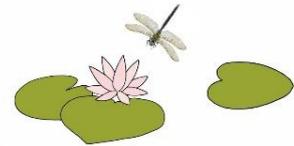


# SPRING



# SYMPOSIUM 28TH

# 2019

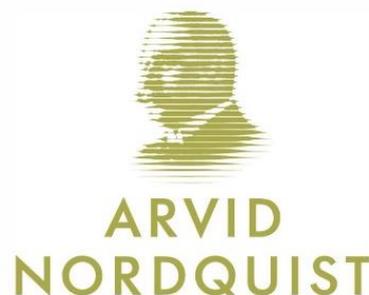
**PROGRAMME AND  
ABSTRACT BOOK**

VIIKKI CAMPUS, UNIVERSITY OF HELSINKI

**4TH - 6TH MARCH AUDITORIUM 2, INFOCENTRE**



# The 28<sup>th</sup> Spring Symposium is supported by the following organizations and companies:



## Organizing Committee

Andrew House

Mikko Kivikoski

Marion Sinclair-Waters

Wenfei Liao

Torsti Schulz

Aina Brias Guinart

## Acknowledgement

The previous Spring Symposium Organizing Team

Otso Ovaskainen, Karen Sims-Huopaniemi

The faculties and the doctoral school

The bosses, colleagues and families

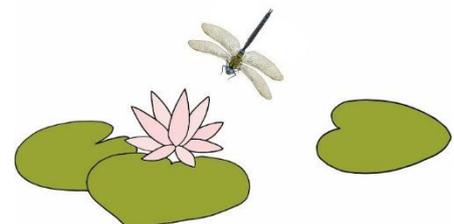
The people and staff of Viikki Campus

... and all those who helped us through the entire project

and whom we could not fit in this limited space

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# Programme 2019

## MONDAY 4TH MARCH 2019

9:15 Otso Ovaskainen Opening Words

### KEYNOTE TALK

CHAIR: ANDREW HOUSE

9:30 Dan Warren The age of big data in correlative ecology

### 10:30 COFFEE

### SESSION I

CHAIR: ANDREW HOUSE

10:50 Joel Jalkanen Spatial prioritization of urban biodiversity, recreation use, and health effects

11:10 Marju Prass Enhancing natural biocontrol: could a snail control the invasive lupine?

11:30 Jussi Mäkinen Predictive species distribution models need to account for spatial confounding

11:50 Sinikka Robinson Impacts of environmental temperature on the stability of terrestrial communities

### 12:10 LUNCH

### SESSION II

CHAIR: MIKKO KIVIKOSKI

13:20 Tuuli Rissanen Importance of cryosphere in studying species' distributions

13:40 Pekka Niittynen Winter outweighs summer climate in driving Arctic tundra vegetation

14:00 Konsta Happonen The causes of plant community functional variation in a tundra landscape

14:20 Julia Kempainen Shrubs constructing tundra soils

### 14:40 COFFEE

### SESSION III

CHAIR: MIKKO KIVIKOSKI

15:00 Sirja Viitamäki Functions and activity of microbial communities in the changing Arctic

15:20 Matti Ruuskanen Sediment DNA in the Northern Hemisphere tracks anthropogenic Hg deposition

15:40 Toni Eerola Mineral exploration company websites in Finland: sustainability, technology and social license to operate

## TUESDAY 5TH MARCH 2019

### KEYNOTE TALK

CHAIR: MARION SINCLAIR-WATERS

9:30 Roosa Laitinen What can *A. thaliana* hybrids tell us about evolution?

10:30 COFFEE

### SESSION IV

CHAIR: MARION SINCLAIR-WATERS

10:50 Twinkle Solanki UV-screening and recovery of spring photosynthetic capacity in evergreen shrubs  
11:10 Samuli Junttila Using multispectral terrestrial lidar for early detection of tree decline  
11:30 Charlotte Angove Nutrient cycling by aquatic plants  
11:50 Suvi Sallinen Plant fitness effects of varying pathogen communities

12:10 LUNCH

### SESSION V

CHAIR: WENFEI LIAO

13:20 Hanna Rosti Identity, population size and conservation status of the enigmatic Taita Dwarf Galago  
13:40 Joni Ollonen Genotype-phenotype mapping of skull development and adaptation in squamate reptiles  
14:00 Katja Koskenpato Geographical variation in plumage coloration in the colour polymorphic tawny owl  
14:20 Irene Conenna Space use and movement seasonality of a desert-dwelling bat

14:40 COFFEE

### SESSION VI

CHAIR: WENFEI LIAO

15:00 Annikka Herrero Formation of local populations for Eurasian lynx  
15:20 Milla Salonen Cat behavior: an evolutionary perspective  
15:40 Linda Loikkanen Antibodies against hepatitis E virus in Finnish moose

16:00 POSTER SESSION

18:00 DINNER\*

\*Please contact marion.sinclair-waters(at)helsinki.fi in advance.

**WEDNESDAY 6TH MARCH 2019**

**KEYNOTE TALK**

**CHAIR: AINA BRIAS-GUINART**

9:30 Philine Feulner Genomics of rapid adaption

**10:30 COFFEE**

**SESSION VII**

**CHAIR: AINA BRIAS-GUINART**

10:50 Xueyun Feng Introgression in the nine-spined stickleback

11:10 Marion Sinclair-Waters Moving beyond single SNP approaches for understanding the genetic basis of complex traits: a case study in Atlantic salmon

11:30 Bohao Fang How parallel is parallel evolution? The case of the three-spined stickleback

11:50 Jack Beresford Gene expression in the genomes of hybrid *Formica rufa* group ants

**12:10 LUNCH**

**KEYNOTE TALK**

**CHAIR: TORSTI SCHULZ**

13:20 Laurent Keller Sex, sociality, and supergenes

**14:20 COFFEE**

**SESSION VIII**

**CHAIR: TORSTI SCHULZ**

14:40 Filipe Chichorro Using computer simulations of virtual organisms to understand which traits drive them to extinction

15:00 Mervi Laaksonen Species and their traits in dead pines

15:20 Janne Koskinen Fungus-associated arthropods

15:40 Ana Salgado Drought alters host plant quality and threatens its insect herbivore

**18:00 GRANDE FINALE (REGISTRATION REQUIRED)**

## POSTER SESSION \*

1	Meri Lähteenaro	The twisted-wing parasitoid genus <i>Stylops</i> (Strepsiptera: Stylopidae) in Finland
2	Sonja Still	Summer and winter leaves of woodland strawberry ( <i>Fragaria vesca</i> ) genotypes
3	Jakke Neiro	Evodevo of insect wing venation
4	Suamya Mehta	Novel inhibitors of intracellular lipid phosphatase SHIP2 and their effects on
5	Anna Lyssenko	Biodiversity and oxygen dynamics within seagrass and macroalgal canopies
6	Heli Kainulainen	Shrubification of the Arctic - Modelling distribution changes of tree species
7	Markus Korpela	Autoimmune Regulator
8	Raphaël Martin-Roy	Can hybridization fuel adaptation under climate change?
9	Assia Pekonen	The nectar source plants in the field margins in Southern Finland

\*The poster session is on Tuesday 5<sup>th</sup> March, 16:00 – 17:20.

