics to elucidate phytoalexins in *Barbarea vulgaris* var *arcuata* against the oomycete pathogen *Albugo* sp.

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The yellow rocket cress *Barbarea vulgaris* var *arcuata*, a member of the mustard family, has two recognised types differing morphologically in leaf pubescence and chemically in their composition of secondary metabolites, i.e. saponins, glucosinolates and flavonoids. The glabrous type (G-type) is resistant to insect herbivores like the flea beetle *Phyllotreta nemorum* or the diamond back moth *Plutella xylostella* but susceptible to the white rust pathogen *Albugo* sp., whereas the pubescent type (P-type) is essentially resistant to the white rust but highly susceptible to herbivores. Several G-type specific saponins were identified cause resistance against herbivores, but it is still unknown what determines the resistance against *Albugo*. Besides short-term responses, i.e. oxidative burst, apoptosis or callose deposition, plants can resist pathogen infection through the production of antimicrobial substances, so called phytoalexins. Our aim of this study was to examine if secondary metabolites are likely to be involved in the resistance of the P-type of *B. vulgaris* against the white rust pathogen *Albugo* sp.. For that we infected second generation offspring of artificially crossed P-and G-type plants as well as offspring of a natural hybrid population with *Albugo* sp. and monitored development of white rust symptoms, which was the case for about 40 % of the inoculated plants. Untargeted metabolomics by LC-QTOF mass spectrometry was used to acquire the chemical profiles of resistant and susceptible hybrids, which were further analysed by univariate statistics and multivariate PLS-DA models to detect compounds correlating with resistance. The data analysis is ongoing and results will be presented.

P028 Grazing abandonment drives community compositional shift in the Tatra Mountains over the past 90 years.

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Mountain and alpine areas are particularly vulnerable to environmental change, including climate warming but also agricultural changes. Resampling of datasets first collected before the onset of anthropogenic climate change has become an established method for monitoring environmental change. Alpine areas are often the focus due to their high sensitivity to climate change, their interesting plant communities, and the fact that they were also attractive sites for study during previous decades. We present results from the first resampling of plot-based vegetation data from Morskie Oko, a valley in the Polish part of the Tatra Mountains. The data were gathered in the 1920s with the intent of describing phytosociological communities. We have found that consistent changes over time have occurred in most habitats. In snowbed habitats the ordination analysis is dominated by the change over time. In dwarf pine and spruce habitats time does not provide a consistent outcome; here it is likely that the long life cycles of the dominant species and the management-driven community structure predominate in structuring the vegetation. In the Tatras, climate warming has been weaker than elsewhere in Europe; indicator value analysis of our dataset suggests that the vegetation is responding to grazing changes rather than warming. Grazing abandonment has led to decreased species richness and an increase in tall herbs and other grazing intolerant species. Supporting the Tatras alpine flora, with its high number of endemic species, may be possible even in the face of climate warming if traditional grazing regimes can be reinstated.

P029 Roads are no barrier for dispersing red squirrels in an urban environment

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In urban environments, roads are one of the major threats for moving animals. Roads can act as barriers to movement either through mortality during crossing attempts or through behavioral avoidance. This can have severe population level consequences such as population fragmentation and demographic or genetic isolation. A major limitation for determining the effects of roads, however, is the lack of studies on responses of animals to roads during dispersal. In a radio-telemetry study, we investigated the responses of dispersing juvenile red squirrels (*Sciurus vulgaris*) to roads in an urban environment in Finland. We observed that, during routine movements within their home range, squirrels were located further from roads and crossed them less frequently than simulated random walk paths, while they did not avoid roads when performing explorative and dispersal movements. Moreover, during routine movements squirrels rarely crossed roads with high traffic volume, while during dispersal they crossed both big and small roads. Traffic did not seem to be a major cause of mortality for juvenile squirrels, based on our observations. Our study provides striking evidence that movement behavior during dispersal differs from that of non-dispersers. For road ecology, this implies that the evaluation of the role of roads as barriers for e.g. gene flow cannot be based on the interpretation of movements of non-dispersers.

P030 An introduced species meets the local fauna

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Crabs are some of the most successful introduced species among marine organisms, and they can be an important structuring force in marine communities. Recently, the mud crab, *Rhithropanopeus harrisi*, has invaded the Northern Baltic Sea. This is an area where no native crab species exist, and the addition of a novel functional species to the low species diversity of the Baltic Sea could have large community-level impacts i.e. modifying biotic interactions and/or altering ecosystem functioning. We examined the predatory behavior of introduced *R. harrisi* both in the laboratory and field focusing in shallow, hard bottom habitats dominated by the alga *Fucus vesiculosus*. In the laboratory environment, *R. harrisi* was an effective predator of littoral grazers, readily consuming both sessile fauna (*Mytilus trossulus*) and also mobile species such as isopods (*Idotea balthica*) and gammarid amphipods (*Gammarus* sp.). When studying the predation of different sized prey items, *R. harrisi* preyed upon small and medium sized prey of both mobile and sessile species. However, in the field experiment with the native faunal community associated with *F. vesiculosus*, *R. harrisi* negatively impacted only the abundance of the snail *Theodoxus fluviatilis*, possibly through indirect effects. Nevertheless, *R. harrisi* significantly decreased both the prey species richness and diversity but not the total number of potential prey individuals associated with *F. vesiculosus*. In conclusion, predatory behavior of this novel crab has the potential to impact the native macroinvertebrate littoral community, but the realized predation pressure in the field is lower than could be expected from laboratory experiments.

P031 Life history trade-offs under dietary stress in the ant *Formica fusca*

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The surrounding environment, to which organisms need to adapt, can vary from benign to highly stressful. Adaptation to prevalent stressors is hypothesized to lead to trade-offs between different functions (e.g. digestion, detoxification, reproduction, defence). For example upon pathogen exposure resources might be allocated to defence rather than growth. Environmental stressors associated with diet and diseases are among the most critical ones. Eusocial organisms, such as ants, have found the way to decrease the effect of the environmental fluctuations on them by forming dense, often well isolated and protected nests. However, foraging workers, who provide the colony with nutrition, can bring various toxins and pathogens to the collective, increasing the vulnerability of the nest. Here, we studied how fitness and phenotype are affected by dietary conditions in the ant *Formica fusca* by exposing colonies to a bacterial pathogen (*Pseudomonas entomophila*) and oxidative stress (hydrogen peroxidase). We demonstrate that dietary stress reduces larval survival, but the effects on eclosion success and adult size vary.

P032 Spatial and temporal variation of stickleback abundance and feeding pressure in the Northern Baltic Sea

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Populations of three-spined sticklebacks (*Gasterosteus aculeatus*) have been increasing in the Baltic Sea in recent years, possibly linked to decreasing numbers of predatory fish and eutrophication. As mesopredators, sticklebacks play an important role in the trophic network, potentially decreasing mesograzers and thus facilitating macroalgal blooms. In this study, we sampled fish populations across the SW Finnish archipelago over three time periods to determine spatial and seasonal variation in stickleback abundance and the factors affecting abundance. We also performed lab and field experiments to determine predation pressure of sticklebacks on mesograzers in different habitats. We found that sticklebacks were most abundant in the outer archipelago, and decreased towards the inner archipelago; this was positively correlated with secchi depth and vegetation cover in the outer archipelago. In early summer, catches were composed of breeding adults, but adult abundance decreased over the summer and in late summer, catches were almost exclusively young of the year individuals. Meanwhile, predation success of adult fish depended on fish size, prey size, species, and habitat, with the highest predation rates on small amphipods. Predation was higher in *Zostera marina* than *Fucus vesiculosus*, but habitat preference followed the opposite pattern, likely linked to higher food availability and prey encounter rates in *Fucus vesiculosus* as well as increased shelter from predators in these more complex habitats. Stickleback abundance and predation thus seems to be linked to a combination of turbidity, habitat complexity, and food availability.

P033 Responses of subarctic plant phenology to natural microclimatic gradients

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Snow manipulations have commonly been used to simulate the effect of changing winter conditions on tundra plants. While these experiments are useful for evaluating the short-term plasticity of plants, they cannot detect the long-term evolutionary adaptation of plants to small-scale climatic differences in their current habitats. Here, I used a natural snowmelt gradient above the alpine treeline in Finnish Lapland to assess how well subarctic dwarf shrubs are naturally adapted to different microclimates. The timing of snowmelt differed by up to 1.5 months between microhabitats, causing a broad range of growing season lengths for plants separated by only a few meters. The effect of this was seen especially in the plant phenology which showed species-specific and aspect-specific responses. Interestingly, such differentiated patterns could also be seen in the end of the growing season and in some species there was a carry-over effect of the timing of spring snowmelt on the timing of senescence. In order to find out whether these phenological differences are temperature-controlled alone, the effect of temperature sums on the timing of phenological events was estimated. I considered canopy-height as well as rooting zone temperatures as these may both cause the seasonality in plants. It is ecologically significant to find out how conservatively plant phenology is coupled to current microhabitats as this greatly determines a species' survival during climatic changes. Those species which are more plastic in their phenology across their current habitats are more likely to cope with future climate changes.

P034 Individual based modelling of European Anchovy (*Engraulis encrasicolus*) and climate driven marine habitat changes in the North Sea

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Reappearance of the Anchovy population in the North Sea after 1990s makes the research scope to do an intensive modelling study, when they were absent in the North Sea fishery stock for 40 years. So far, it has been referred in several studies that alternated climate conditions could force European Anchovy to return to the North Sea territory, and otherwise, it could be the revival of limited old stock with their optimal environmental condition after 90s. A fully parametrized Individual Based Model is implemented in this exploration of early stage dynamics (2.85–21 mm). The IBM results have indicated a very positive appearance of larval growth and survival in the North Sea average condition as well as sensitive Progression to the changing extrinsic parameters of temperature, daylight, turbulence and to prey biomass variability. Larval growth has been found very sensitive to zooplankton biomass levels in the model runs, while they couldn't grow well with lower amount of biomass levels (100–300 mgCm⁻³). Also, model results have shown an optimum temperatures range 8–12°C for smooth growth development for larvae for North Sea average conditions and similarly, they can grow well in the extended daylight hours and found that European Anchovy prone to grow well in higher turbulent condition. IBM long term simulation tests along with multi-decadal environmental data (Temperature, Prey biomass) exhibit a well existence of European Anchovy after 90s in the North Sea and but Norther North Sea signify a poor larval growth possibility in the observed 61 year period (1948–2008).

P035 Surface and subsurface macroinvertebrate community differences across a thermal gradient in Icelandic streams at two spatial scales

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Macroinvertebrate communities and food webs have been thoroughly studied in small streams, but there has been relatively little research done on the linkages between surface and subsurface communities (i.e., within hyporheic habitats). Hyporheic habitats and communities may play a major role in shaping stream processes and are likely very susceptible to warming temperatures. Climate change and resource development may alter the linkages between surface and subsurface habitats upon which stream food webs depend. Understanding these linkages better, in the face of increasing resource development and climate change, will help inform aquatic resource management. The objective of this study is to determine how temperature influences invertebrate community assemblage, density, and diversity in the surface and subsurface of streams. To address this objective, we are studying streams on two spatial scales: landscape and catchment. In the landscape-scale study, we are using thermally-stable and thermally-variable streams from multiple catchments. In the catchment-scale study, we are using only thermally-stable streams. At both scales, we selected streams that provide a thermal gradient across which to study community differences. We sample from four stations within each stream. At each station, we are collecting surface samples and subsurface samples at 25 and 50 cm below the streambed.

P036 The diet of otters (*Lutra lutra*) in Denmark based on morphological and DNA analysis of stomach and intestine contents

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Knowledge about the diet of the Eurasian otter (*Lutra lutra*) is very important to reveal their ecological role and for conservation of the species. The otter is an omnivorous animal and forages on many different groups of species. The majority is fish, but amphibians, invertebrates, small birds and mammals can also be part of their diet. Most dietary studies have been done on the analysis of spraints, but the use of stomachs is also a used method. This project is based on almost 100 otter stomachs and intestines, collected in years 1991-2014. Stomach contents analyses can provide us with information on prey items with few indigestible parts, whereas spraints contain those parts of the food that cannot be digested (scales, hair, feathers, bones etc.). Stomach contents analyses can also provide a better insight into the number and size of prey items taken. Traditionally, morphological characteristics of undigested hard parts, e.g. fish scales and vertebrates, bird feathers, bones and hair have been used to identify prey species. However, some prey species cannot be differentiated from morphological characteristics. Furthermore, soft tissues are generally poorly preserved, difficult to identify and remain unstudied. This study will combine and compare a morphological approach with a DNA based approach. Sanger sequencing will be used on the food items that cannot be differentiated by their gross morphology. This is carried out to identify more items to species level and give us more detailed information on otter diet.

P037 Genetic structure of a re-establishing wolf population

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The grey wolf is one of Europe's most evocative predators. In Finland, the wolf population has expanded rapidly since protection in 1995. Re-establishment in human-populated areas for the first time in >100 years has led to an acrimonious national debate over wolf population control. Here, we present an ongoing genetic strategy to inform this debate, using family relationships to characterise pack dynamics in the wolf population in south-west Finland. We obtained DNA from 254 samples, mainly non-invasive scats collected opportunistically by volunteers, which were genotyped at 17 established microsatellite loci. We fitted a pedigree in a Bayesian framework, decreasing bias in parental assignments by simultaneously estimating other unknown parameters (unsampled population size and genotyping error). We identified 55 individuals and confidently assigned at least one parent to 46. We found a clear family structure in the population, which consisted of three main parent-offspring groups. These groups were related but showed no strong evidence of recent inbreeding. Simulations using more genetic markers showed that this family structure, with consequently low within-population variation at certain loci, limits our confidence in resolving the remaining relationships. Nonetheless, mapping this family structure onto sample locations revealed true pack structures that were previously disputed. In combination, this volunteer-based genetic sampling and unbiased parentage analysis allows continuous monitoring of pack movements and reproductive events. Our approach is currently being applied more extensively within Finland, and the tools we develop will enable evidence-based decision-making in similar systems.

P038 Microrefugia and stepping stones - climate driven range shifts of northern and southern species

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We study forest plants in the transitional region that is called *Limes Norrlandicus*, where many northern and southern species have their range limit. Climate warming will probably shift these limits. However, local climate is strongly modified by topography and forest structure, creating spots, which are colder or warmer than the surrounding landscape. Therefore retreating cold-adapted northern species may survive in microrefugia with a colder microclimate, whereas pioneer populations of advancing warm-adapted southern species possibly will establish in warmer stepping stone habitats. Our project aims to understand these mechanisms and to provide advices for society to adapt biodiversity conservation to climate change. The project has four components: First, we will create a microclimatic model over the study area that allows the identification of locally colder or warmer microclimates in the landscape and by which site features (e.g. forest age) they are created. Second, we will identify localities with refuge populations of northern species and compare the microclimate in these sites with the regional climate to assess if these species at their range limit stick to certain (colder) microclimates or if they rather occur at sites with little competition. Third we try to identify possible habitat quality constrains for warm-adapted southern species to establish in stepping stone habitats, for example due to time lags in soil development. Finally we will evaluate to what extend our model of refugia and stepping stones is part of the current reserve network and how conservation and forestry management can adapt to climate change.

P039 Regime shifts in exploited marine food-webs: detecting mechanisms underlying alternative stable states using size-structured community dynamics theory

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Resolving mechanisms up-holding alternative stable states in natural food-webs is of key importance for the prospects of ecosystem recovery and for management of human activities affecting such systems. We show how mechanisms underlying alternative stable states caused by predator-prey interactions can be revealed in field data, using analyses guided by theory on size-structured community dynamics. This is achieved by combining data on the performance of individuals (such as growth and fecundity) with information on population size and prey availability. We use Atlantic cod (*Gadus morhua*) and their prey as an example to discuss and distinguish two types of mechanisms, 'cultivation-dependence' and 'overcompensation', that can cause alternative stable states preventing the recovery of overexploited piscivorous fish populations. Importantly, the type of mechanism can be inferred already from changes in the predators' body growth in different life stages. Our approach can thus be readily applied to e.g. monitored stocks of piscivorous fish species, for which this information often can be assembled. Using this tool can help resolve the causes of catastrophic collapses often observed in marine predatory-prey systems. Without such knowledge of ecological mechanisms governing food-web dynamics, attempts to restore collapsed predator populations risk being a shot in the dark.

P040 Phylogenetic relationships of Finnish *Coptoformica* species

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Formica exsecta group (subgenus *Coptoformica*) is a group of c. dozen species of ants that typically live on open grassy habitats and build small nest mounds. Several *Coptoformica* species build supercolonies, where populations consist of large networks of nests, with numerous queens in each nest. The most recent addition to the group, *F. fennica*, was described as late as 2000 from Finland and Caucasus (Seifert 2000). The description was based on morphological characters but the species status has not been confirmed by molecular methods yet. In this study, we use mitochondrial sequences (COI & CYTB) and 14 DNA microsatellite markers to assess the phylogenetic relationships and spatial population structure in five boreal *Coptoformica* species, including *F. fennica*. Our results suggest that the species studied form discontinuous clusters in phylogenetic and spatial analysis, showing only little intraspecific genetic variation in general. However, mitochondrial genes failed to separate the species pair *F. exsecta* and *F. fennica* despite established morphological differences. Spatial genetic difference within this group was extensive, but can be mostly attributed to the founder effect in connection to the establishment of various genetically separated supercolonies.

P041 Are changes in solar radiation flux and spectral composition reflected in leaf pigment dynamics of the forest understorey species?

