



# Programme and Abstract Book

Viiikki Campus, University of Helsinki  
2<sup>nd</sup> March to 4<sup>th</sup> March, 2020



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## **Acknowledgement**

The previous Spring Symposium Organizing Team  
Otso Ovaskainen  
Karen Sims-Huopaniemi  
Petri Nummi  
The faculties and the doctoral school  
The Finnish Museum of Natural History (LUOMUS)  
The bosses, colleagues and families  
The people and staff of Viikki Campus

## Welcome to Spring Symposium 2020

*“If I have seen further it is by standing on the shoulders of Giants.”*

Isaac Newton

We are honored to welcome you to the 29th Spring Symposium. Already from 1992, the Spring Symposium has been organized yearly by the Doctoral Programme in Wildlife Biology Research (Finnish acronym LUOVA) of the University of Helsinki, in collaboration with the Faculty of Biological and Environmental Sciences, the Faculty of Agriculture and Forestry, and Finnish Museum of Natural History.

Every year, the Spring Symposium brings together PhD and MSc students from a range of research fields related to ecology, evolution, systematics, and nature conservation. The Spring Symposium provides the students an opportunity to present their research in a friendly atmosphere and receive invaluable feedback on scientific content and presentation skills from fellow students, colleagues and three international evaluators.

The best talk will be awarded with Olli's prize, which is a 1000 € sponsorship for an international conference. There will also be prizes for the runner-ups and a prize for the best poster. Our international evaluators will announce all prizes at the Grande Finale on the last evening.

In this booklet, you can find the programme of the symposium as well as all abstracts listed chronologically. We hope that you will join the poster session and can attend as many talks as possible to provide valuable feedback to the students as well as engaging in lively discussions.

We hope you find the symposium inspiring and beneficial!

The Organizing Committee,

Katarina, Elena, Antti, Marju, Luisa, Kati, Miisa

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# PROGRAMME

2020

MONDAY 2<sup>nd</sup> MARCH 2020

9:00 – 9:15 Coffee

9:15 – 9:30 Otso Ovaskainen Opening words

## KEYNOTE TALK

9:30 – 10:30 Hanna Kokko Gentlemanly males: always, sometimes, never?

10:30 – 10:50 Coffee

## SESSION I

10:50-11:55 Iris Orizar Intra-specific trait variability and plasticity at different salinity levels in two species of phytoplankton

Clio Hall Impact of salinity change on food web interactions in marine plankton communities

Elena Kochanova Phylogeography of freshwater copepods: revealing the complex cryptic structure in Palearctic

11:55 – 13:15 Lunch

## SESSION II

13:15 – 14:20 Roxana Preston The origin and regeneration of free-living populations of *Fucus vesiculosus* in the Baltic Sea

Christina Elgert Reproduction under light pollution: maladaptive responses to artificial light in a glow-worm

Pinja Näkki The effects of tire rubber particles on the Baltic clam (*Limecola balthica*)

14:20 – 14:35 Coffee

### SESSION III

14:35 – 15:40	Leena Hintsanen	Research plan for species communities under a climate change in North America
	Wenfei Liao	From diving beetle diversity to biodiversity conservation in urban wetlands
	Aku Korhonen	Urban forests as potential biodiversity hotspots for wood-decayers

TUESDAY 3<sup>rd</sup> MARCH 2020

9:00 – 9:30 Coffee

KEYNOTE TALK

9:30 – 10:30 Susan Johnston Micro-evolution of recombination rate variation in wild populations

10:30 – 10:50 Coffee

SESSION I

10:50-11:55 Marion Sinclair-Waters Beyond large-effect loci: large-scale GWAS reveals a mixed large-effect and polygenic architecture for age at maturity of Atlantic salmon

Mikko Kivikoski Are you related to your siblings - check your crossovers

Antti Miettinen A large Baltic salmon population is genetically differentiated within, but not between, rivers

11:55 – 13:15 Lunch

SESSION II

13:15 – 14:20 Jack Beresford Introgressed loci under selection are associated with differentially expressed genes in hybrid wood ants

Suvi Sallinen Host genotype and local population context are the key determinants of disease in the wild

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14:20 – 14:35 Coffee

14:35 – 16:35 POSTER SESSION

19:00 - DINNER

## WEDNESDAY 4<sup>th</sup> MARCH 2020

9:00 – 9:30 Coffee

### KEYNOTE TALK

9:30 – 10:30 Jane Reid Integrating individual movements into evolutionary ecology: dynamics of fitness, dispersal and seasonal migration

10:30 – 10:50 Coffee

### SESSION I

10:50-11:55 Marju Prass Timecourse of an invasive non-native species: the effect of large-leaved lupine on plant communities

Camila Souza Beraldo Diversity, transmission mode, and evolution of symbiosis in an insect community

Nadja Verspagen Stress tolerance of a butterfly across a latitudinal gradient

11:55 – 13:15 Lunch

### KEYNOTE TALK

13:15 – 14:20 Tanja Pyhäjärvi The evolutionary genomics of conifer reproductive peculiarities

14:20 – 14:35 Coffee

### SESSION II

14:35 – 16:35 Sonja Saine Reintroducing the threatened fungi of Finnish forests - the ecological foundations of a novel conservation tool

Janne Koskinen Fun with fungi – fly larvae in mashed mushrooms

18:00 – 23:00 GRANDE FINALE (REGISTRATION REQUIRED)

# KEYNOTE SPEAKERS

(ALSO EVALUATORS)



**Susan Johnston**

Institute of Evolutionary Biology at the University of Edinburgh, United Kingdom.

Susan is a Royal Society University Research Fellow using genomics to understand evolutionary puzzles in natural populations. At present, her main interests are the evolution of recombination rate variation and understanding the genetic architecture of ongoing sexual conflict.



**Hanna Kokko**

Department of Evolutionary Biology and Environmental Studies, University of Zurich, Switzerland

Her research focus is on evolutionary ecology of sexual and asexual reproduction, analysis and management of animal populations, evolution of reproductive and social strategies, sustainability science.



**Tanja Pyhäjärvi**

University of Oulu, Finland

She is an Academy Research Fellow in the Department of Ecology and Genetics. Her research group works on evolutionary genetics and are interested in various aspects of population genetics and molecular evolution. Genetic basis of environmental adaptation, haploid life stage evolution and effects of natural selection on molecular variation are in our focus. They mostly work with plants: *Pinus sylvestris* (Scots pine), *Arabidopsis lyrata* and *Betula pendula* (Silver Birch).



### **Jane Reid**

Centre for Biodiversity Dynamics, NTNU, Trondheim, Norway, and at the University of Aberdeen, United Kingdom

My research aim is to understand the genetic and environmental causes of variation in individual life-histories, and to understand the consequences of such variation for population and evolutionary dynamics. I achieve these aims by applying sophisticated statistical, quantitative genetic and molecular genetic analyses to long-term data from wild populations, coupled with mathematical and simulation modelling, and thereby develop and test ecological and evolutionary theory. At present, my main interests are in mating system evolution (especially inbreeding and polyandry) and eco-evolutionary dynamics driven by seasonal migration.