# Welcome to Spring Symposium 2019

Ladies and gentlemen, students and faculty members, presenters and evaluators, peers and colleagues,

We are honoured to welcome you to the 28th Spring Symposium. The Spring Symposium is organised annually by the Doctoral Programme in Wildlife Biology Research (Finnish acronym LUOVA) of the University of Helsinki, in collaboration with the Faculty of Biosciences and Environmental Sciences, the Faculty of Agriculture and Forestry, and Finnish Museum of Natural History.

The Spring Symposium brings together PhD students active in research fields related to ecology, evolution, systematics, and nature conservation. This event gives students an opportunity to present their work in a friendly atmosphere and to gain valuable feedback from other students and three international evaluators.

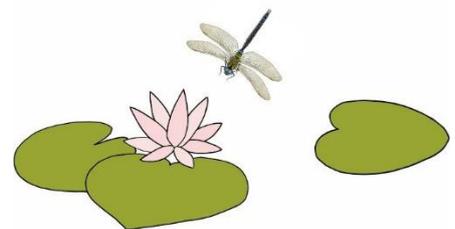
This year, we have interesting oral presentations and posters addressing important issues related to different aspects of ecological, evolutionary, and conservation biology. The best talk will be awarded with Olli's prize, which is a 1000 € sponsorship for an international conference. There will also be nice 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 all abstracts listed chronologically according to sessions. We hope that you can attend as many talks as possible to provide valuable feedback to the speakers as well as engaging in lively discussions.

We hope you will enjoy the symposium!

The Organising Committee,

Andrew, Mikko, Marion, Wenfei, Torsti, Aina



# Evaluators

## **Dan Warren**

**Researcher of evolutionary ecology at the Senckenberg Biodiversity and Climate Research Center in Frankfurt, Germany**



I have broad interests in evolution, ecology, conservation, and animal behavior. My primary research program focuses on the evolution of species' environmental tolerances and spatial distributions, with frequent applications to conservation-oriented empirical studies. My work includes both basic and applied research, with a particular focus on developing novel quantitative methods. I also maintain active research programs in phylogenetic methods and theory, as well as the neuroecology of marine fishes.

## **Roosa Laitinen**

**Researcher from the Max Planck  
Institute of Molecular Plant  
Physiology, Germany**



My research focus is to investigate mechanisms of hybrid incompatibility in plants using *Arabidopsis thaliana* (*Arabidopsis*) as model system. Knowledge of this process will further our understanding of the first steps towards reproductive isolation and speciation, even before species have diverged. I take advantage of both, publically available accessions from diverse geographical locations and local accessions collected in recent years. My work combines methods of traditional and modern genetics and genomics to state-of art molecular methods available for model system *Arabidopsis*.

## **Philine Feulner**

**Researcher at the Center for Ecology, Evolution and Biogeochemistry, Swiss Federal Institute of Aquatic Science and Technology, Switzerland**



**My research focuses on identifying the evolutionary processes relevant for shaping genetic diversity and on understanding how evolutionary processes constrain or facilitate adaptive evolution and speciation. To do so, I build new genomic resources and generate and analyse large-scale genomic data sets. Ultimately, I aim to understand which evolutionary processes drive molecular change that occurs rapid enough to allow a feedback between ecology and evolution and how ecological and evolutionary processes influence the rate of molecular adaptive change at a genome-wide scale. Largely, I work on freshwater fish, recently with a major focus on the adaptive radiation of Alpine whitefish, but I also study the dynamics of genomic change in an experimental algae virus system attractive due to the short generation times and the ability for experimental manipulations.**

# KEYNOTE TALK I

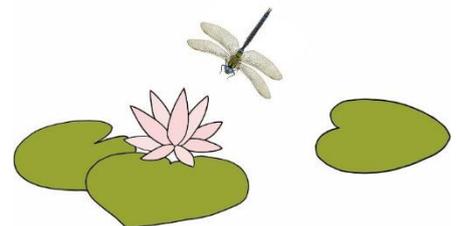
## Dan Warren:

### **The age of big data in correlative ecology**

The rapidly expanding pool of large data sets on species distributions, community composition, and environmental factors has been paralleled by an increasing number of methodological approaches to analyze this data. If done correctly, this represents an unprecedented opportunity for understanding ecological processes at large scales. However, it also represents an opportunity to be wrong about those same processes at a scale that was previously not possible. In this talk, I will use examples from ecology and other fields to discuss some of the issues that arise when we take big data approaches to ecological questions, and how we might avoid some of the known issues that await us as correlative approaches to ecological questions become increasingly prevalent.



**SESSION I**  
**MONDAY 4<sup>TH</sup> MARCH 2019**  
**10:50 -12:10**  
**INFO 2**



# Joel Jalkanen<sup>DENV1</sup>:

## **Spatial prioritization of urban biodiversity, recreation use, and health effects of urban green**

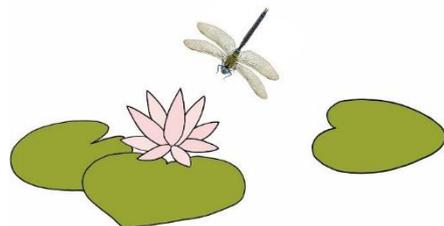
Urban green improves urban peoples' physical, mental, and societal health and well-being in many ways. Urban areas can also harbor great biodiversity with various kinds of habitats and associated communities. However, in growing cities, there is a need to balance, and manage trade-offs, between human use and biodiversity in green areas. In the presentation, I will introduce my study plan for spatial prioritization between these different dimensions of urban green. Biodiversity data includes maps about various urban habitats and different types of community attributes they support (richness, abundance, biomass, etc.). Human use will include demographic information and point-to-point accessibility data from Helsinki. With this data, many types of accessibility to green areas, and the associated health effects, can be estimated, based on demographic groups and travel types. The spatial prioritization will be done with the Zonation software.



## Marju Prass<sup>LUOVA</sup>:

### Enhancing natural biocontrol: could a snail control the invasive lupine?

The non-native herb *Lupinus polyphyllus* has invaded road verges and disturbed grasslands in Finland. Specialist herbivores are usually absent, but a generalist snail is consuming the lupine vigorously. However, the impact of generalist invertebrates has often been regarded negligible. Yet, long-term research on herbivory opposes this concept. Our aim is to enhance the natural biocontrol by snails with liming: high soil pH stunts lupine growth, and calcium could attract snails. In 2017, we set up a 3-year experiment at seven grassland sites and monitored seedling emergence, plant growth and fecundity of lupines in study plots. Results indicate that snails decrease the biomass and density of lupine populations. Yet, snail herbivory did not influence the fecundity and growth of individual plants. However, we hypothesise that the negative effect of herbivory on lupines will increase with time, and that snail herbivory in combination with liming could be a promising biocontrol solution.