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The light environment experienced by forest understorey plant species changes from early spring to summer due to the flushing of the canopy trees and thus results in different absorption, reflectance and transmittance of solar radiation within the canopy. The understorey species adjust their phenology to canopy closure to best utilise the favourable light conditions, particularly species such as spring ephemerals. To best describe the realistic environmental conditions that understorey species experience, it is necessary to measure not only photosynthetically active radiation (PAR), but a full solar spectrum including UV-radiation. Here, we investigate the relationship between changes in the spectral composition and radiation flux under forest canopies, and the pigment composition of leaves and UV-screening of the species growing in the forest understorey. Plants produce UV-screening flavonoids in epidermal cell layer as a response to UV-B radiation, thus making seasonal changes in leaf flavonoid content in the forest understorey interesting to study. We report how the species-specific and time-dependent patterns under different canopies reflect differing strategies of understorey species, and further how solar radiation flux and spectral composition change in different forests, with spectral changes composing a possible signal for plants to fine-tune their growth.

P042 Vascular plant responses to moss cover changes in intact and restored tundra ecosystems

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Mosses are an important component in many tundra ecosystems. In ecological restoration mosses may play an important role by stabilizing the soil. As the moss cover develops, the effects of mosses on ecosystem processes and the performance of vascular plants may change. To investigate these relationships, we established a moss thinning and removal experiment in an intact heathland and a 30 year-old restoration site in the subarctic-alpine highland of Iceland. Dominating bryophyte species were *Racomitrium lanuginosum* and *Sanionia uncinata* in the intact and restored heathlands, respectively. The effects of moss thinning and removal on selected soil properties (temperature, moisture, respiration, TOC, available NO₃⁻ and NH₄⁺) and on four target species (*Betula nana*, *Empetrum nigrum*, *Silene acaulis*, *Carex rupestris*) were measured in 27 plots (50x50cm) at each study site in 2011-2013. Soil temperature generally increased when the moss was removed, while no effects were detected on other soil variables. The vascular plant responses were positive (increased growth) or negative, depending on site. In the intact heathland the growth of *Betula* and *Carex* decreased when moss was removed, but no responses were detected in *Empetrum* and *Silene*. However, at the restoration site *Empetrum* responded significantly to the treatments with an increased growth. This discrepancy in responses between the two sites may be due to generally younger individuals at the restoration site. The relatively young plants may have experienced a competitive release when the moss was removed to such an extent that it outweighed any negative impacts of moss removal.

P043 The bigger takes it all: the triple costs of mate attraction for small females

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Sexual selection on females is poorly studied. For capital breeders, using energy to attract males is likely to reduce fecundity so individuals should aim to mate quickly. In the common glow-worm (*Lampyrus noctiluca*) wingless females glow to attract males, which fly in search of females. Females do not eat and have limited resources for glowing and egg production. Males prefer large and bright females, which are then likely to mate sooner than small dull females. Large females also have more eggs. We explored the costs of glowing and whether these costs vary among females. We expected large females to suffer larger costs due to greater energy expenditure from larger ornaments. To study the costs of glowing, we varied the amount of glowing and the length of time before mating. Half the females mated the same day they were captured and the rest after five days. Glowing was manipulated by regulating the light rhythm. Our results showed that waiting, but not glowing, had a significant negative effect on the number of eggs laid, but only in small females. In large females, there was no discernible difference between the groups. This is the first study we know of to examine the costs of ornamentation in females. Small females are likely to suffer greatly, as they start off with fewer eggs, have to wait longer before mating and have higher costs of waiting than large females.

P044 Temporal and spatial variation in reproduction and vegetative growth of a rare terrestrial orchid

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Plant reproduction and growth vary temporally and spatially due to both extrinsic (e.g., climate) and intrinsic (e.g., plant's own resource status) factors. Differentiating between these two is an important goal in population biology. We studied individual-level temporal and spatial variation in flowering intensity (proportion of flowering ramets) and vegetative growth (number of ramets) in a rare terrestrial orchid, *Cypripedium calceolus* L., using long-term monitoring data from Finland and Estonia (five populations in total). Autocorrelation analyses suggested a two-year cycle in both reproduction and growth, indicating that these two vital rates depend on individual demographic history. The flowering intensity of clumps showed no temporal trend, while clump size increased over time in both countries, probably via rhizome branching as clones aged. Previous clump size had a positive effect on current reproduction and growth. Both vital rates were also affected by past weather conditions, with the cumulative temperature sum of the previous growing season and the maximum snow depth of the previous winter being the most influential weather variables that either increased or decreased the performance of clumps depending on the country. However, analysis of pairwise cross-correlations showed only little synchrony in flowering intensity and vegetative growth among clumps both within and between populations, suggesting that climatic control of reproduction and growth is sufficiently low to be masked by high annual variation that arises due to cyclicity and microhabitat effects. Together, these results indicate that the reproduction and growth of *C. calceolus* depend on both individual demographic history and past weather conditions.

P045 Degradation in matrix is associated with biotic homogenization in protected areas

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The main goal of protected areas is to maintain species diversity and the integrity of biological assemblages. For the integrity, functional and phylogenetic diversities are at least as important as taxonomic diversity. Functional diversity refers to the functioning of ecosystems and phylogenetic diversity consists of evolutionary lineages, the maintenance of which ensures that future evolutionary potential is safeguarded. The process where taxonomic diversity is maintained but parts of functions and evolutionary history are lost is called biotic homogenization. Human population growth and intensifying land use in the surrounding matrix create a challenge for biodiversity conservation based on protected areas. Earlier studies have mainly focused on taxonomic diversity and characteristics within the protected areas. However, functional and especially phylogenetic homogenizations are less studied phenomena, especially with respect to matrix effects on protected areas. We studied whether intensity in land use in the matrix has an effect on bird community assemblages in protected boreal forest areas. We used line-transect count data from 91 forest reserves in Northern Finland, and land-use data from buffer zones surrounding the reserves. We studied if the intensity of forest management has a consistent effect on taxonomic, functional and phylogenetic diversities. We found that forest management intensity in matrix may have strong effects on the diversity of bird assemblages in protected areas. This indicates that boreal forest reserves are not able to maintain integrity if embedded in severely degraded matrix. We also point out the importance to focus on several different aspects of biodiversity when studying biotic homogenization.

P046 Eurasian red squirrel (*Sciurus vulgaris*) in an urban environment - Habitat and nest use during natal dispersal

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Urban habitats usually differ from species' natural habitat by being extremely fragmented. In the cities semi-natural areas are often divided by roads and buildings, which can act as barriers for movement and affect habitat selection. In many mammalian species, habitat selection occurs mainly during natal dispersal, when young individuals leave their mother's home range and find their own home range. Thus habitat selection during natal dispersal determines where animals are found in the city with implications both on individual fitness and population dynamics. We study the habitat and nest use of juvenile Eurasian red squirrels (*Sciurus vulgaris*) in an urban area, with our main focus being to study changes in habitat use during natal dispersal. We conducted our study by monitoring movements of young squirrels by radiotelemetry in southwestern Finland, in the city of Turku. Our preliminary results show that squirrels are located in a variety of habitats in the city, from forest-like parks to totally treeless built areas. Squirrels preferred coniferous and deciduous trees but also used constructed areas when moving in the city area and also occasionally for nesting. Squirrels used mostly twig dreys in trees as their nests in an urban area, but sometimes took advantage of manmade structures as their nest places. Our results show that in urban areas squirrels are not restricted to their natural habitat type, coniferous forest, but use different habitats including totally constructed areas with only few trees or no trees at all.

P047 The Shining guest ant and other associates of red wood ants

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Ant nests are rich with various other fauna, and they may be seen as resources for these guest species. We studied the species richness and abundance of ant guests in the nests of *Formica polyctena* by addressing the resource concentration hypothesis which predicts that nests in high densities would support higher species richness and abundance of associates. We did find support for this hypothesis as the species richness was higher in nests with close neighbours. There was no relationship between the abundance of guests and the nearest neighbour distance. In addition, we studied the occurrence of the Shining guest ant *Formicoxenus nitidulus* in the nests of *Formica rufa* and *Formica polyctena*. *F. nitidulus* was more likely to be met with the polydomous *F. polyctena*, preferring large and well-connected nests. For maintaining and conserving high arthropod diversity in temperate and boreal forests, forest management practices preserving dense red wood ant populations should be used if the habitat cannot be protected.

P048 Fighting disease in space and time

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How resistance to disease is distributed across space and time can affect fundamental components of disease evolution and epidemiology. Here, our aim was to study how spatial connectivity of host populations, the coevolutionary history with a pathogen and environmental factors shape resistance variation among natural plant populations. We surveyed resistance patterns in a large cross-inoculation experiment and analysed the soil quality of patches to understand whether patch quality differed between isolated and connected populations. Non-infected, well-connected *Plantago lanceolata* populations were the most resistant to *Podosphaera plantaginis* infection and they supported highest phenotypic diversity. In turn, isolated populations were more susceptible, especially if they had no evolutionary history with the pathogen. When infected in the past, isolated populations showed increased resistance suggesting pathogen mediated selection occurring in these areas. We found that populations with higher quality soil did not have greater host resistance. One possible reason for this is that, if there is a trade-off between resistance and reproduction, hosts may allocate more resources to reproduction in higher quality environments with more competition between species. Overall, we conclude that host population resistance is influenced by both, spatial structure and coevolutionary history with a pathogen.

P049 Is the farmer's dream a wader's nightmare? Future developments of agriculture in Iceland

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Intensified agricultural practices have driven biodiversity loss throughout the world, but the extent of the impact on biodiversity can depend on the willingness of the stakeholders to take part in conservation. Knowledge on what farmers are willing and able to do is crucial for successful conservation management. Icelandic agriculture is currently at relatively low intensity but there are many indications suggesting that it will expand. Expansion of agriculture could have negative impacts on Icelandic biodiversity, particularly on northern hemisphere breeding waders. With the aim to understand Icelandic farmers' views towards bird conservation given the current potential for agricultural intensification in that country, 62 were questioned across Iceland. Most farmers think it is very important to have rich birdlife on their land but also most of them are unlikely to take special consideration of birds in land management, even if financial compensation were provided. It should be noted that there are few precedents of this type of conservation in Iceland so the concept is unfamiliar. When asked about different conservation actions to fulfil breeding wader requirements, nearly no farmer was willing nor thought it would be possible to delay harvest, but many were willing to spare important land and/or let pools stay intact. Most farmers do intend to increase their area of cultivated land, which could have negative consequences for birds, but nearly all of them think it is important to have rich birdlife on their land and are willing to participate in some action aimed at bird conservation.

P050 What drives plant species turnover in a global diversity hotspot: the Southwest Australian Floristic Region?

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South-west Australia is a global centre of plant diversity and endemism, threatened by a combination of land use change and projected future climate change. A comprehensive understanding of the drivers of plant species turnover across the region is, however, lacking. Such baseline information is urgently required for management, as well as being of theoretical interest. Our study contributes to filling this knowledge-gap, by modelling native plant species turnover across 650 widely-distributed sample sites, as a function of field-sampled soil data, high resolution climatic and topographic variables, and the geographical distance between sites (a surrogate for the effects of dispersal limitation). We fit generalised dissimilarity models, which allow for non-linear rates of species turnover on environmental gradients, to quantify the effects of these variables. Furthermore, we present a new method for decomposing the unexplained ('noise') fraction of variation, and use this approach to look for the signatures of major missing drivers of species turnover. We interpret these residual patterns using various sources of ancillary data, including predictions of past climate, and information on the life form and broader geographical ranges of associated species. We conclude that whilst current soil and climatic gradients (in particular soil phosphorus and winter rainfall) have strong, independent effects on floristic turnover, significant model error structure is linked to some unmeasured aspects of climate. This could arise from imperfect modelling of current climatic conditions, as perceived by plants. However, it could also reflect the imprints on floristic composition of either ongoing climate change or historical climatic fluctuations.

P051 Vegetation and species richness of a small archipelago in the Bothnian Sea National Park, Pori, Finland

Heli Jutila

City of Hämeenlinna, Hämeenlinna, Finland

The vegetation of Baltic archipelago was studied in SW Finland. The number of vascular plant species on each island (N=25) was counted during several visits (2–13). The average species richness and the cumulative richness were obtained for each island. The area and length of the shoreline of island was measured. The island age was estimated based on the highest elevation. The number of plant species on islands mainly depends on the age and size of the island and length of shoreline. In older islands succession has led to higher species richness and several habitats. Hydro- and geolittoral vegetation is constantly changing with water level fluctuation, wind and waves. Lower geolittoral meadows are characterized by *Deschampsia bottnica*, *Potentilla anserina* and *Glaux maritima* and upper geolittoral with *Rhinanthus serotinus*, *Parnassia palustris*, *Centaurium littorale* and *Ophioglossum vulgatum*. Drift algae accumulates to the uppermost geolittoral and is quickly covered with annuals like *Galeopsis bifida*. In epilittoral typical dry meadow plants are *Deschampsia flexuosa*, *Silene nutans* and *Fragaria vesca*. From juniper bushes succession leads to black alder, rowan and pine forests and finally to herb-rich spruce forests. In depressions succession leads to bogs. On smaller islands only the beginning of succession can be found, while on old and large islands all the successional stages exist. Among threatened species are *Antennaria dioica*, *Galium verum*, *Centaurium pulchellum* and *Linum catharticum*. *Ligusticum scoticum*, *Ranunculus cymbalaria* and *Rosa rugosa* are neophytes. The flora is threatened by eutrophication and decreasing land uplift due to climate change.

P052 The effect of benthic macrofauna on coastal sediment nutrient cycling

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The heterogeneous coastal areas of the Baltic Sea are areas of high biodiversity and support many vital ecosystem functions, such as primary production and nutrient cycling. As the Baltic Sea is suffering from an ongoing eutrophication it is important to understand the different parts of the nutrient cycling processes. The activities of benthic macrofauna are tightly linked to biogeochemical processes included in nutrient transformation and retention in marine sediments, although the importance of these organisms as a part of the coastal filter is not well understood. In our study we focus on the role of benthic macrofauna for nutrient cycling processes in the coastal zone. We sampled sediment at 18 stations on a gradient from silt to coarse sand while ensuring to include the variability of shallow coastal habitats regarding vegetation and exposure. Sediment cores from each station were incubated to measure nutrient and oxygen fluxes before sieving the sediment to obtain information on the infauna. With this information we aim at linking benthic macrofauna in different coastal environments to nutrient cycling processes. In our study we are also focusing on the link between functional traits expressed by benthic macrofauna and nutrient fluxes, as well as identifying differences in trait distribution across habitats.

P053 Exploring the association between telomere shortening and blood parasite disease in the colour polymorphic tawny owl

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Parasites are expected to exert long-term costs on host fecundity and longevity. A molecular marker for senescence, telomere length, has been found to degrade faster in malaria-diseased individuals compared to healthy ones with strong negative effects on longevity and thereby fitness. Here we study the impact of a hemosporidian blood parasite on telomere length in wild tawny owls using real time qPCR methodology. Tawny owls display a plumage colour polymorphism ranging from pale grey to reddish-brown, and infection by hemosporidian blood parasites has been found to have different impact on somatic maintenance of the morphs. We found that the tawny owls are merely infected by one strain of *Leucocytozoon* parasites, whereas no infections of *Hemoproteus* or *Plasmodium* were found. Parasitemia was not associated with colour polymorphism, but probability of infection was associated with early breeding and increased age. Telomeres were significantly shorter in infected than non-infected owls. In addition telomeres length was negatively associated with the degree of reddish-brown colouration in tawny owls. We conclude that blood parasite diseases lead to faster telomere degradation with differential consequences for the colour morphs.

P054 Parallel variation in the growth rate, demography, human-induced mortality and health indicators of the Baltic grey seal population during the 2000's

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We examined the growth rate and demographic structure of the Baltic grey seal (*Halichoerus grypus*) population in the Finnish sea area, size and structure of the catch (hunting bag), body condition and birth rate, and compared temporal changes in these variables between three time periods (2003–2006, 2007–2010 and 2011–2014). Population growth rate was estimated from aerial monitoring counts. Seal samples (n = 1556) were collected from hunters to estimate the demographic structure of the catch and population, and birth rate and body condition of the seals. Changes in population growth rate during the past 12 years took place more or less simultaneously with changes in the other variables examined. The growth rate and the proportion of females at reproductive age in the population, and birth rate of females declined from the first to the second period but then increased again during the third period, whereas the size and sex ratio (males/females) of the catch first increased and then declined. Blubber thickness of pups declined in recent years. The small catch size, high numbers of females in the reproductive age in the population and increased birth rate may be responsible for the high growth rate of the population during the last time period and predict an increase in grey seal numbers, unless the slimming of pups will lead to a decreased survival and birth rate of these cohorts in the future.

P055 Can we predict the effects of multiple stressors in the anthropocene?

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Biological systems must respond to various natural abiotic and biotic stressors, but also to increasing array of anthropogenic environmental stressors. The most important human-induced environmental stressors include climate change, land-use, habitat fragmentation and loss, overharvesting, various forms of pollution, and introduction of invasive species, diseases and pests. Global and local stressors form a complex multi-stressor environment with many potential interactions between stresses. Studying multiple stressors is important, but their combined effects on organisms are particularly difficult to study. Published research in this area is still mainly of a phenomenological and descriptive character, missing mechanistic, predictive understanding. There are many examples on interactive and counterintuitive effects of multiple stressors, which lead to the concern that their complexity will make accurate predictions of the consequences of anthropogenic change impossible. We provide an overview of the current knowledge about the impacts and interactions of different stressors in animals, and assess how well this information transfers to insects. In particular, we note that multiple stressors are perhaps best understood for animals in aquatic ecosystems, but research on terrestrial insects seldom include more than two stressors, and that ecotoxicology seems to be more advanced than other areas of environmental physiology. We also discuss how to extend descriptive understanding of multiple stressors to the mechanistic understanding that would be the necessary next step. There is an urgent need to identify which stressor interactions can be predicted, and which are idiosyncratic, species-dependent.