# MONDAY

2<sup>nd</sup> March

Auditorium 2 Infocenter Korona

# KEYNOTE TALK

9:30 – 10:30

**Hanna Kokko:**

## **Gentlemanly males: always, sometimes, never?**

There is definitely a taxonomic bias in what we study: a sexual selection textbook, for example, is almost guaranteed to show or at least mention peacock males (or perhaps peacock spiders), while theories that are built with such an animal in mind are less applicable to e.g. fungal sex. If one switches the perspective a little, then one can start asking why what we take as 'normal' is a norm in the first place. For example: why are male and female feeding niches typically (though not always) so similar, when in an interspecific competition context species A and B tend to become different for very good reasons to do with resource depletion? In a mathematical model, we show that males may evolve to be 'gentlemen' who leave profitable food to females, but this requires almost complete absence of sexual conflict. I will then also present field data on truly gentlemanly male behaviour on *black coucals*, a bird species where males build nests and care for the young, and females retain harems of such males.

# SESSION I

10:50-11:55

**Iris Orizar (LUOVA):**

## **Intra-specific trait variability and plasticity at different salinity levels in two species of phytoplankton**

Predicted changes in the salinity of the world's ocean are threatening phytoplankton community diversity and structure. However, most studies and models about the response of phytoplankton community to environmental changes have been focused on the species level, neglecting the importance of individual variation within the species. Intra-specific trait variation is an important source of variability in the community and understanding its effect on phytoplankton resistance to the ongoing climate change can help to improve models predicting changes in marine primary production. In this study, we aimed to determine intra-specific trait variability in *Alexandrium ostenfeldii* (Dinophyceae) and *Skeletonema marinoi* (Bacillariophyceae) at different salinity levels (0, 5, 15, 20, 30, 35 psu). We measured morphological and physiological traits of each strain at every salinity level and observed similarities and differences in growth strategies among the strains of *A. ostenfeldii* and *S. marinoi*. In general, dinoflagellate and diatom species had different growth patterns: *A. ostenfeldii* had a long lag-phase and a short log-phase, while *S. marinoi* had a short lag-phase and a long log-phase. Furthermore, cell size distribution varied across strains grown at the same salinity level and between different salinities. Our results demonstrated the potential of intra-specific trait variability and plasticity to broaden the environmental range the species can occupy, which has important consequences for phytoplankton community performance threatened by climate change.

**Clio Hall (LUOVA):**

## **Impact of salinity change on food web interactions in marine plankton communities**

Current climate change predictions indicate increased levels of warming and declining salinity in the Baltic Sea, with negative implications for plankton food webs, which are an important baseline for functioning of marine ecosystems. In this study, we investigate the effect of salinity change on trophic interactions in plankton communities under different scenarios of freshening of the Baltic Sea. Projections for future salinity change derived from regional physical-biogeochemical models were used to set-up an outdoor mesocosm experiment at Tvärminne Zoological Station, Finland in August 2019. Each mesocosm was inoculated with natural plankton using a mixture of both freshwater and marine communities, mimicking the natural influx of a freshwater community from rivers into the Baltic Sea. The plankton food web ranged from bacteria to mesozooplankton. Samples were also taken from one location in the field at the same time and sampling frequency as the mesocosm experiments, to allow for the comparison of natural variability with the experimental set-up. Replicates were independently controlled to operate under different salinity change scenarios. The experiment ran for 4 weeks. Preliminary results from the experiment suggest higher diversity and productivity of phytoplankton as the water column becomes fresher or saltier with implications for higher trophic levels. The results from this project could be used to develop recommendations for new pre-emptive conservation strategies, in which climate mitigation targets are better suited to predicted freshening of the Baltic Sea.

**Elena Kochanova (LUOVA):**

## **Phylogeography of freshwater copepods: revealing the complex cryptic structure in Palearctic**

Harpacticoid copepods are widespread micro-crustaceans with unusually high genetic divergence among conspecific populations. The existing phylogenetic studies of individual taxa have started to challenge the cosmopolitanism paradigm of these animals and to recognize hidden and regional diversity, which can be a result of previous cycles of glaciation or environmental conditions. In order to investigate morphological and genetic variability of freshwater copepods, we 1) sampled hydrobiological materials from various waterbodies in Europe, 2) analysed 30 morphological characters and revealed the most variable, 3) sequenced mitochondrial and nuclear genes to get an insight into the phylogenetic structure of the species. For the analysis, we used three species, which were occurred more often in the samples: *Canthocamptus staphylinus* Jurine, *Attheyella crassa* Sars, *Nitokra hibernica* Brady. All the three taxa are split into genetically distinct clusters of clades and deemed to represent complexes of species with largely (but not completely) non-overlapping distributions. In one case, the geographic subdivision follows an East-West pattern (*A. crassa*) whereas in the other case the division is characterized rather as Continental-Fennoscandian (*C. staphylinus*). The phylogeographic structure of *N. hibernica* is uniform in European populations, however, the clear difference from American populations of the species is observed. Estimates of the inter-clade divergence suggest that the differences are far older than the history of the latest glacial cycles, while the geographic patterns still point to an important role of geological history in determining the biogeography. We also present some scenarios of the copepods distributions and migrations during the last glaciation period.

# SESSION II

13:15 – 14:20

**Roxana Preston (LUOVA):**

## **The origin and regeneration of free-living populations of *Fucus vesiculosus* in the Baltic Sea**

*Fucus vesiculosus* is a foundation species within the Baltic Sea, forming two distinct morph types: benthopleustophytic (free-living) and epilithic (attached). Intriguingly the taxonomic designation of free-living *Fucus* within the Baltic Sea is still questionable. Using microsatellites and DNA barcoding we aim to measure the levels of relatedness between populations and thus infer the population connectivity and taxonomic classification. We hypothesise that free-living ecads are genetically distinct ecotypes, forming spatially confined populations maintained predominantly through asexual reproduction. Similarly to attached *F. vesiculosus*, free-living morphs have demonstrated extirpation from areas they were once commonly recorded within. The status of this morph type is thus of huge import, with concerns being demonstrated through the classification of four biotopes as endangered by HELCOM (2013). As a species ability to adapt to environmental change is related to the level of genetic diversity within the population; it is imperative that the gaps in knowledge relating to the levels of genetic diversity between these morph types are resolved. With this understanding effective conservation measures could be established to safeguard *F. vesiculosus* populations, both the free-living and attached morphs, and the consequential ecosystem function and services provided. Our preliminary analyses indicate differences in the levels of genetic variation between attached and free-living individuals, suggesting some degree of isolation between the two morph types. Through this we propose that free-living ecads form separate populations that have at least some capability to sustain themselves.