# Jussi Mäkinen<sup>GEODOC</sup>:

## **Predictive species distribution models need to account for spatial confounding**

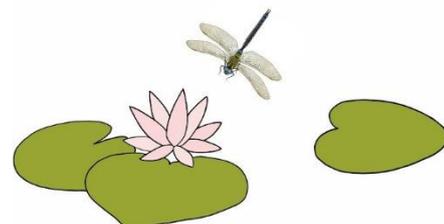
Transferability of a species distribution model depends on the accuracy of the estimates for the fixed effects of environmental covariates. However, estimates may be confounded by spatially constructed errors which reflect unmeasured environmental and ecological processes. Moreover, spatial errors may correlate with measured covariates, which increases uncertainty about the covariate effects. The model transferability is dependent on how accurately the covariate effects are estimated and distinguished from spatial errors. Here, I constrain the proportions of spatial and environmental effects with respect to the explained variation of the species occurrence and abundance data. Prior distributions on environmental and spatial functions restrict the variation of the functional values. I demonstrate the approach on occurrence data of vascular plants, where occurrence patterns are unevenly explained with the available covariates. The bias and variance of extrapolation are key elements in the use of models and highly dependent on prior assumptions about the occurrence pattern.



# Sinikka Robinson<sup>LUOVA</sup>:

## Impacts of environmental temperature on the stability of terrestrial communities and food webs

Understanding and quantifying impacts of warming across multiple levels of biological organisation is important for modelling the ecological and evolutionary dynamics of ecosystem change. I use a natural warming experiment in Iceland to investigate the impact of temperature on the stability of terrestrial communities and food webs. Sample collection over several time points within a season allows assessment of whether temperature alters temporal variability in terrestrial communities and compositional turnover. I construct food webs based on consumer-resource feeding links, exploring the topological structure of food webs along the temperature gradient and temperature effects on their stability. These data are used to test if with increasing soil temperature: (1) temporal variability in community composition increases; (2) species turnover through time increases; (3) food web complexity decreases; (4) temporal stability of food web properties decreases. Results remain forthcoming.



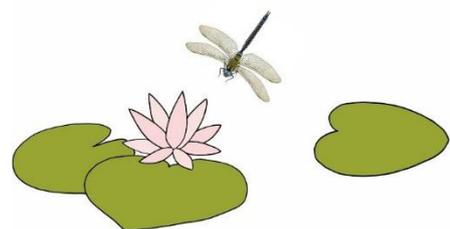
**SESSION II**  
**MONDAY 4TH MARCH 2019**  
**13:20 -15:00**  
**INFO 2**



# Tuuli Rissanen<sup>GEODOC</sup>:

## Importance of cryosphere in studying species' distributions

Majority of the biogeographical research has focused on the role of climate when current environmental conditions and species' distributions are concerned. However, in high-latitude and –altitude regions there are also other highly important drivers shaping species' biogeographical patterns. Cryosphere, the frozen part of Earth system, has rarely been discussed in terms of species' distributions even though it is a crucial feature of cold environments. Below ground permafrost drive Earth surface processes and control water and nutrient cycle and thereby may affect species' occurrences. Above ground snow is a key feature determining both wintering and growing season conditions. To address these often neglected issues, we examine the effect of permafrost and snow cover on vascular plant species' patterns, while controlling for climate and soil factors in a multivariate setting. The study is based on over 8 million observations of ca. 800 species surveyed in Fennoscandian mountain environment.



# Pekka Niittynen<sup>GEODOC</sup>:

## Winter outweighs summer climate in driving Arctic tundra vegetation

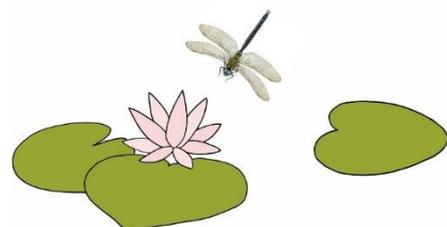
Recent reviews suggest that winter conditions are key drivers of composition and functioning of various ecosystems. During the previous decades, winter season has warmed faster than summer climate across most of the high-latitude regions. Notwithstanding, the importance of winter climate in driving Arctic ecosystem processes is still poorly understood and far less frequently taken into account than summer conditions in climate change impact modelling studies. Furthermore, in the Arctic no robust quantitative analysis has ever been performed that compared the importance of winter vs. summer climates based on direct field measurements. Here, we conduct such comparison of winter and summer temperatures by using unique plot-scale data for three taxonomic groups – vascular plants, lichens and mosses – in an Arctic landscape, while accounting also for the impacts of other key non-climatic environmental factors on the studied species. We show that winter temperatures are far more important than summer thermal conditions in determining species distribution, community, and richness patterns of tundra vegetation, especially for vascular plants and lichens. This is an alarming finding as climate models for high-latitudes project continuing trend of greater winter than summer warming and predict major changes in snow conditions that control the winter temperatures at the ground level. Better accounting of winter conditions in climate change impact models would increase model realism and credibility, potentially revealing significant hidden ecological responses in ecosystems and species assemblages.



# Konsta Happonen<sup>LUOVA</sup>:

## The causes of plant community functional variation in a tundra landscape

The functional composition of plant communities is only weakly related to macroclimate, meaning that landscape and local scale factors are highly important for understanding trait composition and its responses to climate change. Here, we study causes of variation in plant community functional composition in a tundra landscape by investigating the responses of community averaged traits to locally measured environmental conditions. We also quantify intraspecific variation (ITV) and its importance for between-community functional differences and trait-environment relationships. We find that the magnitude of ITV relative to between-species variation differs between traits, and that ITV is not very important for trait-environment relationships. We show that vegetation height increases with temperature, while leaf economics are controlled by snow depth and soil resources. Our results show that predicting ecosystem functional change from temperature changes alone is impossible, and that concurrent changes in snow and soil conditions need to be taken into account.