P056 High genetic variation for the critical day length in diapause induction in *Drosophila montana*

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At high latitudes, changes in environmental cues e.g. the day length can help the insects to predict the forthcoming winter and get prepared for it in advance. Photoperiodic adult diapause, where the emerging females will enter diapause under short day conditions, is one of the most common overwintering strategies of insect species living in the temperate zone. The timing of diapause measured as a critical day length (CDL; half of the females of a given population enters diapause) is under a strong local selection pressure as females that enter reproductive diapause too early or too late may have reduced over-wintering survival. We have traced genetic variation in CDL in a northern *Drosophila montana* population by performing quasi-natural selection favoring the females that reproduce under short day conditions. We also traced the effects of selection on other life-history traits, including cold tolerance and egg-to-adult developmental time. Selection was started in the day length corresponding the CDL of the base population, and in each generation the progeny flies were transferred into a shorter day length, where only the non-diapausing females produced progeny. After seven generations of selection, the CDL of the selection line replicates had shortened by 3.5 hours, which shows that this trait has high genetic variation and evolutionary potential in *D. montana*. In future we will perform genome scans through resequencing to detect genomic regions diverged between selection and control lines.

P057 Intriguing behaviour in *Littorina* species promotes the survival of juvenile snail.

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Marine *Littorina* species inhabit the intertidal rocky zone along the coast of Skagerrak and Kattegat, where they feed on different fucoids and epiphytic microflora. Two species, *Littorina fabalis* and *L. obtusata*, are closely related and separated only about 1.3 million years ago. The aim of this study was to compare these two species regarding their propensity to select between *Fucus* and *Ascophyllum* when placing their egg sacs. We also investigated the natural distribution during the spawning period. Both *Littorina* species prefer *Fucus* to *Ascophyllum* as substrate for placing their egg sacs on. The egg sacs were mainly found just below the floating bladders and on older parts of the *Fucus* thalli, with a richer epiphytic microflora. This lush microflora was absent on *Ascophyllum*, making it a less favourable substrate for juvenile snails. Later in the summer, juvenile *L. obtusata* were found to migrate from *Fucus* thalli back to *Ascophyllum*, which is their main food source as adults, while *L. fabalis* remained on *Fucus*. In conclusion, the two *Littorina* species were found to have different spawning behaviour as *L. obtusata* exhibit a seasonal migration pattern, where the adults move to place the egg sacs on *Fucus* and the juveniles later move back to *Ascophyllum*. We suggest that this pattern has developed due to the lack of a suitable epiphytic microflora on the surface of *Ascophyllum* combined with a radula that makes it possible for *L. obtusata* as an adult to graze directly on *Ascophyllum* thalli.

P058 Demography and genetics of the introduced white-tailed deer in Finland - from few individuals to an important game species

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Immense amounts of animals have been introduced by humans to new areas and some of these introductions have resulted in highly successful populations. In the rare occasion the introduction history (number of founders and growth rates) is well documented, these populations provide valuable case studies for detailed mechanisms of both population demographics and genetics. The introduction of white-tailed deer to Finland from North America in 1934 by just four animals provides this type of case study. We studied sex and age specific growth patterns of 451 individuals collected during hunting season 2012 in Southwestern Uusimaa. We determined exact ages, measured body mass and jaws for both sexes and skulls and antler scores for males. As expected, females seemed to gain their body size earlier than males. However, the age structure was skewed i.e. a deficit for older males warrants for future attention in the management of this strongly hunted species. Moreover, as these morphometric traits likely correlate to fitness, we combined this data (N=422) to genetic diversity to investigate inbreeding depression. Though the overall genetic diversity of the population has not reduced much compared to the population of origin, we found even with 14 microsatellites individual heterozygosity explaining considerable amount of inbreeding. This in turn explained a small but significant amount of the variation in body mass. The study of Heterozygosity-Fitness-Correlations is attractive for game and conservation-oriented wildlife management because it presents an affordable approach for genetic monitoring identifying fitness costs. The implementation of SNPs in this project is discussed.

P059 Understanding the characteristics of forest encroachment into tundra ecosystems along environmental gradients in central Norway.

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Encroachment of trees into tundra ecosystem is a fundamental aspect and indicator of high-mountain vegetation response to climate change. In this study we analyze variation in mountain birch (*Betula pubescence* ssp *tortusa*) recruitment along coastal/inland and altitudinal gradients (treeline to summit level) in the central Norwegian mountains. Four study areas were used and analyses included age, stem height, basal diameter, and crown size of birch recruits (< 2 m), and environmental data for each specimen (vegetation composition, ground conditions, altitude). No significant differences between recruitment pattern along coast-inland and vegetation composition were found. Altitude has a controlling effect on the encroachment at site-level, but, at the regional scale, encroachment pattern seem not to be climate-driven. Effects of regional climatic differences are confounded by other factors (mainly grazing) that prevent development of distinct area-specific recruitment patterns. Our results highlight the importance of considering the interplay of regional and local facilitation agents on forest encroachment into tundra, and the importance of multisite studies when addressing responses to warming.

P060 Evolution and extinction in global change: Do biological interactions obscure abiotic selection pressures?

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Climate change is expected to put species directly in the jeopardy via limits of physiological tolerance or indirectly via changes in species competitive interactions. Even though extinctions as well as evolution in the wild occur in multispecies communities most of the information on environmental adaptation is based on single species studies without consideration on how biological interactions could affect selection and extinctions. Experiment done with tens of different bacterial communities revealed strong community and key species effects on evolutionary trajectories. Moreover, in experiment with six species of *Drosophila* -flies the increased mean temperatures affected strongly competitive interactions between the species. Based on these results it is clear that species respond to environmental selection pressures also indirectly via biological interactions: altering evolutionary trajectories, likelihood of species coexistence and predictability of evolutionary change.

P061 The mercury content in organs and tissues of mammals from Cherepovets and Kirilov Districts, Vologda Region

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The aim of the study was to determine the level of mercury in the bodies of mammals from different trophic levels. The samples of tissues were collected in 2014–2015. The material gathered consisted of 394 samples from 88 individuals from 35 rodents, 39 artiodactyls and 14 carnivores. The mercury content in samples were determined on a mercury analyzer (PA-915+ with PYRO device, Lumex®). The mercury content in organs of animals from different trophic levels is different: the maximum observed in carnivores (0.17 mg / kg wet weight). The maximum concentrations of mercury are registered in liver. The liver of animals used by man for food contained mercury: boar 0.02 mg Hg/kg of raw weight and moose 0.01 mg Hg / kg of raw weight. The mercury content in mammals from protected territory – the National Park "Russian North" is lower than from the Cherepovets District.

P062 Thermal plasticity of growth and development varies adaptively among alternative developmental pathways

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Polyphenism, the expression of discrete alternative phenotypes, is often a consequence of a developmental switch. Physiological changes induced by a developmental switch potentially affect reaction norms, but the evolution and existence of alternative reaction norms remains poorly understood. Here, we demonstrate that, in the butterfly *Pieris napi* (Lepidoptera: Pieridae), thermal reaction norms of several life history traits vary adaptively among switch-induced alternative developmental pathways of diapause and direct development. The switch was affected both by photoperiod and temperature, ambient temperature during late development having the potential to override earlier photoperiodic cues. Directly developing larvae had higher development and growth rates than diapausing ones across the studied thermal gradient. Reaction norm shapes also differed between the alternative developmental pathways, indicating pathway-specific selection on thermal sensitivity. Relative mass increments decreased linearly with increasing temperature and were higher under direct development than diapause. Contrary to predictions, population phenology did not explain trait variation or thermal sensitivity, but our experimental design probably lacks power for finding subtle phenology effects. We demonstrate adaptive differentiation in thermal reaction norms among alternative phenotypes, and suggest that the consequences of an environmentally dependent developmental switch primarily drive the evolution of alternative thermal reaction norms in *P. napi*.

P063 Biocidal use of anticoagulant rodenticides results in the secondary exposure of non-target animals

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Anticoagulant rodenticides (ARs) are the primary rodent control method in most European countries. ARs can be transferred to non-target animals when they prey on poisoned rodents. Here we studied, for the first time in Finland, prevalence of AR residues in non-target animals. Main focus was on species, which are susceptible to secondary exposure due to their diet. ARs bromadiolone, difenacoum, brodifacoum, flocoumafen and coumatetralyl were analysed in 136 liver samples by an HPLC-triple quadrupole mass spectrometric method. One or more ARs were detected in 87% of samples. ARs were frequently found in eagle owls, tawny owls, raccoon dogs, foxes and mustelids. The most commonly found AR was bromadiolone, which was also found in the highest concentrations. Bromadiolone was the most frequently used AR in Finland in 2014. The second most common AR present in the livers was coumatetralyl followed by difenacoum, brodifacoum and flocoumafen. Overall, the prevalence of ARs in non-target species correlated well with the sales of these substances. A high variation of concentrations was found within and between animals. Our results show that the biocidal use causes frequent exposure of non-target animals. ARs are authorized only as biocides in Finland and the use for the crop protection can be considered negligible. Majority of concentrations found were assumed to be sublethal, but in 15% of species concentrations were so high that ARs could have contributed to the death of these individuals. Secondary exposure of non-target animals should thus be taken into account when reassessing AR use restrictions.

P064 Effects of insect herbivory on bilberry production and the attractiveness of berries to frugivores

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The evolutionary purpose of a fleshy fruit is to attract seed dispersers and get the seeds dispersed by frugivorous animals. For this reason, fruits should be highly rewarding to these mutualists. However, insect herbivory can alter plant reproductive success e.g. by decreasing fruit yield or affecting the attractiveness of the fruits to mutualistic seed dispersers. Under natural conditions, we tested the effects of experimental larval-defoliation on berry ripening and consumption of a non-cultivated dwarf shrub, the bilberry (*Vaccinium myrtillus*), which produces animal-dispersed berries with high sugar and anthocyanin concentration. Bilberry ramets with high fruit yield were most likely to get their berries foraged, indicating that frugivores made foraging choices based on the abundance of berries. Moreover, the probability for berries being foraged was the lowest for non-defoliated ramets that grew adjacent to larval-defoliated ramets, even though larval-defoliation did not seem to affect the biochemical composition (concentrations of anthocyanins, sugars and organic acids) or the probability of ripening of berries. We hypothesise that the lower probability for berries being foraged in these ramets may be a consequence of rhizome-mediated communication between ramets, resulting in a priming effect of the herbivore defence and lower attractiveness of the non-defoliated ramets.

P065 What function do pigment absorption measurements really serve?

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Leaf pigment absorption spectra are routinely used by ecologists as functional response traits. Common spectrophotometric analysis of biochemical extracts in solvents involves the harvesting of leaves, whereas repeated non-destructive measurements of the same leaf can be taken using a portable 'leaf-clip' devices. Many such devices are now available to measure chlorophyll and leaf epidermal flavonoids, providing index values adopted as proxies for photosynthesis, productivity, nitrogen status and UV-screening. We consider what 'easy' leaf pigment absorption measurements really tell us about function and how far we can legitimately generalise and compare treatment effects using leaf-clip data. (1) We tested variation among 'identical' DUALEX devices, and other SPAD and DUALEX devices: Correlations of in vivo measurements against absorption values obtained from spectrophotometric scans of leaf extracts were used to determine (2) species specificity, (3) and wavelength dependency of these relationships, (4) and their consistency among equivalent plants grown under different conditions. These tests allow us to describe how factors like chloroplast arrangement and orientation, and leaf morphology, can affect the results of in vivo measurements. The capacity of leaf clip devices to detect this sort of variation can be considered advantageous, if aiming to demonstrate functional differences in plant-light relations in response to treatments. However, if a mechanistic physiological explanation for these responses is required, only extracts for spectrophotometer/HPLC can provide qualitative information on leaf biochemical composition. Sometimes both approaches are required e.g. to determine whether diurnal changes in leaf optical properties result from pigment relocation or changes in metabolism.

P066 Macroinvertebrate biodiversity in Icelandic freshwater springs

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Freshwater springs are ecotones between surface and subsurface water habitats and have the potential to house a diverse and highly-specialized invertebrate fauna. In Iceland, an abundance of cold and thermal springs can be found, which makes the country a perfect place to study temperature influences on stygobiont and crenobiont macroinvertebrates. The aim of this study is to analyse community composition in Icelandic freshwater springs at the surface-subsurface water interface and assess how temporal, environmental, and spatial factors shape biodiversity. We have sampled 35 warm and cold freshwater springs all over Iceland using a modified electric fishing gear. Macroinvertebrates clinging to the source duct are detached by the electric shock and washed into a driftnet fixed in front of the source. Additionally, water samples for eDNA analysis have been taken. Since the water temperature for each spring is seasonally and annually stable, community composition is expected to be similar all year round. For a biogeographical approach, springs both within and outside the volcanic active zone in Iceland will be compared in order to assess whether spring type (limnocrene or rheocrene), water temperature, or geographical distribution have greater influence on macroinvertebrate composition. Warm springs could act as habitat islands across the Icelandic freshwater landscape and thus may represent a unique ecosystem which requires special protection. So far, Chironomidae, Copepoda, Cladocera, and Hydracarina (Acari) seem to be the most abundant invertebrate taxa in Icelandic freshwater springs.

P067 Molecular determination of the diet of seals in the Baltic Sea

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The conflict between seals and fisheries has been present for centuries. In recent years, many fish stocks have declined because of overexploitation and now it is relevant to investigate how much seals can affect fish abundance and damage fishing gear. The seal populations have increased rapidly since the 1970s where a total protection was introduced in Denmark and Sweden. The consequence of high seal abundance for the already impaired fish stocks is as yet relatively unknown. Seals are opportunistic feeders, but their diet is often dominated by a few key species. Previous studies on seal diet have relied on identification of otoliths found in scat or stomach of the seal. This method can be inaccurate because of the erosion of hard parts in the stomach, and because seals are known to sometimes only eat parts of the fish, making the otolith count underrepresented. This study will use molecular methods to analyse the diet of Grey seal (*Halichoerus grypus*) and Harbour seal (*Phoca vitulina*) from faeces collected on Christiansø, Denmark and Falsterbo, Sweden over several seasons. Each scat was sequenced to identify the seal species. The diet determination will rely upon molecular analyses made with next generation sequencing. To compare the results with hard part analysis, otoliths found in the scats will be identified and counted. The results of this study will help determine which fish stocks are preyed upon by seals, providing a tool for the continuous conservation of species in the Baltic Sea.

P068 The combined effects of biotic and abiotic stress on biodiversity and connectance

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Food webs are determined by two main factors namely their number of nodes i.e. species richness, and the links between species i.e. connectance. Both these properties are subject to biotic (predation pressure and food limitation) and abiotic (environmental change) stress. We developed a community model, which considers both intra- and interspecific variability in tolerance to both types of stress, to describe effects on richness and connectance in a two trophic level food web. First, we used this model to investigate how the effects of abiotic stress on biodiversity propagate in food webs by changing biotic stress levels (i.e. whether a stress-induced reduction in predator richness influences prey richness and vice versa). The effects of biotic stress were either top-down (predation pressure reducing survival) or bottom-up (food limitation reducing reproduction) control, and abiotic stress was modelled as adverse effects on survival and reproduction. Second, we also evaluated the corresponding changes in connectance over time. Model simulations showed that under top-down control, a stress-induced reduction in predator richness increases prey richness at low initial connectance but not at high initial connectance; and realised connectance decreased as a function of initial connectance, with the highest effect seen when the predator community was stressed. However, under bottom-up control, a stress-induced reduction in prey richness does not affect predator richness. Furthermore, top-down control decreases connectance while bottom-up control increases connectance. Our results suggest that biotic and abiotic stress combine to indirectly influence diversity and directly influence connectance.

P069 Temporal and spatial variation in correspondence between boreal production measures and recorded climate data

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In Northern-Europe, land temperature and precipitation are primary determinants of boreal vegetation growth. Both factors have increased over the last century, particularly during last decades, and are expected to continue increasing throughout current century. Spatiotemporal variations of these growth determinants modify vegetation composition, growth and productivity. Thus, knowledge of how correspondences between vegetation production-measures (here tree diameter, height growth, and NDVI) and primary climatic determinants vary thorough time and space is essential from climate change impact and resource management points of view. In this study, we analyse growth-climate correspondence along coast-inland and north-south gradients in Norway for 1960–2012 and successive intervals therein. Scots pine is used as model species for diameter and height growth measures. A complex set of growing season and non-growing season temperature and precipitation factors affect growth with diameter-current July temperature being the long-term dominating correspondence. However, this dominance was inconsistent both thorough space and time. In coastal north, no such long-term correspondence was found, although intervals from mid 1980s to late 1990s indicated substantial July_t temperature importance. Further, at sites with dominating July_t importance the correspondence was temporarily lacking. August_{t-1} temperature was most important factor affecting height growth, but with changing significance through time and with negative effect in north and positive in south. NDVI was not significantly correlated to either diameter or height growth at any of the included study sites. The spatiotemporal variation in climate-growth correspondence, and limited explanation power of NDVI for local forest production, makes extrapolation beyond scale of empirical evidence challenging.

P070 Kinship effects on tree seedling growth and behavior

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Kin selection can lead to cooperative behavior among related individuals, and unlike commonly assumed, plant interactions can also be guided by recognition mechanisms. Birch growth is commonly limited by soil N availability and the N in shed leaves can be considered as common goods that after litter decomposition and N release benefit the individual and the neighboring plants. Birch trees have high genetic variance in the proportion of N they can withdraw from their leaves to the stem in the fall, and they also face a tradeoff between efficient N retention and growing season length. Moreover, soil N levels likely affect the shape of this tradeoff. If the plants can recognise their kin among the neighbours, they have a possibility to plastically optimise their N-retention behaviour. Plants are also known to signal about herbivore damage through volatiles and it is possible that kinship either directly or through plastic responses affects the herbivore damage. We use ESS and individual-based, spatially explicit models to understand the coupling between kin-effects, tradeoffs, phenotypic plasticity, and nutrient cycling in plants. We also set up a large-scale field experiment in 2015 manipulating kinship of two birches, *Betula pendula* and *B. pubescens*. Results of the modelling and experiment are discussed.