**Christina Elgert (LUOVA):**

**Reproduction under light pollution: maladaptive responses to artificial light in a glow-worm**

The amount of artificial light is growing worldwide with potential impacts on the behaviour of nocturnal organisms. Females of the common glow-worm *Lampyris noctiluca* glow in the night to attract flying males and could be negatively affected by light pollution. We investigated if females mitigate the negative effects of light pollution by adjusting their timing and location of glowing to spatial variation in artificial light. When we exposed females to a gradient of artificial light, they did not move away from the light, but instead delayed or even refrained from glowing. To investigate the impact that staying at an illuminated location has on mate attraction, we exposed dummy females to a gradient of artificial light in the field, mimicking conditions under a streetlight. We found success in mate attraction to be lower at the illuminated spot, but higher only a short distance away, where it was darker. Because female glow-worms do not move during the day, and glow only during a few nights (as capital breeders, that use stored energy for their reproduction), remaining at an illuminated location increases their risk of staying unmated. Thus, our results indicate that glow-worms are not able to cope with spatial variation in artificial light. This could have contributed to their global decline.

**Pinja Näkki (LUOVA):**

## **The effects of tire rubber particles on the Baltic clam (*Limecola balthica*)**

Microplastics (plastic particles <5 mm) are ubiquitous pollutants in the marine environment. One of the potentially largest sources of microplastics are tire rubber particles (TRP), which are generated from car tires undergoing friction on the road. Some components of tire rubber (e.g. heavy metals and polycyclic aromatic hydrocarbons; PAHs) are known to be harmful, and are able to leach out from TRP. As recent studies have shown that marine sediments often act as accumulation hotspots for microplastics, the aim of this study was to follow the leaching of PAHs and heavy metals from TRP, and to investigate their accumulation and effects on one of the key invertebrate species of the northern Baltic Sea seafloor, the Baltic clam (*Limecola balthica*). The experiment was conducted in mesocosms, and consisted of acute (4 days) and chronic (1 month) exposures. TRP (2190 µm) were added to the mesocosms in concentrations representing their occurrence in natural sediments (approx. 1.4 g/kg of dry sediment). The leaching of contaminants from TRP was verified from water samples, and their uptake by clams was analysed from their tissues at the end of the experiment. The impacts of exposure were studied by combining physiological biomarkers and histopathological examination of clam tissues. The results show leaching of heavy metals and PAHs from TRP to seawater. The concentrations of some PAHs measured from the water exceeded their environmental quality standards, indicating a potential risk for the clams. The exposure to TRP did not affect the survival of the clams, but accumulation of both heavy metals and PAHs to clam tissues was observed. The preliminary results of the integrated biomarker response also show an elevated stress in clams chronically exposed to TRP. The results demonstrate the potential of environmentally relevant concentrations of TRP to affect the clams and emphasize the importance of tire rubber as a yet understudied environmental contaminant.

# SESSION III

14:35 – 15:40

**Leena Hintsanen (LUOVA):**

## **Research plan for species communities under a climate change in North America**

Climate change is expected to cause drastic changes in ecosystems and already redistributions of species due to altering climate are well knowledged. An important question is how living organisms can cope with this rapid change in climate, together with other anthropogenic pressures. In addition, the protected areas are the cornerstones of our conservation politics but we don't know how good their ability to mitigate the impacts of climate change on biodiversity is. I evaluate this in my research plan by presenting my main research question, can protected areas reduce the speed of climate driven community changes in North America. I present also the dataset consisting North American breeding bird surveys and the network of protected areas. The aim for the study is to compare how the community temperature index (CTI) reflects the low- or high temperature dwelling species for a given species assemblage outside and inside protected areas. Also the possible approaches for research methods are presented. The hypothesis is that the protected area network mitigate the climate driven changes in birds and the CTI of breeding birds in North America has increased during the study period.

**Wenfei Liao (LUOVA):**

## **From diving beetle diversity to biodiversity conservation in urban wetlands**

From diving beetle (Coleoptera: Dytiscidae) diversity to conservation in urban wetlands Authors: Wenfei Liao\*, Stephen Venn, Jari Niemelä Abstract Urban blue infrastructure plays important roles in the ecology of cities, such as supporting aquatic biodiversity; yet, it has received little attention compared with urban green. As consequences, little is known about how urbanization has affected aquatic biodiversity and what habitat features are essential to support biodiversity in urban blue. We surveyed diving beetles (Dytiscidae) in 26 urban ponds at 11 sites in Helsinki, Finland, with 1-litre activity traps. With generalized linear mixed models (GLMM), we analyzed how dytiscid species richness and abundance were associated with the percentages of impermeable surfaces, pond margin slopes, and emergent plant coverage in ponds with and without fish. Our results revealed that dytiscid species richness, but not their abundance, was negatively associated with the surrounding impermeable surfaces. Dytiscid assemblages were lower in ponds with predatory fish than in ponds without fish. At the trap level, their species richness and abundance decreased with increasing margin slopes and decreasing emergent plant coverage in ponds with fish, but not in ponds without fish. At the pond level, emergent plant coverage determined the presence of dytiscids. Urban wetlands can support a diversity of dytiscids at the regional level. Ponds free from predatory fish are ideal habitats for dytiscid diversity. In ponds with fish, emergent vegetation can be planted to create microhabitats for dytiscids to avoid predators. It is important to create microhabitats for other invertebrates that prefer open water. We recommend maintaining a diversity of wetland habitats to support aquatic biodiversity in urban areas. Keywords: biodiversity, dytiscid, invertebrate, margin steepness, pond, urbanization, vegetation.

**Aku Korhonen (LUOVA):**

## **Urban forests as potential biodiversity hotspots for wood-decayers**

Urban forests are managed primarily for recreation and amenity value, and management practices applied in them are usually less intense than in rural production forests. Therefore, urban forests could be expected to retain more natural-like characteristics and higher biodiversity value than most non-protected forests. We propose that urban forests could provide valuable habitat patches that could be significant for preserving biodiversity, not only within cities, but also at a larger landscape scale. To investigate this potential, we have studied urban spruce-dominated forests in southern Finland, focusing on dead wood and wood-decaying fungal communities. So far, our results have revealed that urban forests typically contain ca. 10 m<sup>3</sup> ha<sup>-1</sup> of dead wood, although densities over ten times higher have developed locally. While dead wood availability is probably the most important factor limiting wood-decaying biodiversity in urban forests, it is unclear how sensitive wood-decaying species and communities are to urban stressors such as edge effects and wear. To address this question, we will use HMSC approach to disentangle the effects of substrate-level and stand-level environmental variables in shaping wood-decaying fungal communities in urban and rural settings. The goal of this study is to guide urban forestry towards smarter management with limited dead-wood resources.