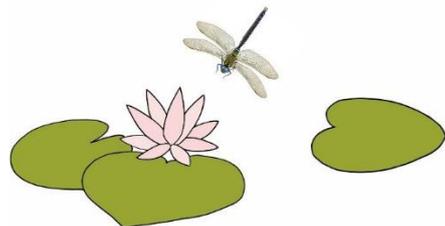
# Julia Kemppinen<sup>GEODOC</sup>:

## Shrubs constructing tundra soils

Tundra biogeography is changing, as shrubs are expanding their distribution towards higher latitudes and altitudes. In a dwarf shrub dominated tundra, we examined the impacts of shrubs on multiple soil conditions, namely soil moisture, soil temperature, and soil organic matter (SOM). These soil factors are resources and direct drivers of tundra ecosystem functions. Thus, they are vital for the carbon and water cycles, and for the growth and distribution of tundra flora and fauna as well. Our *in situ* data were collected from 178 plots located in northern Fennoscandian mountain tundra. In addition to species-specific shrub coverage, the data consist of field-quantified soil properties and snow depth measurements. We measured surface soil moisture and temperature throughout the growing-season, and analysed SOM from both organic and mineral layers. We controlled the influence of landscape factors, such as climate and topography, on soil conditions. We used high-resolution LiDAR (Light Detection and Ranging) based variables and structural equation modelling (SEM). SEM enables building a hypothesis-based model, which takes into account the hierarchy as well as the direct and indirect relationships in the study system. We found direct shrub effects on all soil properties. Shrubs act as mediators on the indirect impacts of snow and landscape. We found no direct links between snow and soil properties. Shrubs lower soil temperatures, decrease soil moisture, and increase the amount of SOM. Our results shed light on how dwarf shrubs affect tundra soil conditions. Observational studies, such as this, are valuable for understanding tundra vegetation relations, as these systems show slow responses to manipulation. The expected changes in vegetation of the high-latitudes are likely to alter the very foundations of entire tundra system.



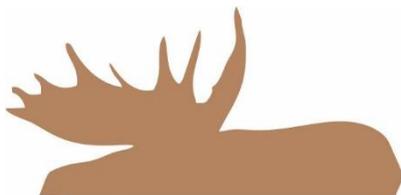
**SESSION III**  
**MONDAY 4TH MARCH 2019**  
**15:20 -16:00**  
**INFO 2**



## Sirja Viitamäki<sup>DPPS</sup>:

### Functions and activity of microbial communities in the changing Arctic

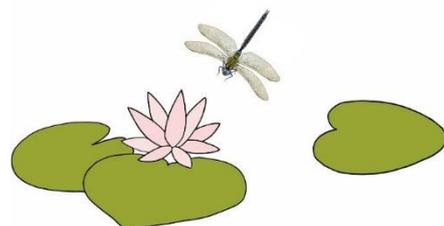
Soil microbial communities have critical role in biogeochemical processes on Earth, but our understanding of their response to the ongoing climate change is poor. Arctic and subarctic soils harbor approximately 50 % of Earth's below ground carbon. Warmer climate leads to increased rate of soil organic matter decomposition in polar regions, but the overall impact to carbon and other biogeochemical cycles is difficult to predict without a deeper understanding of the soil microbial ecology. Our aim is to improve the knowledge of the ecology of microbial communities in subarctic soil in changing climate conditions, and to consider how this data could be used to predict the microbial feedback to environmental change. Metatranscriptomics was applied to elucidate the functions and activity of microbial communities in subarctic soils collected from Kilpisjärvi, northern Finland. The sampling site forms a climate gradient, which represents the possible scenarios of the impact of climate change to soil microbial community functions. Various metadata including pH, carbon content, soil organic matter, support the metatranscriptomic data. Our data shows differences in the composition and activity of the microbial communities along the climate gradient. Soil pH, organic matter and moisture were the main drivers of activity in organic layer, whereas pH was in the mineral layer. Our results give information on how environmental factors contribute to microbial activity and again its feedback effect to warming climate.



# Matti Ruuskanen<sup>UNIVERSITY OF OTTAWA</sup>;

## Sediment DNA in the Northern Hemisphere tracks anthropogenic Hg deposition

Anthropogenic remobilization of toxic heavy metals such as mercury (Hg) has considerably increased since the Industrial Revolution in the late 1700s, and these remobilized pollutants have reached environments far from their emission point. Furthermore, microbially mediated transformations of bioavailable Hg in the sediment can produce bioaccumulating methylmercury, which has serious toxic effects in higher organisms. We analyzed DNA in sediment cores from eight lakes on the Northern Hemisphere. We establish that the microbial mercury resistance gene (*merA*) can likely act as a biomarker for historical Hg deposition. We were able to pinpoint the start of a drastic increase in its effective population size to year  $1783.8 \pm 3.9$  CE. These results suggest that increasing global atmospheric loadings of Hg affect the evolutionary dynamics of microbial mercury reduction and that in turn, these dynamics can be used to track historical Hg bioavailability.

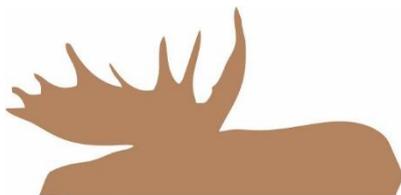


# Toni Eerola<sup>DENVI</sup>:

## **Mineral exploration company websites in Finland: sustainability, technology and social license to operate**

A survey on websites of mineral exploration companies operating in Finland is described. The surveyed topics were the origin of the companies, websites and their language, responsibility reporting, use of new technology, and social media, as well as mentions on social license to operate (SLO). The purpose of the survey was to find and analyze companies which use new technologies, and to define their understanding of SLO. Their relationship with the local communities was reflected through a media analysis.

The results of the survey and their implications are presented. The survey is part of the EU Horizon 2020 financed New Exploration Technologies (NEXT) Project, and it is related with a similar ongoing survey of mineral exploration company websites in Sweden, as well as literature review on SLO in mineral exploration.

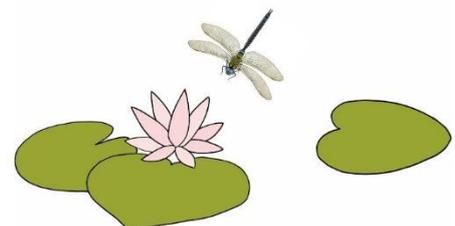


# KEYNOTE TALK II

## Roosa Laitinen:

### What can *A. thaliana* hybrids tell us about evolution?

Hybrids occasionally exhibit problems that result in reduced fitness when compared to their parents. These hybrid incompatibilities exist throughout taxa and can restrict gene flow in populations and thereby lead to genetic differentiation between populations and ultimately speciation. In the past ten years, natural variation in *Arabidopsis thaliana* has proven to be an excellent model to investigate intraspecific hybrid incompatibility and several studies have reported how conflict between gene variants can result in hybrid dysfunction in this species (Vaid and Laitinen, 2018). The most common type of post-zygotic hybrid incompatibility in *Arabidopsis* and in plants is hybrid necrosis, in which hybrid problems are associated with autoactivation of immune responses (Bomblies and Weigel, 2007). Yet, the diversity of different molecular mechanisms contributing to hybrid incompatibility and the evolutionary forces maintaining the incompatibility alleles in populations are largely unknown. Our research focus is to investigate different mechanisms of hybrid incompatibility in plants using *A. thaliana* (*Arabidopsis*) as model system. We take advantage of both, publically available *Arabidopsis* accessions from diverse geographical locations and local accessions that we have collected in recent years. In my talk, I will introduce our recent findings of three new hybrid incompatibility cases highlighting that not only rapidly evolving, but also genes involved in conserved processes



may underlie hybrid incompatibilities (Plötner et al. 2017; Alhajturki et al. 2018). I will also discuss our future plans on characterizing the function of genes involved in different hybrid incompatibilities and investigating their role in local adaptation and evolution.