P071 Tick ecology and tick-borne pathogens in Finland - the tick project of the University of Turku

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Ticks and tick-borne diseases constitute a growing problem in northern Europe and Russia. The tick project of the University of Turku was started in 2012, with the objective of producing novel data on tick abundance, ecology and tick-borne pathogen diversity in Finland. Since the start, blanket dragging has been conducted at many locations around southwestern Finland to survey tick abundance and tick-borne pathogens prevalence. Furthermore, a long-term surveillance site for tracking annual changes in tick abundance, seasonal questing activity patterns and pathogen diversity was established on Seili island in 2012. Similar surveillance sites were established at several university research stations all around Finland in 2015. We also wanted to produce nationwide data on the geographical distribution of the two currently known disease-transmitting tick species in Finland, *I. ricinus* and *I. persulcatus*. To accomplish this, we organized a national tick collection campaign in 2015, where we asked citizens to send ticks to us at the University of Turku. The collection campaign was a success, with nearly 7000 letters received, containing approximately 20 000 individual ticks from all around Finland. Our field studies suggest that both the abundance and pathogen prevalence of ticks have increased in Southwest Finland. Currently, we are working on the massive data gathered in the national tick collection campaign. While laboratory analyses have just been started, identification and mapping of the received tick samples have already revealed that *I. persulcatus* is much more prevalent in Finland than previously thought. The main bulk of contemporary spatial distribution and mapping studies analyse species occurrence data instead of density measurements. However, the present study shows that the information loss from spatial generalization can be larger for taxonomic occurrences and rare species than for species abundances and aggregated community parameters like total abundance or taxonomic richness.

P072 RADSeq genetics of resident and migratory brown trout within and among rivers

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Migration is almost ubiquitous biological phenomenon within animal kingdom. Salmonids are among the most famous and economically important migratory species. Brown trout *Salmo trutta* forms both partially migrating and entirely resident and migratory populations. Migration behaviour correlates with many other life-history traits forming migration syndromes. However, while the phenotypic plasticity in migratory decisions is known to be large and under strong environmental control, it is still unclear if resident individuals within a same watershed differ genetically from migratory individuals, and whether the potential differences are more or less pronounced than those observed among watersheds and tributaries. We are starting a project in which we use next-generation sequencing of RAD tags to compare 50 000 SNPs: in 14 populations (5 migrants, 9 resident) in River Olanga and River Oulujoki watersheds. For each population, 30 individuals are sampled and sequenced. By comparing both neutral and functional markers among the populations, we are looking for genomic regions associated with the different migratory patterns. If the resident and migratory individuals from a same watershed appear to represent population genetically a uniform gene pool, the remaining last wild resident populations will offer invaluable genetic material to be used in restoring the wild-type fitness qualities in domestication-impacted hatchery strains of migratory trout. A better understanding of the genetic underpinning of migration behaviour and population structure can lead to major advances in the management and the conservation of brown trout all over the world.

P073 Revealing historical linguistic contacts in Finland with population genetic methodology

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Historical migration of people leaves its imprints on both genetic and linguistic data, since both types consist of features that vary in space and are passed on in time. By using the present distribution of variants of these features, their historical distribution can be estimated, revealing contacts among groups of people. Sometimes these contacts may be detectable only in genetic or linguistic data, sometimes in both. Similarities between genetic and linguistic data enable us to apply the same framework to both types of data, opening an opportunity for multidisciplinary research. There is growing number of studies applying statistical methodology from evolutionary biology to study linguistic variation among language families. Here we focus on linguistic variation within a language and study historical contacts among the speakers of the Finnish language. By using historical linguistic data, we estimated 'flow of linguistic variants' among the dialects by applying Bayesian clustering methods, originally designed for population genetics. The detected flow among dialects suggests that people have spread linguistic variants by the way they spoke and gave names to places. The results indicated a major east-west division in the data, and a source-sink dynamics of dialects mainly within these major clusters. We will discuss the strength and direction of linguistic flow among the Finnish dialects in the light of the previous knowledge on biogeographical separation of the dialectal areas. Our results will set the stage for combining linguistic and genetic data to provide a more comprehensive picture of the historical migration of Finns.

P074 The Impacts of Sheep Grazing on Bryophyte Communities

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Bryophytes play an important role in tundra ecosystems. Bryophytes are sensitive to trampling and grazing by large herbivores, such as sheep. This disturbance can have strong effects on bryophytes in terms of species diversity and composition of the community. This depends on grazing intensity and the growing conditions. It is not well known how grazing affects bryophyte communities in tundra ecosystems. This study aimed at assessing the impact of sheep grazing on bryophyte species diversity, and the abundance of growth forms and life-history strategies, in tundra regions of Iceland. A vegetation survey was conducted in six grazed and ungrazed valleys in two regions. The survey was stratified at three different landscape scales within each valley to reflect environmental variation and growing conditions, i.e., exposure, elevation, and topography. This hierarchical stratification allowed for analyses of the communities within different combinations of growing condition, and to determine where the disturbance was detectable. Bryophyte species diversity and abundance was measured, and species were grouped based on growth form and life-history strategy. Results indicate that grazing activity had more pronounced effects on the bryophyte communities in the west-facing slopes of the valleys than the east-facing slopes. Species diversity and the abundance of pleurocarpous moss were greater in grazed valleys than ungrazed, while colonist species were less abundant, especially in the more favorable concave landforms. Perennial stayer stress tolerant species were more abundant in grazed valleys in general, particularly in the most favorable conditions, i.e., on west-facing slopes, at low elevation, and in convex landforms.

P075 Spatial arrangement for the function of midfield islets to preserve grassland plant species.

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To identify the most important spatial factors in fragmented landscapes to mitigate species loss is essential to conservation strategies. However, with few species-rich habitats left, small remnant grassland habitats, e.g. midfield islets, might have an important role for biodiversity and ecosystem functions in intensively used agricultural landscapes. The habitat amount hypothesis, proposed by Fahrig (2013), suggest that the amount of a habitat type is a simplified way of predicting species richness in fragmented landscapes, compared to species area relationship and isolation of the habitat. Species richness in equal-sized samples should increase with the total habitat amount in the closest surrounding. Here, we have tested the hypothesis against the spatial variables: habitat size and isolation of the focal habitat, using data on species richness from 133 midfield islets (size between 148–4876 m²) in 30 landscapes in eastern Sweden. In total I found 306 species. Many (74) so called grassland specialists, i.e. plants associated to semi-natural grasslands with a long continuity of managed still remained on the midfield islets. Mean species richness within sampled area (8 plots of 0.5*0.5 m) was 32 species (± 7.8 SD) and the mean number of grassland specialist species was 7 (± 4.1 SD). Preliminary analyses show that habitat amount was a good predictor of species richness, yet it performed less well compared to habitat size and distance to the nearest habitat patch, thus being the best combined predictors of species richness.

P076 How should we define a plankton population?

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Long-term monitoring data of phytoplankton are collected annually from multiple stations to cover vast areas, typically without replicates from the same stations. To further analyse time-series of individual species' population densities, it is important to understand whether data from stations close to each other can be viewed to represent one large population, or spatially separated populations with either similar or different dynamics. To investigate these questions we studied the population dynamics of some phytoplankton species present at three offshore stations in the Baltic Sea proper and in the Gulf of Finland using multivariate autoregressive state space modelling. The time-series has been collected by the Finnish Environment Institute since 1979. We compared models where samples from the three stations were considered the same population and models where they were considered separate populations. We further tried models with different kinds of behaviour and finally, we considered different correlation structures between the three stations. We investigated different models and evaluated their support according to their AIC scores. Preliminary results indicate that the most parsimonious model was the one considering the data from different stations as belonging to the same population. This is an indication that it might be viable to consider the annual population dynamics of the investigated species to act uniformly over a large area, and e.g., to pool data from stations close to each other. This, however, needs to be investigated over a larger range of stations and species before generalisations can be made.

P077 Mums who have sex produce better quality sons? Effect of copulation and diet quality on the fitness of haplodiploid *Diprion pini* pinesawflies

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Toxic defences of an individual contribute to the 'common good' by educating predators to avoid prey of similar appearance in future encounters. However, sometimes it benefits the individual to avoid production of costly defences by exploiting the common protection. Sociality in predator defence is quite common in haplodiploid pine sawflies. Their larvae feed in large aggregations and regurgitate a resinous droplet of fluid from their mouth and perform defensive movements in concert when threatened by predators and parasitoids. Based on our own data, defensive display is costly and its efficacy can depend on both the sex of the individual as well as environmental conditions. Here we took a closer look on these sex-linked differences and tested how the chemical defence, performance and immunology of female and male larvae differed in low and high resin acid diet. In addition, we compared the quality of the sexually (females were allowed to copulate) and asexually produced haploid male offspring. We found that copulated females had better reproductive output as they produced larger amount of eggs and offspring. Females had better immunological defence in comparison to males, but there were no differences in the immunological defence among asexually or sexually produced haploid males. Interestingly, asexually produced males regurgitated higher quantities of defence fluid, but grew slower and were smaller than sexually produced males. In sexually produced clutches, female larvae were always more likely to defend and produced higher quantities of defence fluid than male larvae indicating potentially parasitic relationship between males and females in terms of cooperative defence.

P078 Guardian or threat: cascading effects of golden eagle predation risk on forest grouse

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Previous studies on intraguild predation have mainly focused on within-class assemblages, even though avian top predators may also influence mammalian mesopredator prey. By using nation-wide long-term data from Finland, northern Europe, we examined the impacts of golden eagles (*Aquila chrysaetos*) together with red foxes (*Vulpes vulpes*) and pine martens (*Martes martes*) on forest-dwelling herbivores, black grouse (*Lyrurus tetrix*) and hazel grouse (*Tetrastes bonasia*). We hypothesized that eagles may indirectly benefit grouse if the intraguild predation risk imposed on mesopredators alleviates the overall predation pressure on grouse. The predation impact of eagles was modelled using density estimates and distance to eagle nest. Wildlife triangle counts were used as predation impact proxies of mammalian mesopredators and as measures of response in grouse. Our results show that eagle density correlated negatively with black grouse abundance while being positively associated with the proportion of juveniles in both grouse species, irrespective of the abundance of mesopredators. Yet, foxes and martens alone had a negative effect on both the abundance and the proportion of young in the two grouse species. This suggests that the possible cascading effects of eagles are not mediated by decreased numbers of fox and marten but instead through intimidation, which may change mesopredator hunting behaviour and microhabitat use. In conclusion, we found support for the hypothesis that eagles provide protection for juvenile black and hazel grouse, whereas they are a threat for adult grouse. This kind of information helps us to better understand the role of avian top predators in terrestrial ecosystems.

P079 Pollinator deception increases outcrossing and effective population size in patchy habitats

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Non-rewarding plants are common especially in the huge orchid family, where every third species is deceptive. There is some consensus that pollinator deception – if adaptive – might be a way to increase cross-pollination and therefore seed quality, but on the cost of seed quantity. However, the role of habitat structure of such plants in their pollination dynamics has remained unclear. Effect of spatial structure of plant populations (homogenous/patchy) and rewarding of pollinators (reward/no reward) on the degree of cross-pollination was tested in this factorial experiment. The study was carried out in laboratory conditions with bumblebees (*Bombus terrestris*) and with a new type of computer controlled artificial flowers we developed. In non-rewarding treatments pollinators moved longer distances between visitations than in rewarding treatments, indicating higher outcrossing. In patchy-rewarding treatment most movements between flowers happened inside a patch with little variance. With no reward, a higher proportion of movements happened between separate patches and with much greater variance. In both spatial structures rewarding of pollinators induced short flight distances with small variance between individual bumblebees. In non-rewarding treatments it was not only the average flight distances that were higher, but also the variance between individual bumblebees, indicating considerable variability in the learning abilities of naïve bumblebees. This also suggests higher likelihood for long flight distances between visitations and at plant's point of view, possibly a higher quality of pollen, an important feature especially for epiphytic orchids with naturally fragmented habitat structure and generally low effective population size.

P080 Environmental and spatial effects on the determination of shell traits of the common whelk (*Buccinum undatum* L.)

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The expression of heritable characteristics determining phenotypic traits can be affected by interactions with the environment. Mollusc shells exhibit wide variation of easily measurable phenotypic traits including colour, thickness and shape, which make molluscs ideal for the study of relative genomic and plastic contributions to phenotypic determination. Variability in shell shape and thickness have been linked to environmental factors such as wave action and presence of predators using model species such as *Littorina saxatilis* and *Nucella lapillus*. The documented variability in shell morphology of the subtidal gastropod *Buccinum undatum*, along with its limited dispersal capacity, makes it another fitting candidate for in-depth research on trait determination. In Iceland the highest density of whelks is in Breiðafjörður, where whelks differ in life history traits between sites as well as in shell colour, shell shape and shell thickness. The species distribution across Breiðafjörður covers a diverse area and many environmental factors that could influence shell morphology. The aim of the project was to understand the causes of the phenotypic variation in the common whelk, with respect to spatial and environmental variation. A combination of traditional morphometrics, geometric morphometrics and shell colour analysis was used to classify shell phenotypes of whelk in Breiðafjörður and their correlation with environmental factors was tested. Results indicate that a combination of environmental and genetic factors affects the shell phenotype of the whelk. The next steps in the project, analysis of genotypic variation and a common garden experiment, will shed better light on this.

P081 Phenotypic responses of a water flea population to rapid environmental change

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A powerful way to reconstruct past responses of populations to human-induced environmental changes is to investigate their fossils. Cladocera (water fleas) have been shown to undergo changes in morphology in response to changes in the environment, and to leave subfossils that provide valuable material for long term studies of phenotypic changes. We investigate how a common Baltic Sea cladoceran, *Eubosmina maritima*, has phenotypically changed in response to eutrophication during the past decades. Sediment cores from sites with different eutrophication history have been sampled, and fossils from sediment layers from periods before, during and after the most severe eutrophication are being measured. We will present our preliminary results on how morphological changes (such as changes in overall size of the organism and in the length of appendages) correlate with eutrophication induced changes in the food web (such as primary production and predator community). The results will reveal the magnitude and rate of phenotypic responses of this common species to past environmental changes, and thus help to predict its future success in the face of new challenges.

P082 Trans- and within generational effects of sublethal pyrethroid insecticide exposure on an invasive pest insect

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Pesticides are widely used in agriculture to manage pest species and form a major anthropogenic stressor shaping many ecological and evolutionary processes. Tolerance to insecticide stress may be influenced by the parental exposure to the same stressor. Here we investigated whether sublethal pesticide exposure has within and/or transgenerational effects on the invasive Colorado potato beetle (*Leptinotarsa decemlineata* Say.). Stress caused by low sublethal insecticide dose can either increase or decrease fitness. In the current study larvae were treated with either sublethal pyrethroid insecticide (LD 10) or equal amount of water (control) survival and adult body mass were recorded (first generation). Thereafter control males were mated with females descending from both the first generation insecticide and control group to investigate the transgenerational effects of maternal exposure on the offspring susceptibility to insecticides. Thereafter the second generation larvae were treated similarly as the first generation and, in addition to larval survival and adult body mass, lipid content was analysed from surviving adults. The results suggest both within- and transgenerational effects of sublethal insecticide exposure. Survival varied between life stages from negative to positive effects, while the effect on beetle's body mass was sex-specific and varied from neutral (in males) to positive (in females). No changes were found in lipid content depending on treatment. To conclude, positive maternal effects that are translated into their offspring's fitness can be adaptive. Therefore exposure to sublethal insecticide can potentially contribute to unwanted evolution of pest species, which should be considered in the integrated pest management strategies.

P083 Light sheep grazing on poorly vegetated sites – does it influence succession?

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Land degradation and soil erosion have shaped Icelandic ecosystems and are regarded among Iceland's largest environmental problems. Today, 40% of the country suffers from considerable erosion but many such areas are still grazed by sheep. This practice is controversial, but often justified with reference to the small stocking rate, and the belief that it could not have any significant effect on the ecosystem recovery. In harsh environments where growing conditions are poor, it can take decades before the cessation of grazing produces noticeable changes at community level. Changes at the level of individual plants are likely to be much quicker and with time these will be expressed at higher levels of organization. In this study we evaluate the impact of light summer grazing (<0.01 sheep ha⁻¹) on plant performance on Skeiðarársandur, a 1000 km² glacial outwash plain in SE-Iceland. While parts of Skeiðarársandur have continuous vegetation, most of it has <10% vegetation cover. Ecosystem development has been studied there since 1998 and in 2004, 10 large plots were fenced to exclude sheep grazing. We compared growth and seed production in three common plant species, *Cerastium alpinum*, *Arabidopsis petraea* and *Juncus trifidus*, inside and outside enclosures. None of these species is regarded as particularly palatable. Our results indicate that even such a low stock rate has a significant negative effect on growth and seed production. Clearly, this has implications for grazing management, supporting the view that such poorly vegetated sites, should not be used as grazing land for domestic stocks.

P084 Biological control of environmentally growing pathogens

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Many pathogens, such as *Vibrio cholera*, *Pseudomonas aeruginosa*, *Legionella pneumophila*, *Listeria monocytogenes* and many species from genus *Mycobacterium*, *Flavobacterium* and *Serratia*, are able to use outside-host resources for growth. Due to their ability to grow independently of hosts in the environment, these diseases are impossible to fully eradicate with antibiotics. Control methods that target the outside-host pathogen population likely are more efficient than use of antibiotics in preventing environmentally growing disease outbreaks. Potential methods include using predation of pathogenic bacteria by protists and phage therapy in the outside-host environment. I consider how outside-host predation of the pathogen and phage therapy could be utilized in biological control of environmental diseases. Toward this end, novel epidemiological models for environmentally growing pathogens are developed. The results suggest that both outside-host predation and phage therapy can be successful in eradicating the disease. This outcome depends, however, both on the efficiency of predators and phages as well as the trade-off between the level of virulence and the ability to develop resistance towards phages.