# TUESDAY

3<sup>rd</sup> March

Auditorium 2 Infocenter Korona

# KEYNOTE TALK

9:30 – 10:30

**Susan Johnston:**

## **Micro-evolution of recombination rate variation in wild populations**

Meiotic recombination is often essential for proper chromosome segregation and generates new allelic combinations on which selection can act. However, it is also mutagenic and breaks up previously selected allelic combinations. These relative benefits and costs of recombination are likely to vary with differences in strength of selection and population demography: if recombination rate itself is heritable, then it has the potential to evolve within contemporary populations. We investigate the evolution of recombination rates in wild populations in Soay sheep (*Ovis aries*), red deer (*Cervus elaphus*) and house sparrows (*Passer domesticus*) by identifying genomic regions associated with recombination rate and investigating: (a) the age of allelic variation; (b) changes in allele frequency over time; and (c) the relationship between individual genotypes with reproductive success and survival. I will discuss how and why genetic variation is maintained in a trait thought to be under strong selection, and how our findings shed light on the evolutionary importance of recombination rate variation more broadly across taxa.

# SESSION I

10:50 – 11:55

## **Marion Sinclair-Waters (LUOVA):**

### **Beyond large-effect loci: large-scale GWAS reveals a mixed large-effect and polygenic architecture for age at maturity of Atlantic salmon**

Understanding genetic architecture is essential for determining how traits will change in response to evolutionary processes such as selection, genetic drift and/or gene flow. In Atlantic salmon, age at maturity is an important life history trait that affects factors such as survival, reproductive success, and growth. Furthermore, age at maturity can seriously impact aquaculture production. Therefore, characterizing the genetic architecture that underlies variation in age at maturity is of key interest. Here, we refine our understanding of the genetic architecture for age at maturity of male Atlantic salmon using a genome-wide association study of 11,166 males from a single aquaculture strain, using imputed genotyped at 512,397 single nucleotide polymorphisms (SNPs). All individuals were genotyped with a 50K SNP array and imputed to higher density using parents genotyped with a 930K SNP array and pedigree information. We found significant association signals on 28 of 29 chromosomes (P-values:  $8.7 \times 10^{-133}$  -  $9.8 \times 10^{-8}$ ), including two very strong signals spanning the *six6* and *vgl13* gene regions on chromosomes 9 and 25, respectively. Furthermore, we identified 116 independent signals that tagged 120 candidate genes with varying effect sizes. Five candidate genes found here were previously associated with age at maturity in other vertebrates, including humans. These results reveal a mixed architecture of large-effect loci and a polygenic component that consists of multiple smaller-effect loci, suggesting a more complex genetic architecture of Atlantic salmon age at maturity than previously thought. This more complex architecture will have implications for selection on this key trait in aquaculture and for management of wild salmon populations.

**Mikko Kivikoski (LUOVA):**

**Are you related to your siblings - check your crossovers**

Siblings share parts of their genomes which means that they are related. Relatedness is a key factor in kin selection and cooperation in the wild, for instance. In diploid sexually reproducing organisms the expected relatedness between siblings is 0.5 (i.e. half of their genomes are identical by descent). However, the relatedness varies and may deviate from the expected value. Degree of variance in relatedness is affected by the number of chromosomes, number of crossovers and localisation of crossovers. Variance estimators in the literature are based on these three factors, but their assessment with empirical data are scarce. In my talk, I will explain how each of the three factors affect on the variance of relatedness and assess variance estimation with empirical data from the nine-spined stickleback (*Pungitius pungitius*).

## **Antti Miettinen (LUOVA):**

### **A large Baltic salmon population is genetically differentiated within, but not between, rivers**

Atlantic salmon (*Salmo salar*) are widely distributed across Europe and North America, and exhibit a broad range of life history diversity. Anadromous Atlantic salmon return to their natal location to spawn, which frequently results in strong geographical population structuring. Consequently, there is potential for substantial local adaptation within and among salmon populations. This creates management challenges, as geographically close salmon populations may not be evolutionarily or ecologically interchangeable. Managing such distinct populations sustainably is essential in order to maintain the genetic resilience of salmon stocks as a whole. The Baltic Sea contains an evolutionarily distinct lineage of Atlantic salmon. The genetic structure of the largest wild Baltic salmon population, in the interconnected Tornio and Kalix River systems, has not yet been comprehensively studied. In my study, we used microsatellites to characterize the fine-scale population genetic structure within the river systems. We find genetic differentiation within the Tornio and Kalix Rivers, but not between them: salmon in the upper reaches differ genetically from salmon in the lower reaches, regardless of river system. We also find life history variation between salmon from upstream and downstream reaches, associated with the observed genetic structure. I will discuss the results in the context of the history and management of these ecologically, culturally and economically important fish populations. I will also discuss my future studies that use genomic data of Baltic salmon<sup>1</sup>, including comparisons of historical and contemporary samples to study adaptive variation and human impacts on the populations.

# SESSION II

13:15 – 14:20

**Jack Beresford (LUOVA):**

## **Introgressed loci under selection are associated with differentially expressed genes in hybrid wood ants**

As populations diverge, they accumulate mutations in their genomes that, when recombined in hybrids, can result in negative or positive effects for hybrid fitness. Divergence in regulatory gene regions is expected to accumulate faster than in coding regions, owing to a lesser extent of pleiotropy. An important and outstanding question is how introgression impacts hybrid gene expression. Yet, to date, few studies have attempted to associate hybrid gene expression patterns with selection because it is difficult to link expression to hybrid fitness. To begin addressing this I utilized a population of naturally occurring hybrid European Wood Ants, in which previous studies have documented selection associated with introgressed alleles. I used whole-body gene expression profiling of developing hybrid larvae, combined with genotyping of marker alleles linked with selected genomic regions, to characterize gene expression patterns associated with introgressed alleles under selection. I contrasted gene expression patterns, in males of one hybrid lineage, and females of two, with and without key introgressed marker loci under selection. Males and females had overlapping sets of differentially-expressed genes associated with introgressed alleles, but with expression in hybrids tending to be in opposite directions in the sexes. Interestingly, in all of our comparisons we found a significant overlap between differentially expressed genes associated with introgression and genes located in introgressed genomic regions, suggesting that differential expression potentially contributes to fitness differences among hybrid ants. This study takes an important step towards linking gene expression with fitness, by associating gene expression with alleles known to be under selection. Our results highlight the strengths of combining complementary methods to study the effects of introgression on gene expression and fitness, particularly for hybrids in non-model organisms.

**Suvi Sallinen (LUOVA):**

## **Host genotype and local population context are the key determinants of disease in the wild**

Individuals are often simultaneously infected by multiple pathogenic microbes. However, host-pathogen research has traditionally been conducted in the single-host-single-pathogen framework, and the role of host resistance in shaping pathogen communities remains largely unexplored. To test whether host resistance is the key determinant of within-host pathogen communities, or whether infection of one virus is linked to the likelihood of another virus, we performed a field transplant experiment where we placed healthy replicates of multiple cloned *Plantago lanceolata* individuals in wild *P. lanceolata* populations in the Åland Islands to acquire natural virus infections. We sampled these experimental plants multiple times over the growing season to detect five common viruses with specific PCR primers. Our data suggest that both genotype and location are important determinants of within-host virus communities. However, we did not find evidence for virus-virus interactions after the effect of genotype was accounted for. These results suggest that the effect of genotype on within-host virus communities in this system are more constitutive than a result of induced resistance or susceptibility.