### References:

Alhajturki D\*, Muralidharan S\*, Nurmi M, Rowan BA, Lunn J, Boldt H, Salem M, Alseekh S, Jorzig C, Feil R, Giavalisco P, Fernie A, Weigel D, Laitinen RAE. Dose-dependent interactions between two loci trigger altered shoot growth in BG-5 x Kro-0 hybrids of *Arabidopsis thaliana*. *New Phytologist*, 2018.

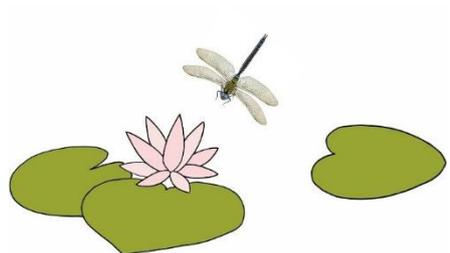
Bomblies K, Weigel D. Hybrid necrosis: autoimmunity as a potential gene-flow barrier in plant species. *Nature Reviews Genetics*, 2007.

Vaid N, and Laitinen RAE. Diverse paths to hybrid incompatibility in *Arabidopsis*. *The Plant journal*, 2018.

Plötner B, Nurmi M, Fischer A, Watanabe M, Schneeberger K, Holm S, Vaid N, Schöttler M, Walther D, Hoefgen R, Weigel D, and Laitinen RAE. Chlorosis caused by two recessively interacting genes reveals a role of RNA helicase in hybrid breakdown in *Arabidopsis thaliana*. *Plant Journal*, 2017.



**SESSION IV**  
**TUESDAY 5TH MARCH 2019**  
**10:50 -12:10**  
**INFO 2**



## Twinkle Solanki<sup>DPPS</sup>:

### UV-screening and springtime recovery of photosynthetic capacity in leaves of *Vaccinium vitis-idaea* above and below the snow pack

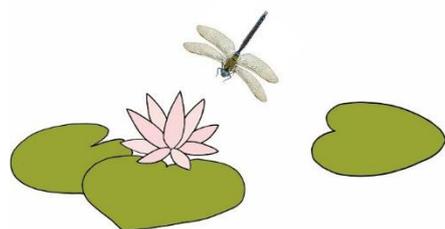
Climate change is expected to affect patterns of snowmelt, changing the depth and duration of the snowpack, which may disrupt the timing of seasonal acclimation in the field-layer community. At Hyytiälä Forestry Station, central Finland, we tested the importance of exposure to fluctuating temperatures above the snowpack on the flavonol concentration and photosynthetic capacity of leaves at different heights on hummocks of *Vaccinium vitis-idaea* L. by monitoring the leaf pigments during the winter and subsequent spring recovery. Our results showed that leaves exposed to colder temperatures and higher solar radiation towards the top of hummocks suffered greater photoinhibition with higher epidermal UV-screening than those at the base of hummocks. Irrespective of timing of snow-melt, photosynthesis fully recovered in all leaves, suggesting that *V. vitis-idaea* has the potential to exploit the continuing trend for longer growing seasons in central Finland without incurring significant impairment from reduced duration of snow cover.



## Samuli Junttila<sup>AGFOREE</sup>:

### Using multispectral terrestrial lidar for early detection of tree decline – from leaf water content to fine structural details

Climate change is causing novel stress to forests that is difficult to predict. New methods for objective estimation of tree decline are required to further understand and evaluate the effects of climate change on forests. Multispectral lidar can provide highly detailed measurements of tree structure and reflectance simultaneously enabling novel approaches for detecting tree stress. A novel method for detecting and evaluating tree decline was developed using multispectral terrestrial lidar. We found that multispectral lidar can detect and assess tree decline of single trees with high accuracy in a forest infested by *Ips typographus* (L.) and its fungal symbionts. The developed methods showed potential in discriminating healthy and stressed trees already in the early stages of tree decline when the foliage did not show visual symptoms. Therefore, the methods could provide new means for objective assessment of early tree decline allowing improved estimation, prediction and mitigation of forest damages.



# Charlotte Angove<sup>LUOVA</sup>:

## Nutrient cycling by aquatic plants

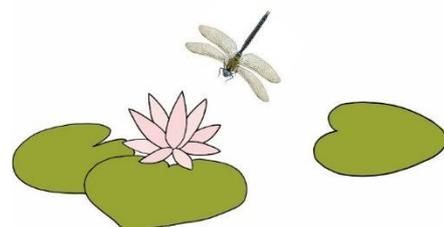
Eutrophication is the greatest risk to coastal habitats in the Baltic Sea. Aquatic plants store and sequester nutrients, and once these nutrients are stored they can no longer be used to fuel eutrophication. Therefore, aquatic plants are valuable for inhibiting the process of eutrophication. We investigate nutrient cycling from the perspective of the plant; what is limiting the plant, what helps the plant to cycle nutrients more effectively, and we do this by conducting *in situ* experiments where we see how plants respond to our treatments. In this talk, I will briefly describe three experiments which we have conducted, in order to communicate their combined message about aquatic plants' nutrient health in the northern Baltic Sea.



## Suvi Sallinen<sup>LUOVA</sup>:

### Consequences of varying pathogen communities on fitness of host plants

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 consequences of varying pathogen communities on host growth and fitness have rarely been explored. To test how the consequences of single pathogens and different combinations of pathogens vary, I performed a common-garden experiment where cloned *Plantago lanceolata* plants of four genotypes were infected with four pathogen treatments: powdery mildew fungus *Podosphaera plantaginis*, stalk disease fungus *Phomopsis subordinaria*, *Plantago lanceolata* Latent Virus (PILV), and a wild virus treatment of pooled inoculum from symptomatic plant collected from Åland Islands. I measured the growth, seed production and symptoms of these plants through the growing season. These results shed light on how the true diversity of pathogens affects wild populations and drives the evolution of resistance.



**SESSION V**  
**TUESDAY 5TH MARCH 2019**  
**13:20 -14:40**  
**INFO 2**



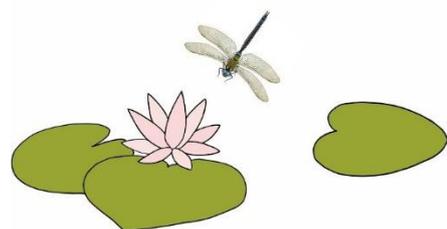
# Hanna Rosti<sup>LUOVA</sup>:

## Identity, population size and conservation status of the enigmatic Taita Dwarf Galago

In 2002 A. Perkin and coworkers reported that a species of Dwarf Galago (*Paragalago* sp.) existed in two relict fragments of indigenous montane forest in the Taita Hills, Kenya. Based on sightings and vocalizations the authors suspected that the animal could represent a Mountain Dwarf Galago (*Paragalago orinus*) or possibly a previously unknown species or subspecies.

We have been able to confirm that a population of Dwarf Galagos exists in Ngangao and Mbololo forests. Since then we have started fieldwork aiming at identifying the species, estimating its current population size and assessing its conservation status.