P085 Smell the danger! Odor-perception of pathogen infection risk in a below-ground parasitoid

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To locate and evaluate host patches before oviposition, parasitoids of herbivorous insects utilize plant volatiles and host-derived cues, but also evaluate predator-derived infochemicals to reduce predation risks. When foraging in host habitats infested with fungal pathogens, parasitoids may reduce the risk of infection to themselves or their offspring by avoiding such patches. In this study, we examined whether the presence of the two fungal pathogens, *Metarhizium brunneum* and *Beauveria bassiana*, in soil habitats of a root herbivore, *Delia radicum*, affected the behavior of *Trybliographa rapae*, a parasitoid of *D. radicum*. Olfactometer bioassays revealed that *T. rapae* avoided pathogen infested host habitats and that this response was dependent on pathogen species and density. In particular, the parasitoid avoided habitats with high densities of the more virulent pathogen, *M. brunneum*. In contrast, host density was found to be important for attraction of *T. rapae*. Volatiles collected from host habitats revealed different compound profiles depending on pathogen presence and density, which could explain the behavior of *T. rapae*. We conclude that *T. rapae* females may use volatile compounds to locate high densities of prey, but also compounds related to fungal pathogen presence to reduce infection risk towards themselves and their offspring.

P086 Exploration of the spatial distribution of bacterial microbiota associated with the Glanville fritillary butterfly *Melitaea cinxia*.

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Bacterial symbionts are interacting with multicellular eukaryotic organisms with a gradient ranging from parasitism to mutualism. Those interactions result in a wide range of effects on their host's life history traits and may participate directly or indirectly to their population dynamics. The Glanville fritillary butterfly *Melitaea cinxia* is one of the most studied insect model system in spatial population ecology. The long term study of the local populations in the Åland Islands archipelago has demonstrated a dynamic extinction - recolonization pattern of this butterfly in this patchy habitat network. Some of the biotic and abiotic factors responsible for the high turnover rate of local populations are well understood. However, the role of bacterial microbiota of *M. cinxia* has been poorly investigated until now. In order to describe its variation within and among natural populations, we sampled 190 individuals of 5th instar, diapausing, larvae as well as leaf samples of their host plant *Plantago lanceolata* from 15 patches in the Sund region of the Åland archipelago. Among them 46% of the individuals were parasitized by the specialist wasp *Hyposoter horticola*. The integrated study of *M. cinxia* midgut bacterial composition, their genetic structure, the parasitism rate and the food plant quality (microbiota and metabolites intake) will be investigated. This project aims to provide one of the first integrated descriptions of those neglected factors potentially impacting the overwinter survival of *M. cinxia*, which is one of the most vulnerable stage of its life and has a great impact on population dynamic.

P087 Sexual difference in the frequency of loss of hind leg in *Parapodisma* adult grasshoppers in natural habitat

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Insects have various defence traits against natural enemies. Autotomy is one of the defence traits against predators. The detailed knowledge of autotomy patterns and frequencies in the wild is required to make more reliable inferences concerning the fitness benefits and costs in the consequences of autotomy. However, few quantitative surveys have been conducted on the autotomy frequencies on the insects in the wild with the traits of insects related to the autotomy. Here, I examined the data on the adult grasshoppers *Parapodisma tanbaensis* and *P. subaestrif*, which are sympatric, closely related species in the wild in Kyoto, Japan, for two consecutive years at the same three sites in Kyoto. I identified the species, and recorded the sex, and body size, and the condition of hind legs after sampling the adults to investigate what trait could influence the frequency of autotomized adults. The results showed a significant effect of grasshopper sex. On the other hand, the results showed no significant effect of species, body size, and season. Those suggest that the sexual difference can exist in the occurrence and disappearance rates of autotomized adults in the wild. We discuss what mechanism and factor in the wild could cause the sexual difference in the autotomy, including the grasshopper mortality caused by the emergence of the parasitoid fly *Blaesoxipha japonensis* from adult grasshopper, which the previous study suggests it could be one of the costs of autotomy of *Parapodisma* grasshoppers in the wild.

P088 Comparative transcriptomics reveals the conserved building blocks involved in parallel evolution of ant phenotypic traits

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Reproductive division of labor in eusocial insects is a striking example of a shared genetic background giving rise to alternative phenotypes, namely queen and worker castes. Queen and worker phenotypes play major roles in the evolution of eusocial insects. Their behavior, morphology and physiology underpin many ecologically relevant colony-level traits, which evolved in parallel in multiple species. We used comparative transcriptomics to test the hypothesis that conserved sets of genes are involved in ant reproductive division of labor. We further hypothesized that such sets of genes should also be involved in the parallel evolution of other key social traits. Applying weighted gene co-expression network analysis to transcriptomic data from 16 ant species, we show the existence of conserved modules of co-expressed functionally related genes that are correlated with phenotypic differentiation between queens and workers. Furthermore, expression of several such modules is strongly associated with key social phenotypes, such as the evolution of complete worker sterility, the number of queens per colony, and even ecological invasiveness. Furthermore, the properties of the co-expressed gene network, such as connectivity and gene expression levels influence selection operating on orthologous protein coding genes. Although caste-biased genes evolve faster than non-caste biased genes, we found no evidence for queen or worker genes evolving faster than one another. These results identify conserved functionally important genomic units that likely serve as building blocks of phenotypic innovation, and allow the remarkable breadth of parallel evolution seen in ants, and possibly other eusocial insects as well.

P089 Predation risk and food supplementation modify egg composition but not offspring condition

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Mothers may affect the future success of their offspring by varying allocation to eggs and embryos. These maternal effects may be adaptive towards the environmental conditions perceived by mothers during early breeding. We manipulated key environmental elements, food supply and nest predation risk, and measured the consequences to egg composition, using a 2x2-factor design in the pied flycatcher (*Ficedula hypoleuca*). Eggs laid in food supplemented nests were heavier and had thicker shells, and eggs laid in nests exposed to cues of nest predators had lower levels of immunoglobulins compared to controls. Two days after hatching a full brood cross-fostering was performed, transferring the chicks to untreated nests, to investigate the impact of egg composition on offspring growth and immune capacity. Offspring mass was not affected by maternal treatment group, neither on the day of cross-fostering or just before fledgling and also immunoglobulin levels did not vary according to food supplementation or nest predation risk perceived by the mother during egg formation. These results suggest that although food supplementation and nest predation risk modify egg composition, these egg-mediated effects may not have consequences on offspring growth or immune capacity. Unpredictable environmental stressors, such as nest predation risk, may thus affect female condition and affect parental investment in the eggs, but the parental care offered by the foster parents may compensate for eventual costs, or benefits, of maternal allocation.

P090 Effect of genetic diversity on ecosystem functioning

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Species diversity is expected to be beneficial to ecosystem functioning. In contaminated soil only few species can survive, so species diversity is diminished. We are interested to know if genetic diversity within a species can compensate for the lack of species diversity: Does high genetic diversity benefit ecosystem function when species diversity is low? We study this question with the earthworm *Dendrobaena octaedra* in a microcosm-experiment that has lasted two growing seasons. In half of the microcosms all the *D. octaedra* earthworms are clones of each other (low genetic diversity) and in half they are all different genotypes (high genetic diversity). There are also microcosms containing other species (arthropods, enchytraeids and one other earthworm species) in addition to *D. octaedra*, both in low genetic diversity and high genetic diversity treatments. The experiment is done both in clean soil and Cu contaminated soil (moderate contamination, 100mg/kg dry mass). CO₂-production and nutrient mineralization is measured from the microcosms, and expression of genes involved in decomposition processes are measured from the earthworms. We compare these variables from the low vs. high genetic diversity treatments in order to make inferences about ecosystem functioning. Preliminary results from the gene expression measurements will be presented and related to CO₂-production.

P091 Color alters thermoregulatory behavior in *Battus philenor* caterpillars by changing the behavior's cue

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When an organism has multiple plastic traits, they can alter each other's expression. This could occur, however, either because one trait changes the environmental cues that the other responds to or because it changes the reaction norm which determines how the other trait responds to those cues. In *Battus philenor* caterpillars, we have previously established through field experiments that a thermoregulatory color change from black to red reduces the use of thermoregulatory behavior to avoid overheating. Subsequently, we have tested which of our proposed mechanisms cause this effect using lab experiments. First, we demonstrated that this effect remains if intense light is used to heat the caterpillars; however, if this light is removed and caterpillars are heated by primarily by conduction, color no longer affects the refuge-seeking behavior. Additionally, color has no effect on the sensitivity of the caterpillar's metabolism to temperature, a potential mechanism for altering the thermoregulatory behavior's reaction norm. As such, we have shown that the effect of color on thermoregulatory behavior is due to how it changes the cues which trigger color change (i.e., body temperature), rather than changing the reaction norm that responds to those cues. Cue-based interactions like this one are likely to be common in thermoregulation, and they also present a novel, within-generation consequence for any alterations an organism makes to its environment (i.e. niche construction). In other circumstances, both mechanisms presented here remain possible and need to be considered more broadly across additional species and ecological contexts.

P092 Temporal and spatial variation of wood anatomical traits in an arctic shrub species

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The changing climate has caused an expansion of shrubs in the Arctic. Growth responses of species differ across climatic and environmental gradients but the mechanistic drivers behind these differences are not well known. Hydraulic efficiency is expected to promote increased growth so here we investigate the hydraulic responses of the Arctic shrub *Betula nana* along a climatic gradient in Western Greenland. We use a dendroecological approach to evaluate how vessel size and vessel grouping are responding to climatic changes in space and time. Linear models show complex temporal responses of vessel size and vessel grouping depending on the climatic conditions under which the individuals grow. Vessel size responds negatively to increasing temperatures along a growing season temperature gradient, whereas vessel grouping responds positively to increasing temperatures along a growing season precipitation gradient. These results indicate a plastic hydraulic system showing the species' ability to respond to climate change. The spatial scale of our study did not catch sufficient variation in wood anatomical traits to explain the spatial pattern of these. This indicates that further studies on this topic on a bigger spatial scale are needed.

P093 Structural properties of benthic food webs altered by point-source organic enrichment

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Anthropogenic impact on coastal ecosystems is primarily monitored with focus on taxonomy, tracking changes in species richness and relative abundances to assess stressor-induced degradation of ecological community structure and processes. Current approaches seldom take into account the fundamental dimension of interactions among taxa. Trophic interactions are central to community ecology given the link between food-web structure and community functioning and stability. Furthermore, extinction of interactions not only accompanies species loss but may even precede it. It is therefore crucial that we increase our understanding of how a changing environment drives biotic interactions. We assessed effects of anthropogenic stressors related to organic enrichment on a range of structural properties of soft-sediment food webs. More specifically, we studied how changes in primarily sediment organic content and bottom-water dissolved oxygen levels influenced the topology of benthic macroinvertebrate food webs, assessing patterns over time and space from point-source organic enrichment. Examining changes in food-web structural attributes, for example the richness of nodes and links, linkage density, connectance, and proportions of basal, intermediate and top-level taxa, we find a general simplification of the trophic network with higher organic loading. In this study, we explore property-specific responses and discuss potential consequences of such restructuring of the interactions within the benthic community. Adding a dimension of interactions (in this case feeding links) to existing biodiversity concepts enhances our understanding of the consequences of environmental degradation

P094 Responses of plant biomass to climate change: a study along temperature and precipitation gradient

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High latitudes and elevations are considered one of the most vulnerable environments to climate change. It has been shown that plants are responding to climate change, either by increasing in biomass or change in the dominant plant functional group. It is not only necessary to determine how plants respond to increasing temperature and precipitation, but also how these trends are evolving over time. For these purposes, I compared total biomass and biomass of three plant functional groups (PFGs) across a climate grid (three temperature levels and four precipitation levels) in Western Norway. Additionally, I compared the biomass of PFGs in 2015 a very cold year with those collected in 2013, which was an average year in terms of climate. Total biomass at both lowland and intermediate sites was relatively high (91.10 g/2,5m² and 92.39 g/2,5m², respectively), whereas the biomass of alpine sites was distinctly lower (61.83 g/2,5m²). Compared to 2013, the total biomass was lower in 2015 and the most significant differences between years were found within the alpine sites. Biomass of vascular plants (graminoids and forbs) and litter increased with temperature. There was no significant correlation between non-vascular plant biomass and either temperature or precipitation. The results of this study confirm that with increasing temperature the biomass of vascular plants increases in addition to litter. Generally, vascular plants become more dominant in plant communities. We are effectively simulating climate change by comparing sites along the temperature and precipitation gradient. Thus, under future climate scenarios, similar trends can be expected.

P095 Factors affecting nest predation in common eider

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The down feathers of eider ducks (*Somateria mollissima*) are used commercially to fill i.e. duvets and pillows. Eiderdown is therefore a valuable product and collected by many farmers in Iceland. By minimizing nest predations it is possible to improve eiderdown yield. The aim of this study was to assess which factors affect predation rate in eider colonies. The research was conducted by visiting each colony twice throughout the incubation period, and by using cameras with motion sensors. Nest predation rate was 14% (n=157 nests). Identified predators were ravens (*Corvus corax*) and great black-backed gulls (*Larus marinus*). The factors affecting predation rate were nest surroundings, nest initiation date and frequency of visits by predators. Predation was lower if nests were surrounded by angelica (*Angelica archangelica*). Near the end of the incubation period, the angelica will overgrow nests and cover them from above and thus hide the nests from avian predators. Predation rate was highest on nests initiated early in the season, and decreased linearly as the incubation period progressed. Early in the season there are proportionally more predators relative to number of nests, vegetation is less advanced and nest density is low and therefore there is limited benefit from nearby eiders or gulls. Predator visits were more common on nests which eventually were predated, or on average 1.7 times/day compared to 0.7 times/day on successful nests. Predators possibly identify nest locations and visit to see if the female eider is present, and eventually try to flush her of the nest.

P096 Genotype by genotype interactions govern pathogen-hyperparasite relationships

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Many organisms employ a parasitic lifestyle and, through their antagonistic interactions with host populations, have major impacts on human, agricultural and natural ecosystems. Parasite dynamics are generally considered within a framework of coevolution with their hosts and competing parasites, mediated by the abiotic environment. However, most parasites and pathogens are also likely to host parasites of their own, i.e. hyperparasites. The impact of hyperparasites on disease epidemiology, and the ecological and evolutionary relationships between parasites and hyperparasites remains greatly underrepresented in the current literature. Here, we use laboratory experiments to demonstrate the impact of a mycoparasitic fungus (*Ampelomyces* sp) on key life-history traits of a powdery mildew (*Podosphaera plantaginis*). Further, we determine if there is a signal of coevolution between the parasite and hyperparasite. We show that hyperparasite infection success is governed by pathogen-hyperparasite genotype combinations and that hyperparasite infection has disparate and surprising effects on key pathogen life-history traits. Finally, we combine these laboratory findings with observations of hyperparasite occurrence and pathogen genetic structure across a natural plant pathogen metapopulation. Our results lend insight to the role of hyperparasites in the ecology and evolution of natural disease and will be important for the application of hyperparasites as biological controls in agriculture and human medicine.

P097 Evolution by natural selection to extinction

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Evolutionary suicide is a process in which natural selection causes a viable population to evolve in such a way that it can no longer persist. In this talk I will investigate how the mechanistic underpinning of a discrete-time model affects the possibility for evolutionary suicide. Relevant theory of adaptive dynamics and bifurcations is discussed. The investigated discrete-time population model is derived from a continuous-time resource-consumer model with processes of harvesting resource, mate finding, and egg production. We observe that a population-level multiplicative parameter is affected both by the egg survival probability and harvest effort. Higher survival probability is selected for, which can result in a period-doubling cascade to chaos, and in evolutionary suicide through a global bifurcation. Also higher harvest effort is selected for, but it becomes a scaling factor for the model without qualitatively affecting its dynamics, and demographically stochastic extinction occurs. To conclude, evolutionary predictions should be based on individual-level traits.

P098 A genomic approach to unravel plant-pathogen coevolution in the wild

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Since the beginning of plant domestication plant diseases have caused concern because of their ability to considerably reduce harvest yields. Given the globally increasing food demand, there is more than ever a need to find durable ways of battling plant disease. The success of pathogens is best explained by their tremendous evolutionary potential that enables them to quickly respond to new host resistances. Theoretically antagonistic survival battle between hosts and their pathogens has been proposed to lead to coevolutionary arms race with balancing selection maintaining variation in both host resistance and pathogen infectivity. Despite considerable efforts, the genetic basis of infectivity traits in pathogens is typically poorly understood. To date, effectors (proteins expressed by plant pathogens to aid infection) have become the best described molecular underpinning of infectivity. The main goal of our study is to find a set of candidate effector proteins responsible for different infectivity levels and investigate their natural diversity in the fungal pathogen *Podosphaera plantaginis* on *Plantago lanceolata* hosts occurring in the Åland archipelago. For that purpose, the genome and transcriptome of two well characterized strains *P. plantaginis* have been sequenced and will be subsequently used for genome annotation. Comparative analyses will provide sufficient information with regard to potential effector repertoire that could be further screened on a panel of strains to unravel how these effectors vary across space and time, and how this variation links to realized epidemiological dynamics.

P099 Annotated genes and non-annotated genomes: use of model organism gene annotation information in ecology and evolution research

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Recent advances in molecular technologies have opened up unprecedented opportunities for ecologists and evolutionary biologists to better understand the molecular functions that regulate traits of ecological and evolutionary importance in almost any organism. Nevertheless, reliable and systematic inference of functionally relevant information from these masses of data remains challenging. Here, I will outline how the Gene Ontology (GO) database can be of use in meeting this challenge. The GO provides a highly structured, largely species-neutral source of information on the molecular function, biological role and cellular location of tens of thousands of gene products. Thanks to its species neutrality, the GO is well suited for cross-species use i.e. functional annotation derived from model organisms can be transferred to inferred orthologs in newly sequenced species. In other words, the GO can provide gene annotation information for species with non-annotated genomes. I will also outline some current weaknesses, as well as possible solutions for using GO for enhancing the understanding of molecular function in ecologically relevant species.