# WEDNESDAY

4<sup>th</sup> March

Auditorium 2 Infocenter Korona

# KEYNOTE TALK

9:30 – 10:30

**Jane Reid:**

## **Integrating individual movements into evolutionary ecology: dynamics of fitness, dispersal and seasonal migration**

Understanding evolutionary dynamics, and associated population dynamic responses to environmental change, requires knowledge of the forms and magnitudes of genetic and environmental variation in fitness, and of selection on key life-history traits. It also requires understanding how the critical genetic variation can arise and be maintained or eroded through combinations of drift, selection and gene flow resulting from dispersal. Yet, such effects have still rarely been jointly quantified, or related to spatio-temporal population dynamics, in wild populations experiencing natural genetic and environmental variation. I will present recent analyses of multi-year data from free-living populations of song sparrows and European shags that aim to explicitly integrate effects of movements, in the form of dispersal and reversible seasonal migration, into empirical understanding of joint ecological and evolutionary dynamics.

# SESSION I

10:50 – 11:55

## \ Marju Prass (LUOVA):

### **Timecourse of an invasive non-native species: the effect of large-leaved lupine on plant communities**

The success of invasive non-native species is attributed to enemy release, increased competitive ability, empty niche and novel weapons hypotheses. Other explanations include disturbance and high propagule pressure. Yet, these mechanisms can diminish over time. For example, enemies accumulate as 1) the invader's enemies and competitors arrive from its native range, and as 2) local species adapt to the non-native species. This has prompted the theory of boom-bust dynamics where the invader would progress from a 'harmful' phase into a 'harmless' phase with lower population size. However, there is still little quantitative empirical support for this theory. To investigate the impact of an invasive species over time, I focused on the large-leaved lupine, *Lupinus polyphyllus*. It is a perennial nitrogen-fixing herb, which is native to North America and has become invasive in many countries within Europe. I aimed to: i) examine whether lupine populations would decrease, and ii) identify plant species that are vulnerable to lupine invasion. I sampled plant communities in young, intermediate and old lupine stands (ca 5, 10,  $\geq$  15 years, respectively). At each site, I examined plant communities within ten 1 m<sup>2</sup> quadrats: five within lupine stands and five in non-lupine areas. I identified all plant species and estimated their ground covers. I analysed species richness and the cover of species with generalised linear mixed models, and community composition with non-metric multi-dimensional scaling (Bray-Curtis index). The lupine abundance did not decrease over time. Lupine reduced the cover of habitat generalists and dry habitat species. Thus, my results suggest that lupine is a strong competitor and conservation efforts should be focused to dry habitat types. My results did not show progression into a 'harmless' phase, but 15 years could have been too short time period. Furthermore, I was not able to find older populations, which indicates the possibility of boom-bust dynamics.

**Camila Souza Beraldo (LUOVA):**

## **Diversity, transmission mode, and evolution of symbiosis in an insect community**

Species communities are shaped by a wide diversity of ecological interactions, including symbiosis. Defined as a long-term interaction between dissimilar species, symbiotic interactions range on a continuum between costly and beneficial, depending on the host-symbiont system considered. For instance, the symbiotic bacterium *Wolbachia*, which is estimated to infect about 60% of all insect species, can either benefit its host in presence of pathogens, or negatively affect its host fecundity. Consequently, symbionts have been suggested to play an important role in the dynamics of the host species populations, and of their host interactions with competitors, predators or preys. Despite this, most eco-evolutionary studies of natural insect communities rarely consider the insect-symbiotic partners. Hence, we lack a comprehensive view on how important symbionts are in the ecology and evolution of natural host communities. I propose to investigate this topic using the insect community associated to the ribwort plantain (*Plantago lanceolata*) in the Åland islands. This system is particularly well described, and includes several species that have been studied for over 30 years (e.g. the glanville fritillary butterfly *Melitaea cinxia* and its associated parasitoids). I aim (i) to characterize the occurrence, abundance and distribution of symbionts in this unique insect community; (ii) to investigate the transmission modes of the symbionts within and between hosts in the field; and (iii) to study whether these different symbiotic interactions have played major roles in the evolutionary history of their insect host species. In order to address these questions, I will combine fieldwork across the Åland islands with experiments in the laboratory, and phylogenetic analyses. My research will contribute to the better understanding of various host-symbiont interactions, and unravel the important role of symbionts in shaping host species interactions in natural communities.

**Nadja Verspagen (LUOVA):**

## **Stress tolerance of a butterfly across a latitudinal gradient**

Climate warming is affecting organisms worldwide. Species can cope with environmental change by avoidance, for example by tracking favourable conditions by moving north. However, this might be prevented by limits such as resource distribution. Adaptation through natural selection or adjustment through phenotypic plasticity are other possibilities but they may be limited by physiological constraints. Understanding the role of adaptation and plasticity in stress tolerance is of great importance if we are to understand how natural populations may mitigate climate change. I recently showed that the thermal reaction norms in the pre-diapause larvae of the Glanville fritillary butterfly (*Melitaea cinxia*) from Finland vary among families and are highly dependent on the host plant the larvae are feeding on. Generally, growth rate increases with temperature but drops after 32 °C and larvae grow faster on host plant *Veronica spicata* compared to *Plantago lanceolata*. However, some families show highly contrasting responses, suggesting a genetic component in thermal response. During my PhD project, I aim to use the *Melitaea cinxia* butterfly as a model system to study tolerance to climate change across a climatic gradient. I will use populations from four different latitudes (Spain, Belgium, Estonia & Finland) to assess direct and indirect effects of stress on all life-stages of the butterfly. Then, I will quantify gene expression differences among populations and environmental conditions to link differences in phenotype to genotype in order to assess whether adaptive potential is present and whether populations vary in their tolerance to the expected effects of climate change. In this presentation, I will show data on pre-diapause larvae from Finland and lay out my plans for the future.

# KEYNOTE TALK

13:15 – 14:15

**Tanja Pyhäjärvi:**

## **The Evolutionary Genomics of Conifer Reproductive Peculiarities**

Gymnosperms have several reproductive biology peculiarities compared to seed plants. They have an extensive haploid megagametophyte life stage, simple and cleavage polyembryony and strong inbreeding depression. From an evolutionary point of view, they provide an interesting comparison to angiosperms. We can use them to answer questions like: Why do angiosperms have closed seeds? Why self-incompatibility systems have evolved? Why diploidy has evolved? Why angiosperms have double-fertilization? and How do organisms cope with inbreeding depression and deleterious alleles? However, they have not yet been widely used in evolutionary genomic studies partly due to their gigantic genome sizes. We study Scots pine (*Pinus sylvestris*) seeds and use new genomic tools and resources to answer these questions. The Scots pine seed consists of both haploid maternal megagametophyte tissue and diploid embryo. We use RNA and DNA sequencing accompanied with population genomic analyses to understand evolutionary dynamics and conflicts of the seed. In addition, we have developed a simulation model that allows us to test different scenarios that could have led to polyembryony. It includes inbreeding depression, early and late expressed deleterious variation, and is flexible in terms of mutation rate and dominance.