Based on our new recordings and photographs galago specialists (Tom Butynski, Andrew Perkin, Simon Bearder and Yvonne de Yong) now suspect that the newly discovered species could, unexpectedly, belong to Kenya Coast Dwarf Galago (*Paragalago cocos*).



# Joni Ollonen<sup>LS</sup>:

## Genotype-phenotype mapping of skull development and adaptation in squamate reptiles

Skull bone diversification has played a major role on the adaptive radiation of vertebrates, and differences in facial morphology have significant ecological and clinical implications. However, the developmental mechanisms leading to different skull phenotypes are incompletely understood in vertebrates. In particular, squamates (snakes and lizards) are the second-most diverse group of tetrapods and show exceptional diversity in skull morphology, making them an ideal group for elucidating the mechanisms promoting phenotypic diversification.

We performed a large-scale and integrative characterization of skull shape evolution in squamates, by covering all major lineages of lizards and snakes, using a geometric morphometric approach integrating developmental, ecological, and phylogenetic data. Strikingly, our data reveal major shape variations in both cranium and mandibular apparatus between major squamate groups, in particular between snakes and lizards, as well as significant cranial shape convergence among fossorial lizard and snake species. Additionally, analyses of morphological modularity and integration further indicate the presence of evolutionary modules in the squamate cranium. Finally, our heterochrony analyses, based on quantification of ontogenetic trajectories in a unique dataset of embryonic squamate skulls, suggest that snakes have evolved novel craniofacial specializations through acceleration of ossification.

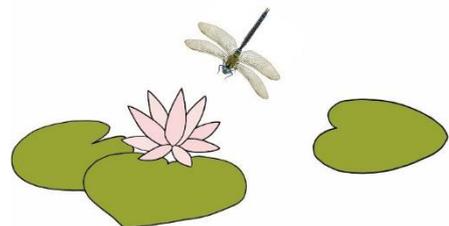
This set of results demonstrates the importance of the relationships between skull shape, ecology, and development in snakes and lizards, and our current analyses involve the identification of the precise developmental mechanisms and signaling pathways underlying skull diversification within squamates, but also within vertebrates as a whole.



# Katja Koskenpato<sup>LUOVA</sup>:

## Geographical variation in plumage colouration in the colour polymorphic tawny owl

Gloger's rule states that animals are expected to be paler with increasing distance from the equator. This cline is predicted to occur also within colour polymorphic species, as morphs are expected to be adaptations to different environments. Tawny owls (*Strix aluco*) have two melanin based colour morphs: reddish-brown and pale grey. The grey morph has higher survival than the reddish-brown under snowy winter conditions, but the reddish-brown performs better in favourable food conditions. We therefore expected that there is a latitudinal cline in colour with the grey morph being more common than the reddish-brown in Northern and harsher environments. We also expect a temporal change in this cline as winters have become milder. With a huge dataset of tawny owl observations across Europe, we aim to find factors affecting the spatial and temporal appearances of the morphs. We aim to shed light on how organisms can adapt to changing climate.



## Irene Conenna<sup>LUOVA</sup>:

### **Space use and movement seasonality of a desert-dwelling bat revealed by miniature GPS loggers.**

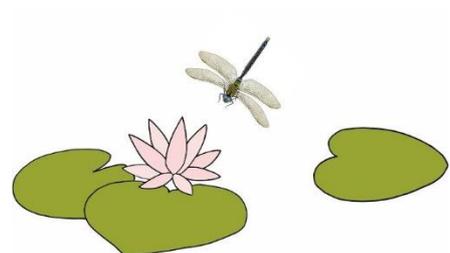
Desert-dwelling bats are believed to be vulnerable to increased aridity predicted under future climate change. However, information on their ecological requirements and strategies to cope with drought is still limited. We employed state-of-the-art GPS loggers to track the yellow-winged bat *Lavia frons* in a desert in northern Kenya, aiming to: 1) describe space use across a desert landscape; 2) identify movement response to seasonal drought.

Bats were tracked during dry and wet seasons. Home ranges were estimated and subsequently used to explore territoriality between neighbouring individuals. We assessed movement seasonality by testing the variation in home range size and activity between seasons.

The bats moved over very small home ranges, with potential members of a pair sharing territory and allowing little overlap with neighbours. During the dry season, when resources are scarce, bats covered larger areas and exhibited high activity levels for a longer time, indicating a trend for high investments to fulfil energy intake. Further exploring these trends will valuably contribute to predicting the impact of future increase in aridity on desert-dwelling bats.



**SESSION VI**  
**TUESDAY 5TH MARCH 2019**  
**15:00 -16:00**  
**INFO 2**



# Annika Herrero<sup>LUOVA</sup>:

## Formation of local populations for Eurasian lynx

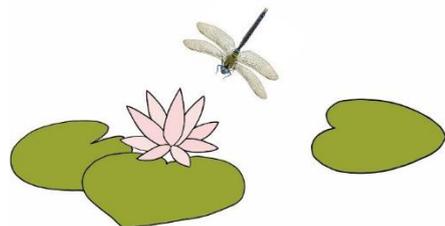
Many highly mobile terrestrial carnivores may exhibit strong genetic clustering and non-random gene flow even in the absence of geographical barriers. Relatedness affects spatial distribution but may differ between sexes due to different evolutionary drivers on for example kin selection. Dispersal often takes place between a young animal on its natal home range and that of an adult, reproducing individual. Dispersal may break the genetic clustering in space unless an adequate proportion of the dispersing individuals either stay or return close to the natal range. The structure, however, seems to be rather dynamic in character. We studied relatedness and dispersal features in the Eurasian Lynx (*Lynx lynx*) in Southern Finland. Our ultimate goal is to explain the formation of lynx populations in a local scale.



# Milla Salonen<sup>ILS</sup>:

## Cat behavior: an evolutionary perspective

The cat is the world's most popular pet, outnumbering even the domestic dog. The modern cat is the result of domestication some 10 000 years ago followed by recent intentional breeding. As a pet living in home environment, domestic cat is seldom the target of evolutionary ecology research. However, domestic animals provide an opportunity to compare historical long-lasting natural selection to recent strong artificial selection. Wildcats, the ancestors of domestic cats, were shy and solitary predators, whereas modern cats seem to enjoy the company of other cats and people. Many behavior traits, including shyness and aggression toward conspecifics, were once beneficial for wildcats trying to survive in a world full of predators and competitors, but these traits are now unwanted and selected against, as social and curious cats make better pets.



# Linda Loikkanen<sup>FOODHEALTH</sup>:

## Antibodies against hepatitis E virus in Finnish moose

Several studies have reported the presence of a zoonotic hepatitis E virus (HEV) in cervids, and in Finland zoonotic HEV-3 genotype has been recorded previously in pigs. In this study, our aim was to find out the presence of HEV in Finnish cervids.