P100 Ant larvae as a secret weapon against social parasites

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Queens of socially parasitic ants initiate new colonies by entering colonies of host species, where they begin laying eggs. As the hosts lose their entire reproductive future, it is important to invest in defences both pre- and post-infection. This should lead to the evolution of precise discrimination systems targeting the parasite queens and their offspring. Ant larvae were recently shown to influence brood composition within conspecific nests by cannibalizing eggs. In social parasite systems, host larvae may therefore aid in preventing colony takeover by consuming eggs laid by parasite queens. If this behavior is adaptive, the larvae of host species would be expected to discriminate between eggs of parasite and non-parasite species. To test whether larvae play a role in anti-parasite defense, we compared the rates at which larvae of a common host species (*Formica fusca*) consumed eggs laid by a parasite queen, a non-parasite queen, a nest mate queen, and a conspecific non-nest mate queen. We show that larvae indeed consume eggs laid by a social parasite queen at a higher rate than those laid by a heterospecific non-parasitic queen. We also show that larvae consume eggs laid by a conspecific non-nestmate queen at a higher rate than laid by a nest mate queen. This suggests the presence of also intraspecific social parasitism in our species. Our study is the first to provide evidence that larvae act as players in colony defence against social parasitism, and points toward a role of social parasitism in shaping discrimination behaviour of larvae.

P101 Long term effects of *Pylaiella littoralis* on benthic macroalgal community structure highlights the need for further life-history studies

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Benthic macroalgal species diversity is low in the Baltic Sea but a wide range of life-history strategies are exhibited including sexual and/or vegetative recruitment and very short to year round recruitment periods. A long-term study was performed to investigate patterns of recruitment and explore possible effects of the annual filamentous brown alga *Pylaiella littoralis* on community development. The main settling period of *P. littoralis* in the northern Baltic Proper is during September to April, with an optimum in October-November, but settlement also occurs during May-August, i.e. year round recruitment. Since few other macroalgal species recruit in late autumn, *P. littoralis* was able to monopolize free space available during this period of the year. Despite its annual life-cycle the establishment of *P. littoralis* was still visible in the benthic community after 2.5 years. Most studies on benthic vegetation in temperate seas are conducted during the prime growth season, i.e. late summer. However, as presented in this study, many critical events occur "off season" in the life-cycles of algal species, events that may have a large impact on benthic succession and community composition. This highlights the need for more life-history studies to improve our understanding of the dynamic processes in benthic macroalgal dominated communities.

P102 The influence of arbuscular mycorrhizal fungi and plant genetic variation on a natural plant-enemy interaction

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Arbuscular mycorrhizal fungi can influence plant performance, but details on how they affect the plant's interaction with natural enemies is less well studied. Here, we set out to investigate how a natural community of arbuscular mycorrhizal fungi affects growth of the perennial herb *Plantago lanceolata*, as well as its interaction with the herbivore *Melitaea cinxia*. To test this, we collected seeds from multiple plant genotypes from the Åland Islands. These plants were grown in the greenhouse either with or without mycorrhizal fungi. After 20 days, *M. cinxia* larvae were placed on a subset of plants and allowed to feed for 12 days. Our findings illustrate that plant genotype had a strong impact on plant performance at an early growth stage, whereas the interaction between mycorrhizal treatment and plant genotype became more important during the later growth period. Likewise, the interaction between plant genotype and mycorrhizal inoculation affected caterpillar growth rate, weight at diapause and fat content. Overall, our findings illustrate that plant genetic variation in response to mycorrhizal fungi may play a key role in the ecology of plant-insect interactions, with consequences for their evolutionary dynamics.

P103 Social behavior and gut microbiota in wild red-bellied lemurs (*Eulemur rubriventer*) — in search of the role of immunity in the evolution of sociality

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Microbiota, the microbial communities living in the gut, skin and glands of vertebrates, are the functional link between an individual and the surrounding ecosystem. Mutualistic microbes might play a role in social systems as well, since they are transmitted through social behaviors and claimed to affect host behavior. In addition, individual stress physiology can affect both behavior and microbiota. With a combination of methods from behavioral and molecular research, we took first steps to describe the gut microbiota and its role in the social dynamics of a group-living cooperative primate, the red-bellied lemur (*Eulemur rubriventer*). Gut microbiota was affected by seasonal change, stress hormonal profile and pregnancy, and individuals were found to have a strongly group-specific gut microbial composition. Unlike expected, individual sociality was negatively associated with gut microbial diversity, and this association was possibly mediated by stress. These results emphasize the role of social environment in determining gut microbial composition of adult animals. Since sociality increases gut microbial transmission and gut microbiota is important for health as well as social recognition, social transmission of beneficial microbiota might have played a role in the evolution of sociality.

P104 Measuring background levels of invertebrate herbivory in the tundra

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Invertebrate herbivores cause extensive defoliation during outbreaks in the forest-tundra ecotone, but we know much less about background (non-outbreak) herbivory levels in tundra. Invertebrate herbivory is generally expected to increase with ongoing warming, but how these changes will influence the ecology of tundra communities are difficult to predict. Initially, a basic understanding of the occurrence, intensity and spatial variability of invertebrate herbivory is critical for the development of monitoring techniques. The goal of this project is to quantify leaf damage by invertebrates at different tundra sites using a common study design, to assess: a) the average levels of background herbivory in tundra, b) how variable the occurrence of invertebrate herbivory is at different spatial scales, and c) which plant species suffer most from invertebrate herbivory. To that end, we designed a hierarchical study design that will allow quantification of invertebrate herbivory at different spatial scales. In summer 2015, samples had been collected from 22 sites across the Arctic. Leaf damage on the most abundant plant species at each site will be assessed in a common lab by the same observer. Community estimates of foliar biomass lost to invertebrates will be calculated using biomass samples harvested at each site. This information will increase our basic understanding of the impacts of invertebrate herbivores in tundra ecosystems and will contribute to the development of a general protocol to measure invertebrate herbivory in tundra.

P105 How do temperate tree species fare under current conditions in Helsinki beyond their natural range?

Matthew Robson

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Climate change is expected to threaten some tree species within their current range and provide opportunities for their replacements. The climate in southern Finland may provide suitable growing temperatures for some European temperate species, but the length of the winter, spectral cues related to day length, and late spring and early autumn frosts may still prohibit their success. The European beech (*Fagus sylvatica*) is facing range constriction in central and southern Europe because of warmer drier summers. Assisted migration of threatened populations holding adaptive genes for abiotic stress tolerance is one suggested solution. Finland is outside its natural range, so to test how suitable Helsinki is for beech, we planted a provenance trial containing four populations from different parts of Europe (Sweden, the Alps, Germany, and Spain). The success of these populations over 5 years is charted and the influence of phenology and nitrogen acquisition on their relative performance is revealed. The beech's South American relative, *Nothofagus*, is also promoted as a tree that might be suitable for forestry across northern Europe in the future. So, we tested the performance of four *Nothofagus* species whose origin spanned a gradient of elevation and latitude. We report that after 5 years; *N. alpina* is largely killed by late frosts; *N. obliqua* shows substantial damage to the buds and meristems; *N. pumilio*, surprisingly, appears to suffer damage to the dark, while *N. antarctica* is able to grow well in the trial (without a nurse species) in Helsinki.

P106 The more the merrier: effects of conspecific density on the ecology of a gregarious butterfly

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Conspecific density in early life can have crucial impact on individual's development and life history in wild populations of insects. High density is often considered a potential predictor of infection risk, as higher crowding allows pathogens to spread more rapidly. In some cases, insects have been shown to respond in a predictive adaptive way by matching early life high density conditions with an increase in immune response. However, other species do not display such mechanisms, and depending on the species and life histories, crowding can have different roles in shaping variety of fitness traits other than immunity. The Glanville fritillary is a gregarious butterfly species occurring in Finland in the Åland islands. Adult butterflies lay clusters of 100–150 eggs in the summer, and the offspring disperse very little from the oviposition site, spending all but the last larval instar in gregarious conditions. The last larval instar consists of a wandering solitary stage. In the present study, the last three larval instars were reared in high and low density conditions. After pupation, either immunity, survival to a parasitoid, or both were tested. Adult immune response was further tested on the survivors. Preliminary results show that larvae reared in high density grew faster and bigger compared to the low density ones. In addition, survival to parasitism alone was higher in the high density group. However, no direct effect of density on immunity was detected. These and other findings are discussed in the context of the ecology of the Glanville fritillary butterfly.

P107 Nordic dung beetles - what are they good for?

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Studies investigating the relationship between biodiversity and ecosystem functioning (BEF) are increasingly focused on multiple functions measured simultaneously, rather than individual functions considered in isolation. Whether different species are needed for different functions, how the importance of species identity compares to that of species diversity, and whether individual functions will trade off against each other are questions at the core of current research. Dung beetles offer an ideal model system for answering such questions, as realistic manipulations of dung beetle diversity can be achieved in mesocosm experiments. In this poster, we showcase our recent studies of both individual functions and patterns of multifunctionality.

P108 Evolution of generalist insect herbivores: diet dependent metabolic readjustments in three *Spodoptera* moths

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Why are not all plant-feeding insects specialists due to of co-evolution with specific host plants? Closely related insect taxa with different degrees of polyphagy are ideal for specialist / generalist and evolutionary comparisons sharing a common genetic background, with differences mainly in their feeding ecology, thus avoiding “phylogenetic noise” when comparing phylogenetically distant taxa. In *Spodoptera*, we have three taxa available within a single genus that are diverse in feeding ecology: a broad generalist species *S. littoralis* (SL) and two strains of a less polyphagous species; *S. frugiperda* Corn strain (SF-C) and Rice strain (SF-R). We compared larval performance in a feeding bioassay on artificial diet or maize leaves. On diet, all taxa showed good performance, while on maize the two taxa non-adapted on maize showed lower survival, growth rate, and pupal weight compared to the maize-specialist SF-C. Differential metabolic responses after feeding on either of the two diets were characterized with RNA-Seq analysis of midgut transcriptomes from the 3rd instar larvae. After feeding on maize, the generalist SL showed broader transcriptional changes in the expression levels of digestive and detoxifying enzymes, transporters, immunity, and peritrophic membrane associated transcripts compared to SF strains. The maize adapted SF-C-strain had high background expression level of a group of maize benzoxazinoid detoxifying enzymes, UDP-glucosyl transferases, contributing to its fitness on maize. Altogether, these findings provide evidence for evolution of divergent diet specific remodelling of digestive physiology among these three *Spodoptera* taxa: both going towards specialisation and keeping induction of generalist responses.

P109 Survival of a marine macroalga and its meso-grazer under the predicted future environmental conditions

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Climate change may be the most important driver of both the biodiversity loss and geographical shifts in distribution ranges. Herbivory that creates the trophic link from producers to consumers is one such a crucial ecosystem function. We tested the tolerance of the brown alga *Fucus vesiculosus*, and its meso-grazer *Idotea balthica* to the predicted changes in salinity and temperature. We conducted the tests separately for populations sampled from the entrance, central, and marginal regions of the Baltic Sea, by rearing them with simulated future conditions. Overall, future conditions affected negatively the survival rate of both the host and the herbivore. The marginal and central populations were the most affected by climate change treatment for *F. vesiculosus*, while those from entrance showed high tolerance. The central populations of *I. balthica*'s tolerated better than the entrance and marginal ones the future changes. In the entrance region, *F. vesiculosus* presence may allow an expansion of the isopod from central region so that their link may last despite the disparity in their responses. In the marginal region *Fucus vesiculosus* will suffer more than the herbivore the future changes. The synergy between the loss of habitat and the climate changes may cause the loss of *I. balthica* from this part of Baltic Sea, with consequences for the top-down and bottom-up regulation on the rocky littoral ecosystems.

P110 State-and-Transition Models: Process-based modelling of a system's capacity to generate ecosystem services

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State-and-Transition (STM) models are heuristic ecological models of vegetation dynamics that, in contrast to succession theory, recognize that for a specific set of ecological conditions, anthropogenic and natural factors can drive the system into alternate states, from which transitions are irreversible without active intervention. Alternate states are characterized by specific structural and functional properties that are, in turn, indicators of ecosystem condition. Between-states dynamics is defined by negative (degradation) and positive (restoration) transitions. We demonstrate the use of STMs as a model of ecosystem condition as a result of ecosystem management, and further link ecosystem condition to the capacity of the system to generate ecosystem services (ES). We illustrate the STMs and ES model with a case of silvopastoral use of native *Nothofagus antarctica* (ñire) forest in northern Patagonia, Argentina, and we discuss questions about criteria of ecological sustainability.

P111 Egg thyroid hormones: an unexplored mechanism for maternal effects in birds

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Maternal effects via eggs are a powerful way to influence offspring phenotype and fitness, thus strong selection is expected. Although data from other vertebrates suggests a prominent role for maternal thyroid hormones (TH) on growth and survival, sources of variation in avian egg TH levels and its effects on offspring have been largely neglected. We studied environmental variation in yolk TH levels (thyroxine, T4 and triiodothyronine, T3) in wild great tits (*Parus major*) and its heritability in captive-bred siblings of wild origin. We experimentally elevated yolk TH in a wild population to study their effects on fitness-related traits. Yolk T4 (but not T3) concentration was correlated negatively with temperature, positively with laydate and increased with laying order within clutches. Interestingly, T3 (but not T4), was heritable ($h^2 = 0.25$). Experimental yolk TH elevation had a sex-specific effect on offspring growth: it increased the growth of male nestlings, but decreased growth in female nestlings, relative to controls. Yolk TH elevation had no effect on behavior, metabolic rate, hatching and fledging success. These studies demonstrate, for the first time in a wild bird species, the biological relevance of variation in maternal thyroid hormones in egg yolk on offspring development, and open a new, interesting avenue for further research in the field of hormone mediated maternal effects.

P112 The leafcutter lunchbox: Linking digestive physiology and foraging behavior of four Panamanian leafcutter ant species

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Life in societies has made ants dominant consumers in habitats across the planet. The social lives of ants are made possible by unique digestive adaptations that enable food sharing among nestmates. When foraging, these adaptations facilitate transportation of resources both externally in their mandibles and internally in three connected digestive organs (crop, midgut and hindgut), each with different implications for sharing and personal use. Leafcutter ants inhabit tropical rainforests where foragers cut fresh vegetation and carry it in their mandibles back to colonies where nestmates convert the substrate into compost used to produce fungus for food. However, many foragers return without carrying any vegetation, which has been assumed to be wasted foraging effort. We tested an alternative hypothesis, that these 'unladen' foragers are actually transporting liquid resources. In a Panamanian rainforest, we studied four species of leafcutter ants and found high frequencies ($\geq 41.6\%$) of unladen returning foragers and used dissections to determine if these foragers transported liquids internally in their crops. While unladen foragers were not likely to transport liquids, our results showed that foragers tend to leave colonies already having full midguts. We hypothesized that full midguts function as 'lunchboxes' that are depleted according to work performed outside the colony. We thus tested depletion rates by experimentally manipulating foraging distance, load mass, and leaf-cutting activity in laboratory colonies of the leafcutter ant *Acromyrmex echinator*. The transportation of a heavy load resulted in significantly greater depletion of midgut liquids, a result linking digestive physiology, nutrition, and social organization.

P113 Geographic variation in predation pressure toward warning coloration of an aposematic moth *Arctia plantaginis*

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The wood tiger moth (*A. plantaginis*) is an aposematic species of which hind wing coloration can be white, yellow, orange or red combined with variable amount of black pigmentation. Throughout its Holarctic distribution both monomorphic and polymorphic populations exist. We asked whether differences in frequency dependent selection by predators could explain geographic differences in warning signals. We recorded local passerine and Lepidoptera communities during large-scale field experiments in four geographic locations (in Estonia, Scotland, Georgia and Southern Finland) where artificial moths of white, yellow and red hind wing coloration were exposed to natural predators. In Estonia white morphs, in Scotland yellow morphs and in Caucasus red morphs dominate whereas in Finland white and yellow morphs coexist. Predation pressure differed between the populations and natural selection seemed to favor locally common morphs in Scotland (yellow) and in Georgia (red) as expected according to the theory of aposematism. However, in Finland and Estonia we did not find evidence of positive frequency dependent selection. In addition to the local wood tiger moth population, we found some evidence that the structure of predator populations as well as local alternative prey communities influence the strength and direction of selection contributing to warning signals.

P114 Spatial composition of females' preference of the Glanville fritillary butterfly (*Melitaea cinxia*)

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Nutritional conditions during development can have a great impact on individual life-history, and subsequently influence individual survival. Lepidopteran larvae, especially during the early stages of their development, are very sessile, and therefore their survival relies highly on their mother's oviposition site decision. I am utilising the Glanville fritillary butterfly (*Melitaea cinxia*) and its two larval host plants, *Plantago lanceolata* and *Veronica spicata*, in Åland Island as a study system. I aim to understand the potential environmental factors that determine females' oviposition preferences and how this influences her offspring survival. I will link within patch information on environmental data, such as host plant density and quality, and on microclimatic conditions, such as temperature and precipitation, with localities of egg and larval groups found in the wild. In the first season of my PhD, I gathered information from 19 local populations and more than 120 larval groups. I will here present the preliminary results of the analysis of the data we collected and discuss how female oviposition preference influences the survival of her offspring and how this may subsequently influence the population dynamic in the wild.