# SESSION II

14:35 – 15:15

**Sonja Saine (LUOVA):**

## **Reintroducing the threatened fungi of Finnish forests - the ecological foundations of a novel conservation tool**

Local species communities result from environmental and biotic filters and stochastic processes, i.e. assembly processes. Understanding on how these processes affect communities is central for predicting biodiversity responses to the ongoing environmental change, and thus for developing effective conservation tools. Wood-inhabiting fungi provide an interesting study system for testing the relative effects of assembly processes because they are highly interactive and environment-sensitive. Moreover, many of these species are of high conservation concern. By reintroducing threatened wood-inhabiting fungi, I study how biotic and environmental filters affect fungal colonization and conversely, how successfully introduced species influence the resident fungal communities. Additionally, I will assess the level of stochasticity in fungal colonization. Beyond the case study of fungi, the study will advance our understanding on general community ecology. In addition, the results are essential for the development of reintroductions as a novel conservation tool for wood-inhabiting fungi.

**Janne Koskinen (University of Eastern Finland):**

**Fun with fungi - fly larvae in mashed mushrooms**

Fungus-insect interactions are among the dominant in the world, with hundreds of thousands of species involved. These communities and interactions have been understudied - the immense amount of tiny, difficult-to-identify dipteran larvae, not even to speak of myriad of mites and beetles - have daunted scientists. Building on the work of brave pioneers we ventured into the undiscovered countries - utilizing metabarcoding to determine just what these ultradiverse communities are like. I will show just how these communities vary in regards to resource quality and latitude - and what we can infer from patterns we observe.

## POSTER SESSION\*

1	Elisa Nygård	Do hybrid wood ants have a fitness advantage due to better temperature tolerance?
2	Beatriz Portinha	Reconstructing the demographic history of wood ant species and their hybrids
3	Reena Karvonen	Changes on Sub-Arctic palsa mires: shifts on vegetation and carbon accumulation during past centuries
4	Norman Göbeler	The role of episodic events for biodiversity and ecosystem functioning in coastal waters
5	Viivi Halonen	Associated benthic macrofauna of free-living <i>Fucus vesiculosus</i> in the Baltic Sea
6	Sofi Heikkilä	Human-carnivore conflict in Finland and which factors influence public attitudes of the animals?
7	Aura Palonen	The effects of prenatal androgen exposure in a cooperative mammal
8	Hanna Finne	Importance of redox potential and vegetation properties to variation in CH <sub>4</sub> flux at a boreal fen
9	Brittni Joette Crosier	Patterns of Distance Decay in Finnish Fungal Communities
10	Inari Nousiainen	Survival of adult male ortolan buntings during years 2013 - 2019 in Finland
11	Elisa Päiviö	Effect of historical predation pressure and current predation risk on genetically determined behaviour of the nine-spined stickleback
12	Laura Puikkonen	Life-history Effects in the Behavior of Svalbard reindeer ( <i>Rangifer tarandus platyrhynchus</i> ): A Focus on Mothers
13	Sanna-Kaisa Kivilompolo	Modelation of cyanotoxins' sediment toxicity in subarctic - temperate lakes due climate stress

\*The poster session is on Tuesday, 3<sup>rd</sup> March, 14:35 – 15:40.

# POSTER ABSTRACTS

*Infocentre Korona (The symposium venue hall)*

Tuesday

Elisa Nygård (EEB):

**Do hybrid wood ants have a fitness advantage due to better temperature tolerance?**

Hybridization between species is more common than previously thought. It is however unclear whether hybrids could adapt to new environmental conditions compared to parental species. In my MSc project I will study thermal tolerance in hybrid colonies of mound-building wood ants naturally occurring in southern Finland. I will test whether hybrid individuals have distinct temperature tolerances and therefore could show adaptive potential compared to parental species. These results will help to clarify whether hybridization could be adaptive. In the light of climate change, the results of my project have conservational implications for these keystone species, and more broadly for many hybridizing species. I am supervised by Jonna Kulmuni and Pierre Nouhaud. Dr. Kulmuni's research group SpeciAnt is a part of Helsinki Institute of Life Sciences (HiLIFE) and Organismal and Evolutionary Biology research programme.

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Beatriz Portinha (EDB):

**Reconstructing the demographic history of wood ant species and their hybrids**

Hybridization leads to the combination of genetic material from previously isolated gene pools and occurs in various animal and plant taxa. However, we know little about the importance of different evolutionary processes shaping hybrid genomes and populations. Haplodiploid wood ant species of the genus *Formica* hybridise in Southern Finland, with hybrid individuals showing sex-antagonistic selection. Theoretical work investigating these opposite selection pressures suggests it could lead to long-term maintenance of hybrids and genetic polymorphisms. To understand how this can be achieved in natural populations, including the causes of the genomic variation patterns in hybrid populations, I will use genome-wide genomic data to test alternative models of divergence, with and without gene flow. We aim to infer the relationship between i) populations of the parental species, ii) hybrid and parental populations, and iii) the hybrid populations themselves, by characterizing the populations under study and reconstructing their demographic history.

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Reena Karvonen (EEB):

**Changes on Sub-Arctic peat mires: shifts on vegetation and carbon accumulation during past centuries**

My Master's thesis work is done as a part of a project that is funded by Academy of Finland, and carried out as an international co-operation. Work is based in Viikki, Environmental Change Research Unit (ECRU). Aim of the project is to evaluate possible effects of recent climate warming on northern peatlands by studying past changes. During my work, I will examine how the peatland of interest (located in Northern Russia) is changed by its vegetation and carbon accumulation, and what is their connection to different climatological phases and significant changes on temperature. My Master's thesis work is focusing on analyzing changes on past and present day plant communities by macrofossil analyses. The samples examined are also dated by using <sup>210</sup>Pb- and radiocarbon <sup>14</sup>C -dating methods.