Our sampling frame was a cervid serum bank at the Faculty of Veterinary Medicine, University of Helsinki. We focused on three different regions in Finland, and randomly selected 162 moose and 50 white-tailed deer samples. We analysed the samples for total anti-HEV antibodies using a double-sandwich ELISA assay.

Anti-HEV antibodies were detected in 10 out of the 162 moose sera (6.2%) but not in any of the white-tailed deer sera. HEV-antibody-positive animals were detected in all three region, indicating exposure could be widespread.

We demonstrated the presence of anti-HEV antibodies in Finnish moose sera, which suggests that HEV is circulating among Finnish moose.

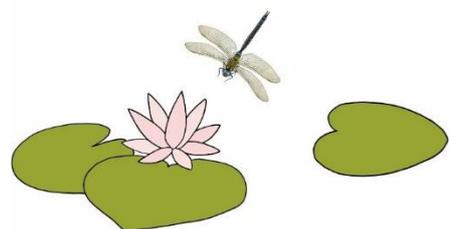


# KEYNOTE TALK III

## Philine Feulner:

### Genomics of rapid adaptation

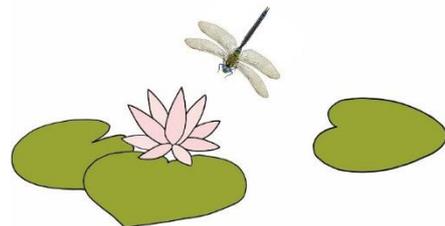
Understanding how rapid adaptive genetic variation builds up, and if so, under which circumstances it is maintained or lost, requires both the identification of beneficial mutations in the genome and the ability to follow the temporal dynamics of such adaptive variants. Novel adaptations are based on underlying genetic variants, which are ultimately generated by mutation and recombination. Genetic admixture and spatially structured populations further allow for the maintenance of genetic variants. In my talk I aim to disentangling processes that drive the dynamics of adaptation making use of two study approaches. (1) I will present results from chemostat experiments, in which a green algal host and its virus rapidly evolved resistance and counter adaptation. We traced rapid genomic changes in coevolving host-virus populations over about 100 generations and show both the influence of antagonistic selection but also demographic changes on genomic diversity during coevolution. A key observation is that the evolutionary dynamics in this system are coupled to demographic changes; i.e. changes in population sizes and abundances of distinct genotypes. (2) I will present genomic data obtained from historical scale collections, which provided us with first insights into the dynamics of change in Alpine whitefish during an intense eutrophication period. We have reconstructed the genome of an extinct whitefish species from Lake Constance and identified about 11% of the



genome of the extinct species across three contemporary whitefish species. This shows that all four species in the lake hybridized during a period of anthropogenic eutrophication of the lake, and before one of the species went extinct. This result uncovers the impact of anthropogenic ecosystem changes on the genomic composition of the Alpine whitefish assemblage.



**SESSION VII**  
**WEDNESDAY 6TH MARCH 2019**  
**10:50 -12:10**  
**INFO 2**



**Xueyun Feng<sup>LUOVA</sup>:**

**Introgression and demographic history in the nine-spined stickleback**

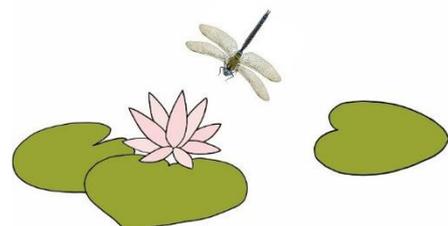
Pleistocene glaciations have strongly affected temperate zone organisms and left footprints on their genetic variability and differentiation. During the last glaciation period, both landscape and sea water levels in Fennoscandia changed drastically, most likely influencing the patterns and extent of introgression, population structuring, and effective size ( $N_e$ ) of nine-spined stickleback (*Pungitius pungitius*) populations. To understand the effects of these complex process on the genetic variability within and among extant *P. pungitius* populations, we obtained Whole Genome Re-sequencing (WGR) data from 530 individuals from 27 localities in Europe, and mapped them to a high quality annotated reference genome. The preliminary results show clear evidence of introgression from the European Western Lineage (WL) to the European Eastern Lineage (EL) in both Baltic Sea and Swedish coastal freshwater populations. This is consistent with earlier findings of widespread mitochondrial genome admixture among WL and EL lineages in the southern Baltic Sea. When an outgroup species was used to polarize the detected variation, we discovered that the proportion of WL ancestry (i.e. admixture) decreased with geographical distance from the southern Baltic contact zone (46% admixture) to the northern Baltic (24%). Interestingly, the Swedish freshwater populations were found to exhibit ~5% WL ancestry, suggesting that WL-EL admixed individuals were involved in the colonization of freshwater habitats ca 10,000 years ago. Analyses of demographic history show that the admixed Baltic populations has higher  $N_e$  than the WL marine populations. In contrast,  $N_e$  of all pond populations has continuously decreased since the start of isolation ca 10,000 years ago. In general, the results paint a clear picture of the significant role of introgression and isolation in shaping patterns of genetic differentiation and variability in sticklebacks. We continue to investigate further questions involving whether the observed introgression is confined to particular genomic regions, and if it is adaptive.



# Marion Sinclair-Waters<sup>LUOVA</sup>:

## Moving beyond single SNP approaches for understanding the genetic basis of complex traits: a case study in Atlantic salmon

A major goal in biology is to understand the genetic basis of phenotypic variation. Genome-wide associations studies (GWAS) are commonly used to identify phenotypic effects of genomic variation. However, GWAS are often based on an oversimplified model that measures the effect of each single nucleotide polymorphisms (SNPs) independently. This single-SNP approach can fail to identify polygenic effects where a SNP can have a small undetectable effect, but in combination with other loci may have a larger effect. In addition, causal variation can emerge via a combination of mutations at linked sites, recombination and/or structural rearrangements. Therefore, studying the phenotypic effects of extended haplotypes and combinations of multiple SNPs can be informative. We investigate the genetic basis of age at maturity in Atlantic salmon using full-genome sequence data for 313 individuals and 220k SNP array data for 1,518 individuals from over 50 populations. To identify associations between genotype and age at maturity, we use single-SNP and haplotype association tests, and Bayesian variable selection regression tests for multi-SNP associations. We find that a single SNP explains the majority of variation in age at maturity associated with a 500k base pair region surrounding *vgll3*, a candidate gene of large effect. Tests for multi-SNP associations reveal additional small-effect loci, providing new insight into the polygenic basis of age at maturity. Our findings show that moving beyond single-SNP approaches is beneficial for refining the genetic architecture of phenotypic traits.