P115 Predation risk on European adders: an experiment with three color morphs

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European adders (*Vipera berus*) exhibit sexual dichromatism, whereby females are generally brownish and better camouflaged while males are light grey especially during the mating season. Both sexes have a dorsal zigzag pattern that acts as an aposematic signal towards visually hunting predators. Adders also have a melanistic (black) color morph which is not sex-related and appears more common in mountaneous areas and other colder environments. Melanistic individuals may enjoy a thermoregulatory advantage over normally-colored adders, but they also lack the aposematic zigzag pattern that may offer protection from predators. Experiments and observations suggest that melanistic adders suffer from higher predation risk, but some studies using black and grey adder replicas have found no difference in avian predation risk between the color morphs. We conducted an experiment in the outer parts of the Archipelago Sea, SW Finland, comparing avian predation risk of black, grey zigzag and brown zigzag morphs. Ten adult-sized plasticine adder replicas of each color were placed on altogether 20 study islands for an average period of 7.7 days. The experiment was repeated in spring (May), midsummer (July) and autumn (September) to examine seasonal changes in predation risk. Beak marks on plasticine were used to identify bird attacks. The overall risk of attack on replicas was 4.6 %. There was no obvious difference in odds between different color morphs or between seasons but predation risk increased both with exposure time and increasing observations of predatory birds on the study islands. Corvids and gulls were the most common birds observed.

P116 Interactive effects of heat waves and pollution on freshwater snail, *Lymnaea stagnalis*

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Extreme summer temperatures have become more frequent in central Europe increasing the stress load in many ecosystems. While heat waves *per se* can have enormous impacts on shallow water bodies, the increased temperature stress might make the organisms more susceptible to other stressors. In this experiment we studied whether temperature stress affects organisms' ability to tolerate micropollutants. We subjected great pond snails (*Lymnaea stagnalis*) to either clean water or a mixture of 17 micropollutants commonly observed in water bodies. After an acclimation period, half of the snails from each chemical treatment were subjected to a 8-days heat wave, followed by a recovery period. The control snails were kept in constant temperature throughout the experiment. We assessed the impact of micropollutants and heat waves on snail physiology, life history and immune defence after the heat wave. To quantify any delayed impacts, we also assessed these parameters after 8 and 16 days of recovery. Heat wave led to increased metabolism with higher respiration rates, growth rates and egg production. While micropollutants alone had only subtle effects on snail fitness, reduced food consumption and lower reproductive input was recorded when micropollutants were combined with high temperature. However, micropollutants increased snails' immune defence during heat wave. The results suggest that heat waves in combination with other stressors can have unexpected ecological consequences.

P117 Experimental manipulation of dietary arsenic levels in great tit nestlings: effects on growth and survival

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The main objective of this study is to explore if environmentally relevant arsenic (As) levels would affect growth and survival of great tits (*Parus major*). Nestlings were orally dosed with As in three experimental groups (Control, Low and High As groups: 0, 0.2 and 1 µg/g/d) and were compared with those living in the vicinity of a copper-nickel smelter in Finland, an As source (Smelter group, 0 µg/g/d). Brood size, number of fledglings, body size (wing, tarsus, and head length and body mass) and growth rate were measured. Faeces were collected to measure As concentrations, and dead nestlings were necropsied to investigate As concentrations in liver, bone and feathers. Faecal As concentrations were significantly higher in the Smelter and High groups, followed by the Low group, and finally the Control group with significantly lowest levels. Arsenic levels in liver, bone and feathers were significantly higher in the High As group, followed by the Low As and Smelter group with similar levels among them, and then the Control group with significantly lower levels. Despite the marked As accumulation, few effects were found on growth and survival. The As levels were below the toxic concentration able to produce effects on growth and survival. Nestlings from the Smelter group showed significantly lower brood size and fledging success. These effects are likely related to decreased food quality/quantity for these insectivorous passerines at the metal polluted environment, showing the importance of secondary pollution effects on birds.

P118 Even plants do it: risk sensitive behavior in an annual plant

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The response of organisms' to variability in resource availability can depend on ecological circumstances. This has been investigated for animals under Risk Sensitivity Theory, but remains unexplored for plants. Plants are known to allocate root growth differentially between patches that differ in mean resource availability. Here we present a test of whether root growth allocation is sensitive to temporal variability in nutrient concentration using pea plants as subjects. We estimated the relationship between nutrient concentration and proxies for fitness (e.g. seed mass) and used this function to predict root allocation strategy under different levels of variability. We then grew split-root plants with one root sector experiencing fixed and the other variable nutrient concentration, equating mean levels, repeating the tests at various combinations of nutrients' mean and variance. The function linking fitness proxies to nutrient concentration was concave, leading to the expectation that variability should decrease fitness under all our experimental conditions. However, plants switched from risk proneness at low mean nutrient availability to risk aversion at high mean nutrient availability. This switch in the sign of risk preferences fits predictions frequently made in animal behavior, but we use our direct measures of fitness proxies to elaborate plant specific theoretical problems.

P119 A transplant experiment of two birch species (*Betula pendula* and *B. pubescens*) along a latitudinal gradient of their natural distribution range

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Transplant experiments offer a powerful method for testing the response of tree species and their associated communities to future climatic changes as translocation towards lower latitudes mimics the shift to future warmer climatic conditions and higher herbivore pressure. We have designed a multi-site common garden experiment to study the acclimation and adaptation capacity of two birch species to the changes in their growth environment. The common gardens with identical set up will be established in 2016 on three locations (Florence, Italy 43°, Punkaharju, Finland 61°, Kolari, Finland 67°), each including two sites of contrasting soil fertility. The plant material has been cloned from trees randomly chosen from *B. pendula* and *B. pubescens* populations growing in North Finland (Kittilä 67°), South Finland (Punkaharju 61°) and North Italy (45°). Due to higher inter-annual variation in growth conditions in North, we expect that northern birch populations have higher acclimation capacity than southern populations in both species. The investigated plant parameters will include plant growth, architecture, leaf traits such as herbivore resistance, genetic markers and leaf litter decomposition and N release. As the effects of soil and day length cannot be separated from the effects of warmer climate in transplant field experiments, we will test the effects of these confounding factors on the growth of the saplings in separate laboratory experiments in the spring 2016. To make good use of a large field trial we are interested in co-operation and during this conference seek for scientists interested in complementing our research approach.

P120 Unravelling top-down versus bottom-up impacts of cormorants on coastal algal communities

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Increasing populations of piscivorous cormorants (*Phalacrocorax carbo sinensis*) have been a concern for coastal ecosystems in the Baltic Sea. Previous studies have shown that cormorants can have both bottom-up and top-down effects: guano runoff from colonies is high in nitrogen and increases filamentous algal growth, while fish predation (1 kg day⁻¹ breeding pair⁻¹) leads to decreased fish populations around colonies, potentially causing a trophic cascade and higher grazing pressure on algae due to higher herbivore abundances. In this study, we measured the importance of these impacts on algal communities experimentally by comparing algal recruitment, growth, and herbivory in herbivore exclusion, fish exclusion, and open control cages around colony and control islands. The foundation species *Fucus vesiculosus* had lower recruitment while filamentous algae had higher recruitment near colony than control islands, likely due to increased nutrient enrichment. Herbivory on some species increased near colonies, indicating that top-down colony effects also occur, but these do not affect all species equally and also vary among years. Cormorants can thus indeed modify lower trophic levels through both top-down and bottom-up processes, though these effects are mediated by local biotic and abiotic factors.

P121 Host-parasite interactions of Icelandic rock ptarmigan and their potential impacts on population dynamics

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The population density of Icelandic rock ptarmigan fluctuates in cycles with peaks c. every 10 years. We investigated how the ptarmigan parasite community acts and parasites relate to ptarmigan age, body condition, and population density. We collected 632 ptarmigan in northeast Iceland 2006 - 2012. Out of those, 630 (99.7 %) birds were infected with at least one parasite species, 616 (98 %) with ectoparasites and 536 (85 %) with endoparasites. The main factors associated with variation in the parasite community were host age and time. Juvenile birds carried overall more parasites than adults and there were distinct annual fluctuations of parasite measures. Ptarmigan population density was associated with the coccidian parasites *E. muta* and *E. rjupa* in juvenile birds. Annual aggregation levels of these eimerids fluctuated inversely with prevalence. Both prevalence and aggregation of particularly *E. muta* tracked ptarmigan population density with a 1.5 year time lag. The cause of the time lag could be explained by the host specificity of the eimerids, host density dependent shedding of oocysts, and their persistence in the environment from one year to the next. Further, ptarmigan body condition was negatively affected at high intensities of *E. muta* and *E. rjupa* marginally, an indication for their pathogenicity. Our findings support the conclusion that *E. muta* and *E. rjupa* through time-lag in prevalence with respect to host population size and by having a negative impact on body condition in juvenile birds could act to destabilize ptarmigan population dynamics in Iceland.

P122 Sex differences in thermal plasticity of development time: a meta-analysis in insects

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Temperature affects nearly all major aspects of organisms' life. In ectotherms, metabolism rates are widely known to accelerate, body sizes to decrease and development times to shorten with temperature, to name just a few responses. Nevertheless, sexes often differ in the degree of plasticity they exhibit in response to environmental variation. In the case of insects, sex differences in phenotypic plasticity have been reviewed for body size (females generally more plastic), but no comprehensive analyses are available for other major life-history traits. In this study, we extend the knowledge on sex differences in phenotypic plasticity by conducting a meta-analysis of sex differences in thermal plasticity of development times. For this purpose, we made use of a broad variety of case studies in which development time of males and females had been reported for multiple subsets of individuals reared at different temperatures. Data on more than 100 species of a wide phylogenetic coverage allow us to make broad generalizations about sex differences in thermal plasticity of development duration.

P123 Phylogenetic comparative studies on the ecology of moths

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The increasing availability of reliable phylogenies and the development respective analytic tools has opened the road for phylogenetic comparative studies. Such studies provide opportunities for rigorous tests of various long-standing hypotheses in evolutionary ecology and beyond. Curiously, the huge potential of insects in comparative studies has not received the attention it deserves. We will report results of our comparative analyses on ecological traits in the Lepidopteran family Geometridae. In particular, we have provided a confirmation to the long-standing hypothesis that larger herbivores tend to be less specialised than smaller species. Our studies on longevity with about a hundred of geometrid species have revealed a surprisingly weak phylogenetic signal, and limited among-species and between-gender differences. Longevity was found to correlate positively with body size but not with expected ecological predictors suggesting the primacy of physiological factors over ecological ones as determinants of the value of this trait. In contrast, the gradation from income to capital breeding, reflecting the importance of adult derived resources in reproduction, is correlated with a number of ecological traits suggesting a potential of this continuum to form an informative ordination axis of life histories. Moreover, we have shown that capital breeding moths tend to have more variable population densities, and are more prone to display regular cyclicity than income breeders, with the causal mechanisms likely to be found in behavioural regulation of population densities.

P124 Does the activity of hikers and grazing animals enhance a range shift of alpine plants toward summits?

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Resurvey of old plant distribution data can provide valuable information about how the plant communities have changed, a topic which is of great interest due to the last decades of climate change and land use changes. Range shifts towards higher altitudes are observed for alpine vegetation in mountainous areas all over the world during the last five to ten decades. A correlation in time between the observed range shift and climatic changes has led to an expectation of climate as the driving factor, while other factors and their interactions with climate have received less attention. One factor which might affect species distribution, both directly and in interaction with climate, is transport of organic material, including seeds, by hikers and herbivores. We investigated the interactions between climate change, hiking activities and amount of grazing animals on summits in three mountainous areas in the Scandes through a resurvey of historical data on maximum altitude for all observed vascular plants on different summits. The time span between the first and the last observation on each summit varied between 80 and 120 years. The results proved a range shift towards higher altitudes in all three mountain areas, as well as an increase in species richness on most summits. Differences in hiking activity or grazing intensity between mountains did not affect the amount or magnitude of elevation range shift. Our results therefore indicate that the consistent upwards range shifts observed in the Scandes are not due to changes in land use.

P125 A new Swedish e-Infrastructure for Biodiversity and Ecosystems Research

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Herein is presented a new national Swedish research infrastructure that will develop and run web-based services enabling access to, and analysis opportunities to researchers using large quantities of historical and recent biodiversity and environmental data addressing ecological, evolutionary and environmental models and forecasts. The services offered are developed in collaboration between five Swedish universities and three governmental research institutes hitherto individually supported by the Swedish Research Council: GBIF-Sweden (Global Biodiversity Information Facility), Swedish LifeWatch, WRAM (Wireless Remote Animal Monitoring), CAnMove (Centre for Animal Movement Research) and RINFI (Research Infrastructure for National Forest Inventory). GBIF-Sweden ranks second in the world by numbers, connecting 53 million biodiversity data from specimen and observation databases to the international GBIF repository that altogether provides access to 580 million species occurrence records worldwide. Swedish LifeWatch presents 50 million georeferenced species occurrence data in the Analysis portal where a host of environmental parameters may be added and data analysed. WRAM and CAnMove publish in excess of 100 million animal positions from remote monitoring projects using sensors to position animals. RINFI covers forest inventory records and analyses from most of the 20th century until present. The new infrastructure aims to consolidate and develop existing services, and to extend sources and methods within four major fields: 1. increased access to historical data, 2. reference libraries and methods integrating DNA-analysis into ecosystems analysis, 3. joining significant national environmental survey systems into a common access system and 4. incorporating imaging techniques into the available toolbox for collecting and analysing marine data.

P126 Effects of acute vs. long term salinity changes on an euryhaline spionid polychaete

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The spionid polychaete *Pygospio elegans* is a common estuarine species that lives on intertidal mudflats, and is thus exposed to frequent salinity fluctuations. Additionally, it shows a broad salinity tolerance occurring in a range from full marine (33 PSU) to brackish (5 PSU) habitats. However, it is unknown how *P. elegans* is able to acclimate to different salinities. We investigated volume regulation in *P. elegans* in response to acute salinity changes. In addition, we studied the long-term effects on survival and reproduction of the worms when exposed to different salinities. *P. elegans* originated from Herslev (Denmark) with an average salinity of 15 PSU and were exposed to salinities of 5, 15 (control) and 30 PSU. We observed a significant increase in body volume of *P. elegans* when transferred to lower salinity (5), while no change in volume was detected when worms were transferred to higher salinity (30). The effect was reversed within a week, but only 60% of the worms survived the treatment. In contrast to the acute experiment, only low mortality was observed after 6 weeks incubation at low salinity (5), probably due to a gradual acclimation. Hence, *P. elegans* is more sensitive to abrupt salinity changes. Moreover, a lower percentage of both asexual reproduction and reproductive males were found at low salinity in comparison to the other treatments indicating that 5 PSU was below the optimal salinity tolerance range of *P. elegans*. Hence, *P. elegans* can better cope with increasing salinities, probably due to its marine origin.

P127 Fallowing strategies to promote different aspects of pollinator diversity in farmland

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Establishing fallows is a potential measure to promote pollinator insects in intensively cultivated agricultural landscapes. We studied the impacts of fallow type and landscape structure on species richness, abundance and trait composition of bumblebees and butterflies in perennial fallows in Southern Finland. The studied species traits were niche breadth and dispersal capacity, which are thought to be the key determinants modifying species' sensitivity to environmental changes. Pollinator counts were conducted in two types of fallows, long-term grassland fallows and short-term meadow fallows, in four contrasting landscape types with different cover of forest and perennial grasslands. Butterflies benefited most from long-term grassland fallows. Species richness within the group was highest in forested landscapes. Butterfly species with narrow habitat breadth and poor dispersal capacity were associated with grassland-rich landscapes. Bumblebees were less dependent on landscape context than butterflies. Bumblebee abundance was highest in short-term meadow fallows. However, diet breadth was narrower in long-term grassland fallows. The results show that fallowing strategies should be differentiated by the landscape character and by the main conservation objective. Short-term meadow fallows attract generalist bumblebees in production landscapes and may contribute to associated pollination service. Long-term fallows in forested landscapes are particularly suitable for many species of butterflies. For the conservation of habitat specialists and less mobile species, long-term fallows in landscapes rich in perennial grasslands are the best option. Our results provide no justification for exempting forested regions or farms with high grassland cover from the ecological focus area requirement under the current agri-environmental policy.

P128 Environmental thresholds and factors structuring biological communities vary seasonally in high-latitude streams

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Understanding the degree to which communities vary as discrete entities or comprise parts of a continuum has important implications for conservation practices. In stream ecology, it has traditionally been proposed that local habitat conditions pose a strong environmental filter resulting in predictable community types. However, recent studies on streams have demonstrated continuous rather than discrete communities along environmental gradients. Our aim was to examine the continuity of stream communities by using functional traits of benthic macroinvertebrates. Data was collected from 50 streams draining into the River Tenojoki (70°N, 27°E). By using multivariate regression trees and ordination methods, we analysed the relationships of taxonomic and functional structure of macroinvertebrate communities to various in-stream environmental factors. Using previous empirical studies and the environmental filtering paradigm as a background, we hypothesised that taxonomic communities should vary continuously over environmental gradients, whereas functional communities should form discrete community types according to specific habitat conditions. As stream characteristics vary between seasons, we also asked if this had an effect on the communities among seasons. Our results suggested that the variation in the importance of environmental factors among seasons combined with the high heterogeneity of habitats precludes the formation of clear taxonomic and functional community types in northern streams. Therefore, conservation efforts should focus on covering varying environmental conditions to embrace all aspects of the communities. However, as responses of individual traits to environmental factors were found, more research on the functional structure of macroinvertebrate communities is needed for developing trait-based biomonitoring tools for high-latitude streams.