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**Norman Göbeler (LUOVA):**

### **The role of episodic events for biodiversity and ecosystem functioning in coastal waters**

Episodic extreme temperatures, upwelling or hypoxic events can alter species distributions and affect marine ecosystem function, such as rates and pathways of nutrient cycling and ecosystem metabolism. An episodic warm event is defined as a marine heatwave (MHW) if it lasts for five or more days, with temperatures warmer than the 90th percentile based on a 30-year historical baseline period. Therefore, a MHW can occur all year around causing possibly season-specific effects. Additionally, satellites allow MHW detection in the sea surface in a 20km<sup>2</sup> grid and are therefore limited in reflecting small-scale conditions in heterogeneous coastal areas and near-bottom water. Thus, there is an urgent need for a refinement of the temporal and habitat-specific effects of MHWs in coastal areas. While it is challenging to assess the ecological importance of extreme events, due to their very nature, controlled experiments are useful for testing mechanistic responses to changing magnitude and frequency of weather. Laboratory experiments are useful for identifying the species and life stages most susceptible to particular types of episodic events. Nevertheless, field studies with natural communities are imperative for providing realism to our understanding of the effects of climate change. Therefore, we need to build on the single-species, life-stage specific experimental studies, and move towards identifying key species and key habitats where changes in important ecological processes are likely to occur because of climate-related shifts in abiotic conditions. In my PhD project investigating the role of heatwaves, I will use a combination of high-resolution environmental data, field observations and biological monitoring, experimentally derived data and modelling in order to link changes in benthic communities (e.g. bioturbation rates and energy budgets) to larger-scale ecosystem changes. I will introduce the plans and this approach in my poster presentation.

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**Viivi Halonen (EEB):**

### **Associated benthic macrofauna of free-living *Fucus vesiculosus* in the Baltic Sea**

The bladder wrack (*Fucus vesiculosus*) is a keystone species of the Baltic Sea that forms large macroalgal forests, providing a habitat and/or a food source to a wide array of animals. Stands of *F. vesiculosus* also function as important carbon sinks. *Fucus vesiculosus* exists in two distinct morphs in the Baltic Sea. The typical epilithic morph is attached to hard substrata via a holdfast, whereas the less common unattached free-living morph lacks a holdfast and lives on soft bottoms. The attached morph has been widely studied, but the free-living morph and especially its functional role have been left understudied. The objective of this project is to investigate the ecological role of the free-living morph by determining the faunal community associated with its presence, as well as identify factors affecting community structure, species abundance and community function. This project will compare the macrofauna of free-living *F. vesiculosus* with macrofauna of soft sediments, using previous work on the faunal community of attached *F. vesiculosus* as reference.

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**Sofi Heikkilä (EEB):**

### **Human-carnivore conflict in Finland and which factors influence public attitudes of the animals?**

Large carnivore conflict is very present in today's Finland, mainly between humans and wolves. To solve these problems, it is important to assess the attitudes of local communities towards large carnivores and to understand factors driving their opinions. This unfinished thesis focuses on people's opinions on the four large carnivores living in Finland, brown bear (*Ursus arctos*), grey wolf (*Canis lupus*), Eurasian lynx (*Lynx lynx*) and wolverine (*Gulo gulo*). With random face-to-face interviews in Eastern and Western Finland complemented with answers from a web survey, the goal was to get a glimpse of the locals' opinions as a first step to better understand the societal roots of the human-carnivore conflict in Finland. With thesis supervisor Julien Terraube a questionnaire was planned to tackle the research questions: 1) is there a difference in attitudes between East and West, 2) do public opinions change with expanding distance from protected areas, 3) are people with

higher education level more positive towards large carnivores, 4) how does persons position in conflict and other personal attributes affect their opinions, and 5) does ecological knowledge of large carnivores affect persons opinions? Analyses concentrated on two main topics: general opinions towards large carnivores and opinions on how their populations should be managed. Neither of these was significantly affected by distance from protected areas, but region (East/West) seemed to have an effect especially in opinions on management strategy, West leaning towards stricter management. People with third level education (University or University of Applied Sciences) were significantly positive on their general opinions of large carnivores, as were people who identified themselves as conservationists. Surprisingly, the trend of hunters opinions was positive. Perceived personal problems and disadvantages had a negative effect on attitudes towards large carnivores and made opinions of management stricter.

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**Aura Palonen (EEB):**

### **The effects of prenatal androgen exposure in a cooperative mammal**

Early development is crucial time for determining life history trajectories that lead to differences in fitness of individuals later in life. Even small differences during the foetal development of mammals may lead to long lasting effects on survival and reproductive success. Many processes are especially sensitive to exposure to hormones in the womb, since hormone concentrations cause for example the development of sex-specific traits. In addition to the hormones the growing foetuses themselves secrete, they may be exposed to additional hormones from their littermates or their mother. Females may alter the phenotype of their offspring via maternal effects, which include regulating hormone concentrations during pregnancy. One example is additional exposure to testosterone during foetal development, which causes masculinization of sex-specific traits in females and may affect competitiveness in pups of both sexes. I aim to study the variation in the anogenital distance, an indicator of androgen exposure in the womb, in the banded mongoose (*Mungos mungo*). For this I analyse images taken by trained field assistants as a part of a long term study in Mweya peninsula, Uganda. Banded mongooses are cooperatively breeding carnivores that live in family groups of 10-30 individuals. Females usually give birth on the same day and pups are cared for by most adults of the group regardless of relatedness. Previous studies indicate maternal effects in that females may manipulate the phenotype of their offspring during more intensive reproductive competition. I will study the effects of sex and body size on anogenital distance as well as the effects of anogenital distance on pup competitiveness: the amount of care received as a pup, weight at maturity, lifespan and reproductive success.

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**Hanna Finne (EEB)**

### **Importance of redox potential and vegetation properties to variation in CH<sub>4</sub> flux at a boreal fen**

Boreal mires contribute considerably to the global methane budget and have, therefore, an important role in climate change models. Methane flux varies between mires, but there is also great variation in methane flux within mires. To understand within-mire variation in CH<sub>4</sub> fluxes, it is essential to identify the related variables. In previous studies, temperature has been shown to influence methane flux, and there are some studies showing that variation in vegetation could also explain within mire variability in CH<sub>4</sub> flux. The net CH<sub>4</sub> flux is a balance of processes in the peat. Reduction oxidation (redox) potential reflects these processes by indicating which electron acceptors and donors are frequently used. Therefore, redox potential could predict, if conditions are suitable for CH<sub>4</sub> production or consumption, which would make redox potential a useful predictor for temporal upscaling of CH<sub>4</sub> flux. CH<sub>4</sub> flux together with CO<sub>2</sub> flux was measured at a boreal fen in Sodankylä during the growing season of 2019. Flux measurements were carried out five to six times per week at three different vegetation types (flark, lawn and string). Plant functional group leaf area indexes and coverages were measured during the summer and continuous redox potential was measured at each measurement plot. The importance of different predictors was assessed using generalized additive models (GAM). Temperature was the main driver of differences in CH<sub>4</sub> flux over the growing season. Classification into the three vegetation types was, however, not a significant predictor of CH<sub>4</sub> flux. A finer scale classification of plant functional groups, on the other hand, improved the prediction capacity of the model. Redox potential was also a significant predictor and improved the model.