## Bohao Fang<sup>LUOVA</sup>:

### How parallel is parallel evolution? The case of the three-spined stickleback

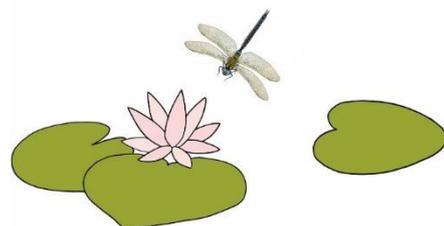
Reuse of standing genetic variation can play an important role in repeated adaptations to similar environments. The most important model system for the study of genomic mechanisms underlying repeated ecological adaptation in the wild are marine three-spined sticklebacks (*Gasterosteus aculeatus*) that have repeatedly colonized and adapted to freshwater streams and lakes. Previous studies have identified numerous large genomic regions showing consistent genetic divergence between freshwater and marine ecotypes globally. Here we re-analyse population genomic data from three-spined sticklebacks with much denser global sampling of populations using unsupervised methods to detect loci involved in parallel evolution. In line with previous findings, we also find that inversions often contribute to marine-freshwater divergence globally. However, outside of inversions, strong and consistent genomic signatures of parallel evolution were only detected in the Eastern Pacific (EP) region, but not in the Western Pacific or Atlantic regions. We further show that this signature from EP is so strong that it has biased earlier studies (that have used supervised methods), resulting in misleading conclusions of the pervasiveness of parallel evolution in the three-spined sticklebacks.



# Jack Beresford<sup>LUOVA</sup>:

## Gene expression in hybrid *Formica rufa* group ants

Speciation, the mystery of mysteries, is the vital biological process that underlies all novel biodiversity. The field of speciation genetics, in trying to understand the process of speciation, is predominantly focused on finding genomic barrier loci that underlie reproductive isolation between diverging lineages. It is in the genomes of hybrids between diverging lineages that we can study the nature of these barriers. Contemporary thinking posits that genes are part of gene networks, and that incompatibilities caused by failed epistatic interactions should be revealed in the transcriptomes of hybrids. Therefore, a significant number of incompatibilities are likely to be caused by regulatory mutations. By leveraging whole transcriptome sequencing, de novo transcriptome assembly and gene network analysis, we here search for candidate genes associated with introgression, agnostic of prior gene information, in a unique model organism, the European Red Wood ants.



# KEYNOTE TALK IV

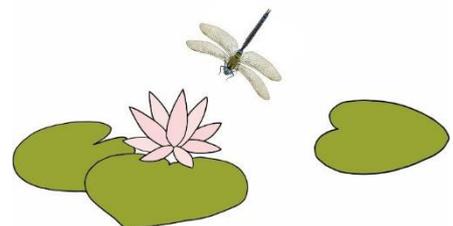
## Laurent Keller:

### Sex, Sociality and Supergenes

Intraspecific variability in social organization is common, yet the underlying causes are rarely known. I will show that the existence of two divergent forms of social organization in six ant species is under the control of a pair of heteromorphic chromosomes that have many of the key properties of sex chromosomes. In particular, this social chromosome contains a large region in which recombination is almost completely suppressed via 3 large inversions. These findings highlight how genomic rearrangements can maintain divergent adaptive social phenotypes involving many genes acting together by locally limiting recombination.



**SESSION VIII**  
**WEDNESDAY 6TH MARCH 2019**  
**14:20 -16:00**  
**INFO 2**



## Filipe Chichorro<sup>LUOVA</sup>:

### Using computer simulations of virtual organisms to understand which traits drive them to extinction

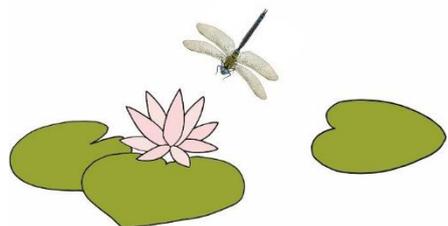
The world is facing its 6th extinction event, but not all species are equally threatened: some of their biological traits may predispose them to extinction. Traits like body size, fecundity, dispersal ability and degree of specialism have shown to correlate with the extinction risk of species. Correlation is not, however, causation. In this study we attempt to uproot the unseen mechanisms working under some of these correlations, either to support or to dismiss them. We do this through the simulation of virtual landscapes, where virtual organisms with different traits try to outcompete each other. When organisms reproduce, their offspring may have different traits through mutation, and therefore the whole simulation evolves over time. By introducing hunting and habitat loss, some traits will be selected against, giving insight into which are the winning and the losing combination of traits.



# Mervi Laaksonen<sup>LUOVA</sup>:

## Species and their traits in dead pines

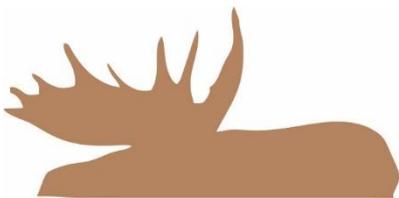
Spatially and temporally dynamic nature of microhabitats in dead wood is one of the key features in understanding population dynamics of saproxylic species that are dependent on dead or dying wood. Species' responses to changes in temporal and spatial aspects of habitat network vary according to species-specific traits. Which traits are significant, is an important question for conservation of species. We collected a beetle dataset from standing pines, which had died less than two years ago. This dead-wood type is present also in managed forests which enabled us to compare forest stands with varying amount of suitable habitat in three landscapes with different forest utilization histories. Our results show that the probability of occurrence of rare habitat specialist beetles has decreased in stands and landscapes with lower amount of dead-wood habitat available whereas the occurrence rate of common generalist species was independent from the density of dead pines.



**Janne Koskinen** UNIVERSITY OF EAST FINLAND.

## **Fungus-associated arthropods**

Fungi and their fruiting bodies, colloquially known as mushrooms, are ecologically important and utilized by a vast number of organisms, including humans and, importantly, thousands of insect species. The fruiting bodies themselves are sometimes superabundant resource, yet their presence is often clustered in time and space. The selection pressures this creates should favour polyphagy and generalism in fungivorous insects, but just what patterns are detectable in the nature remains poorly studied. Utilizing next generation sequencing, we have studied the insect communities in various large and commercially important fungal fruiting bodies. Compared to previous works, we have aimed for identifying all insect OTUs from whole fruiting bodies. In doing this, we have found a highly diverse arthropod community with high degree of generalization. I highlight our recent discoveries that shed light on future studies of this intriguing network.



# Ana Salgado<sup>LUOVA</sup>:

## Drought alters host plant quality and threatens its insect herbivore

Environmental stress impacts the life-history and fitness of herbivore insects, with the potential responses varying along the insect's life cycle. Drought is a significant climate change scenario affecting natural populations, and for herbivorous insects that rely upon their host plants, studying drought effects on their host plant is relevant for understanding adaptation to future scenarios. Using *Melitaea cinxia* and *Plantago lanceolata*, we assessed the responses of its northern population using field and lab experiments. We found that female oviposition site choice is linked to the amount of host plant coverage and the drought prevalence of the host within habitats along nine years. Additionally, drought enhances the nutritional quality of the plants. Furthermore, the life-history responses to feeding on drought-exposed host plants are developmental stage-dependent and individuals enhances fitness by matching preference. Our work demonstrates drought's effects on the host plant, affecting this herbivorous insect and placing at risk the northern populations.