P129 Pelagic food-web indicators accounting for species interactions respond to multiple pressures

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Facing implementation of the Marine Strategy Framework Directive, aiming to reach good environmental status of the marine environment, pelagic food-web indicators are crucially needed. The Baltic Sea pelagic food-web is characterized by strong trophic links between cod (*Gadus morhua*), and its prey sprat (*Sprattus sprattus*) and herring (*Clupea harengus*). Further, these fish populations are affected by density-dependence and changing environmental conditions. Since food-web indicators are aimed to describe the functioning and structure of food-webs, both interactions within and among species and external pressures should be considered when developing indicators. Still, this is rarely done. In our study we apply Multivariate Autoregressive (MAR) models to identify how pelagic fish indicators relate to fishing, climate and eutrophication, while accounting for the linkage between indicators caused by species interactions. We analyzed two sets of indicators based on monitoring data from the Bornholm and Gotland Basins: abundance-based indicators of piscivores and zooplanktivores (cod, and sprat and herring, respectively) and size-based indicators (biomass of large predatory fish (cod > 37 cm) and biomass of small prey fish (sprat and herring < 10 cm)). For both types of indicators, both predator-prey loops and density-dependence contributed essentially in explaining temporal variation in the indicators. Our results suggest that indicators respond to multiple pressures acting simultaneously rather than to single pressures. Variables related to the manageable pressures fishing and eutrophication, as well as to the prevailing hydrological conditions influenced by climate, are all needed to explain the changes in these food-web indicators over the last three decades.

P130 Rodent species and sex determination from single fecal pellets using near-infrared reflectance spectroscopy (NIRS)

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In arctic and sub-arctic ecosystems, small rodents are keystone species affecting plant community biomass and composition, and supporting multi-species predator guilds. While small rodents are central for tundra ecosystem functioning and resilience, effects of warming climate have been associated with the collapse and changes in their population dynamics. With the ongoing acceleration of environmental change in northern terrestrial ecosystems, large-scale monitoring efforts become ever more important. Yet methods for identifying small rodents' species and their key demographic parameters are laborious and costly. Non-invasive, more time and cost-effective methods are thus highly needed. In the current project, we set out to test whether readily available traces of small rodent presence, fecal pellets, can be used to identify species and sex using near-infrared reflectance spectroscopy (NIRS). We used fecal pellets from nearly 500 trapped rodent individuals from a sub-arctic rodent guild of five species and created a calibration set. We also conducted a weathering experiment in order to test if fecal scans of pellets being exposed to weeks of weathering still provide information on species identity and sex. Finally, we assessed if diet was distinctly different between the small rodent species, possibly confounding the identification of species and sex and hence reducing the prediction accuracy. Our results indicate that NIRS is able to accurately predict species identity from single rodent pellets. Success in sex determination within species was species dependent. These results indicate a promising role of NIRS for research and monitoring of small rodents in arctic and sub-arctic ecosystems.

P131 Red squirrels decline in abundance in the boreal forests of Finland and NW Russia

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Large scale studies are needed to reveal patterns and trends that on smaller scale might be masked by local variation and stochastic processes. This, together with global warming and loss of biodiversity, highlight the need to study population trends of even those species that so far have been of least concern. Here, our aim is to study the spatial patterns and temporal trends of red squirrel populations on a large scale with snow track census data from Finland and south-west Russia. The project is collaboration between researchers at University of Turku, Natural Resources Institute Finland, and researchers from Russia and Finland on the European Boreal Forest Biodiversity (EBFB) database project. The data covered 17 years and about 3500 km from west to east and 1700 km from south to north. We used a hierarchical model that allowed for spatial correlations. The results suggested that squirrel populations have declined in both Finland and Russia, and estimated population growth rates show spatial synchrony over large scale. The density of squirrel tracks decreased towards northern and eastern edges of the study area. We also calculated predictions to year 2017, i.e. 5 years after the end of the time series, and found that the northernmost regions have the greatest risk to decline very low.

P132 Angling-induced selection in Eurasian perch *Perca fluviatilis* and brown trout *Salmo trutta*

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Consistent individual differences (CIDs) in behaviour are of interest to both basic and applied research. Any selection acting on them could affect not only evolution of behaviour but the evolution of any co-varying trait. It has been suggested that CIDs in the behaviour of fish might explain individual differences in vulnerability to fishing. We present data from a series of experiments assessing CIDs in the behaviour and their linkage with the vulnerability to angling in both wild-collected and captive-reared Eurasian perch and captive-reared brown trout. Both perch and brown trout displayed individually consistent behaviour across time and context. Our results from perch studies show that boldness, as it is defined to reflect behaviour under predation threat, may not be related to vulnerability to angling in this species, while large size acts as the most obvious trait exposing fish to angling. However, perch captured early in order in ice-fishing showed active exploration behaviour also in experimental groups suggesting that exploration and group leadership expose perch to angling. Also highly explorative brown trout were more vulnerable to experimental fly-fishing than less explorative trout, while enriched hatchery rearing decreased the exploration tendency of trout in comparison to standard rearing. In conclusion, angling was demonstrated to impose selection especially on explorative behaviour that correlated with standard metabolic rate in perch, but was not clearly linked with life-history traits. Due to the state-dependence of behaviour, evolutionary effects of angling are more difficult to predict than those of size-selective harvesting and still require further research.

P133 Function of the eye mask

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Animal coloration can have several functions including intra and interspecific signalling, hiding from prey or predators, or adapting to the abiotic characters of the environment. The coloration of some animals includes an eye mask, the markings running through the eye. The function of these markings is suggested to be connected with concealing the eye, acting as a warning signal, dealing with intraspecific communication and protecting the venom glands of snakes from the solar (UV) radiation. Here we assess the role of the eye mask from the perspective of hiding the snake from predators or prey animals, and whether the eye mask had some function as a warning signal or enhancer of the snake's vision. Based on literature review we determine presence of the eye mask among 99 species around the globe. Among the biological and ecological factors possibly explaining the existence of the eye mask we recorded: activity pattern (diurnal or nocturnal), preferred hunting strategy (active or ambush), habitat according to its openness and the possible venomousness of the snakes. Supporting that the eye mask function as camouflage from prey it was more commonly found among snakes with ambush hunting strategy than those that forage in a more active manner. We did not find any significant connections between preferred habitat type, activity pattern or venomousness of the species and existence of the eye mask. Thus our result does not support the signalling, radiation protection or vision enhancing functions of the eye mask.

P134 Resource partitioning in a changing subarctic climate

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Over the last 20 years perch abundance in the Pasvik watercourse has increased immensely, presumably because of a rise in water temperature due to climate change. In this study, resource partitioning between large sparsely rakered (LSR) whitefish (*Coregonus lavaretus*) and perch (*Perca fluviatilis*) in the littoral zone of two lakes in the Pasvik watercourse was studied. Stomach content and stable isotope ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) analyses were done to determine short- and long-term diets, respectively, of all four populations. The diets of LSR whitefish and perch differed considerably. Diet and isotopic niche overlaps between the two species in Lake Tjærebukta were low (12% and 20.6%). In contrast, in Lake Skrukkebukta the diet and isotopic niche overlaps between LSR whitefish and perch were relatively high (53% and 48.5%). The low overlaps in diet and isotopic niches were a good indication of resource partitioning, on both short- and long-term, between LSR whitefish and perch in the two study lakes. Differences in feeding strategies between the two species, and ontogenetic dietary niche shifts of perch likely strengthened the resource partitioning in both lakes. Resource partitioning was more intense in Lake Tjærebukta than in Lake Skrukkebukta. Potentially this was due to a persistent high density of perch with ongoing inter-specific competition over the last 20 years in Lake Tjærebukta. In contrast, in Lake Skrukkebukta the perch density has continued to increase over the same time interval leading to increased competition with LSR whitefish, which has led to the less distinct division in resources, until stabilized.

P135 Stimulating scientific attitudes in school children through playing

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Didactic of Science (DS) aims to develop scientific attitudes and to recognize and understand our surroundings. Thus, the educational process should be dynamic, flexible, and should integrate different subjects. The conventional methods are not necessarily the most appropriate to achieve this objective. Herein we report on an original DS project with a two months science activity (October to December 2015) in the IPPE (club after school) of Nummenpakka Koulu. The activities were held weekly with children from first to second grade (7–9 years old). We stimulated their skill in *observation* which is the most important a priori to the scientific question. To do this, we developed games and art activities. During the sessions we invented games that integrated and caught the attention of more than 30 children. They were able to create own stories, perceived their environment blindfolded, described the landscape through numbers, observed living creatures, asked questions, took own decisions, solved problems, ran into the forest, recreated animal behaviours, and laughed. In every session, reflexions together with the children about their experiences were made. Our educational plan was always adapted to the interests of the children. Our results showed that with games, art, and non-formal education it is possible to start developing some scientific attitudes. At the same time, these attitudes also help to value what we observe, where we are, and with whom we live.

P136 Who mates with whom? Compatibility issues in fungi

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Parasite strains under coinfection are generally expected to compete for the same limited resources provided by the host. However, for many parasites coinfection is also the pre-requisite for sexual recombination, as the close contact between pathogen genotypes in the context of coinfection allows the generation of novel genetic combinations. Thus, the presence of different strains infecting the same host increases the likelihood for the evolution and emergence of new variation in pathogenicity. To date, the occurrence and frequency of outcrossing in pathogens has remained one of the major unresolved questions in disease biology. We will study how coinfection and outcrossing are linked in the *Podosphaera plantaginis* - *Plantago lanceolata* pathosystem. The powdery mildew *P. plantaginis* is an obligate pathogen naturally infecting the host plant *P. lanceolata*, the ribwort plantain. *Podosphaera plantaginis* is a homothallic fungus (i.e. capable of haploid selfing but also of asexual reproduction and outcrossing). Coinfections are common such as in the Åland Islands where two kinds of strains have been detected: the "Super strains" (i.e. widely distributed and whose presence is stable over the years) and the "Normal strains" (i.e. locally distributed and whose presence varies from one year to the other). We will combine inoculation experiments with molecular analyses and mathematical modeling to test whether this difference is due to different mating choices which could impact on short or long term fitness of infection (i.e. lesion development, overwintering). Resolving this key question "Who mates with whom" is needed to understand the coevolutionary processes of infectious diseases.

P137 Linguistic microevolution: Finnish dialects in population biology framework

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For a decade, lineaging of language families has been studied with phylogenetic approach, i.e. as linguistic macroevolution. We widen the scope of "language evolution" to include also within-language processes. In this approach - which we call linguistic microevolution - we apply the framework of population biology by studying dialectal structure and dynamics of Finnish language with population genetic methods. We also incorporate an ecological perspective to dialect formation by asking how biogeographical aspects, alongside with cultural and administrative issues have moulded the dialectal landscape of Finland. Until now, "language ecology" has referred only to social environment of language speakers, but we address that speaker populations are just as dependent on the environmental resources and dispersal restrictions as other species. Indeed, multiple regression model (MRM) indicated that dialectal differences co-occur not only with cultural but also with environmental differences. We then used Principal Coordinate analyses to locate the environmental and cultural characteristics specific to each dialectal area. MRM showed also that dialectal differences were not caused by geographical distances, but if taken into account also administrative history, there was an effect of geographical separation. We studied this further by creating a cost-distance map over Finland to estimate how the water routes, forests, edgars or routes in 16th century promoted or restricted human dispersal, and studied the dialectal differences and "linguistic flow" (*sensu* gene flow) in the light of this. In general, we will give an overview on how population biology can be applied in dialectal studies.

P138 River specific genetic diversity of *Margaritifera margaritifera* with respect to host fish and population size

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Effective conservation approaches for endangered species require integration of ecological and genetic information. Low genetic diversity is a matter of concern, as it may reduce the ability of the species to adapt to environmental changes. We examined the genetic structure and diversity of 21 *Margaritifera margaritifera* populations located in Finland, Sweden and Norway. We used *COI* sequences and microsatellites to generate genetic information. From 18 observed *COI* haplotypes 7 were restricted to certain populations. The number of observed haplotypes per population ranged from 1 to 10. An average of 5.2 alleles was observed for the 9 microsatellite loci. Hierarchical analysis of molecular variance revealed that 0% of the genetic variation was among drainage systems, 31% among populations within drainages, and 69% within populations. Pair-wise F_{ST} values spanned a wide range, 88% of differences in all pairwise comparisons were highly significant. The results of the Mantel test confirmed that there was no isolation by distance. A regression model was fitted to the four response variables, mean observed and expected haplotype (H) and allelic (A) richness, using the host species and the mussel population size as predictor variables, assuming asymptotic increase in the response variable with the increasing population size. *M. margaritifera* of salmon rivers had a higher asymptotic haplotype and allelic richness than *M. margaritifera* of trout rivers ($p < 0.05$). Allelic richness was at its asymptotic level already in the smallest observed N of < 10.000 while haplotype richness reached its asymptote with N around 50.000 mussels for both species.

P139 Plant Resistance Ecology: The influence of plant resistance on biological control of herbivores

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With the high regulation of insecticide use in crop production, breeding for more resistant plant varieties has regained an important position in insect pest control. Yet, changes in the host plant quality can also impact fitness and performance of higher trophic levels. Parasitoids and insect predators are widely used as biocontrol agents especially in organic grown crops. That raises the question of the importance of plant resistance for ecosystem services. It is still poorly understood how and to what extent the direct and/or indirect exposure to enhanced plant resistance traits of third ecological players alters interaction networks in the field. The framework for this project is to test whether and how variation in plant resistance modulates direct and indirect effects of biological control. The research questions are addressed in the context of the insect community on woodland strawberry (*Fragaria vesca*) with a focus on the Strawberry Leaf beetle (*Galerucella tenella*) and its associated parasitoid *Ascecodes parviclava* (Hymenoptera: Eulophidae). The high within-species genetic variation in resistance in strawberry and the access to a collection of 100 wild *Fragaria* clones in a common garden provides an unique opportunity. It allows to systematically study the magnitude and direction of changes in interactions among the species depending on the resistance level of the host plant. The insights gained throughout the project may open up novel opportunities for breeding strawberry varieties that facilitate improved biocontrol of herbivores.

P140 Maintained functional diversity in benthic communities in spite of diverging functional identities

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Ecological studies based on time-series often investigate community changes centered on species abundance or biomass but rarely expose the consequential functional aspects underlying such changes. Functional diversity measures have proven to be more accurate predictors for ecosystem functioning than traditional taxonomic approaches and hence gained much attention. Studies analysing the functional implications behind decadal changes of entire communities are however rare. We studied zoobenthic communities of two habitats, sheltered and exposed, of a coastal system subject to contrasting changes in community composition over the past four decades. Besides eutrophication and climate-related impacts, the system has been invaded by a non-native polychaete, *Marenzelleria* spp., altering functional properties of the communities. The functional dispersion (FDis) metric was used as a measure for comparing the functional diversity of the contrasting habitats, with special focus on the role of *Marenzelleria*. We highlight changes in the communities' functional identity, expressed as community-weighted means of trait expression (CWM) and investigate the relationship between taxonomic and functional changes. Despite contrasting community developments, the FDis in both habitats remained similar and increased with the introduction of *Marenzelleria*. Although showing maintained functional diversity across time and space, the functional identity of communities changed irrespective of taxonomical differences. Examples include alterations in palatability proxies, feeding position and sediment transportation types, indicating changed functionality of zoobenthos in coastal systems. We show, when focussing on qualitative functional changes of communities, it is important to evaluate the underlying functional identity and not solely rely on measures of the diversity of functions.

P141 Toxic ergot fungus and avoidance mechanisms in reindeer

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Ergots (*Claviceps purpurea* species complex) are a group of fungal seed pathogens that commonly infect grass inflorescences. Ergot sclerotia (dark, protruding seed-like structures) can contain a variety of alkaloids, which makes the fungus poisonous and the infected inflorescence low quality food for grazers. It has been suggested, that ergot may provide protection for its host and have even an aposematic function. In this study, we tested the effect of ergot on reindeer food choice by conducting group cafeteria tests. Ergot and another novel ingredient, wild rice, were added as whole or ground to fodder pellets and offered in different combinations (three-choice tests). Eating decisions were recorded, but actual eating was prevented. As a result, control (plain fodder) was preferred instead of options with added ergot or wild rice. Added rice caused nearly similar rejection than ergot, and a mix of fodder pellets with ground ergots/rice caused stronger rejection than the ones with whole sclerotia/grains. It seems clear, that grazers do recognize ergot, and their preference for "clean" alternative can produce a defensive effect. The similar reaction against toxic and non-toxic novel constituent in food suggests, that food conservatism/neophobia may be a part of the mechanism by which ergot gains and provides protection for infected hosts from mammalian grazers. This mechanism may be complementary to aposematism. Odour seems to function as a signal for herbivores, suggesting a potential role also in aposematism.

P142 Effects of *Epichloë* endophyte on performance and fungal community of local and foreign *Festuca rubra* s.l. grasses grown in subarctic and subalpine meadows

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Systemic grass endophytes (*Epichloë* fungi) have been shown to enhance the performance of their host plants in many experimental settings. Physical growth conditions and interacting community affect the performance of endophyte-grass symbiote and may change the effects of endophyte on host. We explored whether there is local adaptation in natural populations of *Epichloë festucae*-*Festuca rubra* -symbiote in subalpine and subarctic seminatural meadows and whether *Epichloë* affects the fungal community of host grass leaves. We conducted a three year reciprocal transplantation experiment with *Epichloë*-infected and *Epichloë*-free red fescues among Swiss and Finnish meadows. We measured the performance of experimental grasses and the prevalence of pathogens on grass leaves. Fungal community was determined from the grass leaf samples with Ion Torrent sequencing of ITS2 rDNA. In both countries the native grasses performed better than alien grasses. In Switzerland, the Swiss E- grasses had better vegetative growth compared to E+ plants, but both Swiss and Finnish E+ grasses produced more seeds than E- grasses. In Finland, the Finnish originated E+ grasses performed slightly better compared to E- plants, whereas endophyte had opposite effect on Swiss grasses. Fungal community of grass leaves differed among the target countries. *Epichloë* increased the diversity of fungal community of Swiss grasses, but decreased it in Finnish grasses. *Epichloë* affected also the prevalence of some fungal pathogens either decreasing or increasing the infections depending on the pathogen species and the original country of grasses. These results suggest that *Epichloë* affect differently the grasses originating from different countries.