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**Brittini Joette Crosier (EEB):**

### **Patterns of Distance Decay in Finnish Fungal Communities**

Spatial structure of populations is often part of the ground-level knowledge for understanding the evolutionary history, dispersal patterns, and resilience of any given species. One aspect of spatial structure is community distance decay, or the rate at which community similarity decreases with physical distance. Studying community distance decay helps conceptualize dispersal and establishment limitations of different organisms, which is necessary for mitigating biodiversity loss. More and more of the landscape is constantly altered by humans on a very large scale, so it is increasingly important to understand the effects that these anthropogenic changes to the environment has on local populations. Many studies show that habitat fragmentation and loss has greatly impacted the structure of plant and animal communities, but there has been much less focus on fungal communities. The aim of this study is to examine fungal community distance decay from small scale of a couple kilometres or less to a fairly large scale encompassing a landscape of primarily urban, forest, and agricultural areas. Sampling methods were chosen to allow the comparison of communities separated by a mosaic, as well as along a short rural to urban gradient, to assess the effects of habitat change. The role of dispersal ability and functional traits in distance decay is also studied by comparing results from two different methods of fungi sampling. The two methods employed to sample fungal communities were collecting spores from the air using cyclone samplers, and taking fungi biomass from soil cores. All samples were DNA analysed with high-throughput sequencing to get a snapshot of fungal communities in 30 plots around five main localities of middle and southern Finland: Helsinki, Lahti, Tampere, Jyväskylä, and Joensuu.

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**Inari Nousiainen (EEB):**

### **Survival of adult male ortolan buntings during years 2013 - 2019 in Finland**

There has been an European wide decline in populations of birds connected to agricultural areas on last decades. Main reason seems to be the intensification on agricultural practices, but also herbicides use and changes in landscape has been linked to decline. Studying this phenomena gives us more understanding about environmental change and its impact on animal populations, and therefore could give us more insight how to prevent extinctions and loss of biodiversity. My thesis is about a once common agricultural bird, ortolan bunting (*Emberiza hortulana*) and it's decline in Finland. Ortolan bunting has been declining in Finland from 1980- onwards and now it's populations size has shrunk under one percent of what it was before. In the year of 2013 started a research program where they mapped every Ortolan bunting territory and tried to capture and ring the males. Every year, until the year of 2019, they continued this, visited every known territory, counted the birds and tried to capture or see the males. From this data I did survival analysis on Mark- program and population change evaluation on Rtrim -program. Results show that the survival of male ortolan buntings in Finland is quite the same as with other passerines of same size, but the population is still declining. It seems that the reason for a decline of ortolan bunting isn't the adult male survival, but probably survival of the juvenile birds.

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**Elisa Päiviö (EEB):**

### **Effect of historical predation pressure and current predation risk on genetically determined behaviour of the nine-spined stickleback**

Predation is an important driver shaping animal behaviour in the wild. However, it is not easy to demonstrate that specific behaviours are adaptive to certain levels of predation, since behaviour displays notable phenotypic plasticity. We studied how predation shapes genetically determined behaviour of the nine-spined stickleback (*Pungitius pungitius*) through historical predation pressure and by inducing phenotypic plasticity. We reared nine-spined sticklebacks derived from

coastal marine (predator-sympatric) and pond (predator-naïve) populations in a common garden experiment and quantified their behaviour in the presence or absence of natural predators. Pond sticklebacks tended to be more explorative and more risk-taking during foraging than marine sticklebacks regardless of predation risk. In all fish, predator presence decreased the propensity to take risks during foraging, but not exploration tendency. Despite showing similar levels of behavioural plasticity as marine fish, pond fish were still inappropriately active in the presence of predators, and would have a low survival probability in a predator-sympatric environment. Our results provide evidence of local adaptation in behaviour to differing levels of predation in these populations, and that this adaptation comes about as differences in the overall level of behaviour rather than in phenotypic plasticity.

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**Laura Puikkonen (EEB)**

### **Life-history Effects in the Behavior of Svalbard reindeer (*Rangifer tarandus platyrhynchus*): A Focus on Mothers**

Senescence and terminal investment hypotheses are two non-mutually exclusive hypotheses based on the life history theory explaining changes in reproductive success along an individual's age. The senescence hypothesis predicts that due to age-related deterioration of cellular and physiological functions, a parent has less resources to be allocated to reproduction with increasing age. On the other hand, terminal investment hypothesis predicts that as the expected number of future offspring decreases, a parent's investment in reproduction should increase with age. Physical aspects of life histories and reproductive success have been studied in multiple ungulate species such as reindeer (*Rangifer tarandus*). However, the processes of senescence and terminal investment are believed to have an effect on long-living iteroparous individuals' behavior and care of offspring, but studies of the effects are limited. In this study, Svalbard reindeer is used as a model species to analyze the effect of the age to ungulate maternal, social and vigilant behavior and time budget. In addition, the documentation of the behavior of Svalbard reindeer in the summertime provides a baseline for further studies. Behavioral data from marked wild individuals of Svalbard reindeer was collected in the field by focal animal watches and instantaneous scan sampling. These observations were combined with age data from a long-term monitoring program run by the Norwegian Polar Institute and University Centre of Svalbard.

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**Sanna-Kaisa Kivilompolo (ECGS)**

### **Modelation of cyanotoxins' sediment toxicity in subarctic - temperate lakes due climate stress**

Recent climate warming is suspected to be cause to many changes in aquatic ecosystems. In the Arctic freshwater ecosystems Climate Change has already induced and is at risk to cause longer ice-free periods, stronger stratification, browning and shifts in microbial communities. The phenomena are suspected to grow stronger and to cause unpredictable changes in high latitude lakes. Climatic changes may have significant effects on microbial community structure and abundance of species. Especially concerning is predicted and observed increase in cyanobacterial species due to rising temperature. Many cyanobacterial species produce harmful metabolites called cyanotoxins. Chemically cyanotoxins are variable group of organic toxins. Cyanotoxins with variety of harmful effects pose a threat to water safety and health of humans and animals. For example microcystins are known hepatotoxins, anatoxin-a and saxitoxins known neurotoxins and cylindrospermopsin produces wide variety of toxic effects including cyto-, geno- and hepatotoxicity. Sediment may act as a storage of cyanotoxins in aquatic ecosystems. There is some evidence of sorption tendency of cyanotoxins but the topic needs to be studied in more detail. Mobilization of these entrapped toxins may be caused by many variables. For eg. changes in redox-conditions, pH, temperature, oxygen concentration, microbiota and bioturbation. This study is focused in cyanotoxins stored in sediment and possible higher rate of mobilization of cyanotoxins due to climatic change. The goals of this study are to assess ecotoxicity of cyanotoxins in sediment and water column due temperature change, assess potential threat to water safety and aquatic ecosystems and provide new information on behavior and toxicity of cyanotoxins in the environment. The hypothesis 1.1. is that higher temperatures increase sediment ecotoxicity of cyanotoxins and 1.2. is that increase in ecotoxicity is more pronounced in lakes influenced by human activity.