



Abstract booklet for 22nd. Kaamos
Symposium 12th and 13th of December,
University of Oulu

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Program

Wednesday 12.12.2018

Location: L4

09:00 – 9:10 Opening words Prof. Jouni Aspi, University of Oulu

Chair: Dr. Eva Kallio

09:10 – 10:10 Keynote session

Adapting to a warming world. Prof. Marcel Visser, Netherlands Institute of Ecology, the Netherlands

10:10 – 10:30 Coffee break

10:30 – 10:50 Viivi Puoskari - Calving site criteria of wild forest reindeer (*Rangifer tarandus fennicus*) in Kainuu population – Implications to conservation

10:50 – 11:10 Jim-Lino Kämmerle - Fox hunting for conservation? Grouse, red fox populations and the effects of predator control

11:10 – 11:30 Jannikke Räikkönen - Skeletal malformations and inbred wolf (*Canis lupus*) populations

11:30 – 11:50 Jussi Jyväsjärvi – Fungal decomposer assemblages in stream bioassessment: a cross-taxon comparison

11:50 – 13:00 Lunch break

Chair: Dr. Fríða Jóhannesdóttir

13:00 – 14:00 Keynote session

The evolutionary dilemma of ant supercolonies. Associate Prof. Heikki Helanterä, University of Oulu

14:00 – 14:20 Coffee break

14:20 – 14:40 Johanna Honka – Over a thousand years of evolutionary history of domestic geese from Russian archaeological sites, analysed using ancient DNA

14:40 – 15:00 Matti Heino - Ancient DNA provides insights into the population history of the reindeer

15:00 – 15:20 Jaakko Tyrmi - Discovering genetic diversity and molecular basis of local adaptation of Scots pine

15:20 – 15:40 Emmi Alakärppä -Variable DNA methylation and gene expression in Scots pine adaptation

Thursday 13.12.2018

Location: L4

09:00 – 9:10 Opening words

Chair: Prof. Dr. Phillip C. Watts

09:10 – 10:10 Keynote session

Toolbox for studying microbial metaphenomics. Prof. Marja Tirola, University of Jyväskylä, Finland

10:10 – 10:30 Coffee break

10:30 – 10:50 Kaisa Lehosmaa - Arctic plants and microbes in purification processes

10:50 – 11:10 Katharina Kujala - Little helpers – Microorganisms in the passive treatment of mining-affected waters in Northern peatlands

11:10 – 11:30 Nga Nguyen - Transcriptional changes during bilberry (*Vaccinium myrtillus* L.) fruit ripening – focus in analyses of the high throughput sequencing data

11:30 – 11:50 Jaana Jurvansuu - Rest in pee: corpse management of the invasive Argentine ant inhibits growth of pathogenic fungi

11:50 – 13:00 Lunch break

Chair: Dr. Seppo Rytönen

13:00 – 14:20 Invited session

13:00 – 13:40 Plant biodiversity losses in the Anthropocene: evidence for underlying mechanisms, Dr. Risto Virtanen, University of Oulu / German center for Integrative Biodiversity Research (iDiv), Leipzig, Germany

13:40 – 14:20 Parental care in the context of intra- and interspecific interactions, Dr. Topi Lehtonen, University of Oulu / Monash University, Victoria, Australia

14:20 – 14:40 Coffee break

14:40 – 15:00 Sanja Hakala - How to treat a daughter who refuses to leave the nest?

15:00 – 15:20 Niina Nurmi - The tolerant chimpanzee - quantifying costs and benefits of sociality in wild female bonobos (*Pan paniscus*).

15:20 – 15:40 Maria Rajakallio - Diving into murky waters – studying brownification effects on communities in headwater streams

15:40 – 16:00 Nico Alioravainen - Fisheries-induced selection on brown trout behaviour

16:00 – 16:10 Closing words

18:00 – Conference party and poster session at the new Botanical gardens

1. Adapting to a warming world

Marcel E. Visser

Spring temperatures are increasing due to climate change and in the Northern Hemisphere this has had profound effects on the spring phenology of many organisms. These shifts in phenology however vary substantially among species, with predatory species shifting only at half the rate as their prey. This leads to so-called phenological mismatches: the phenology of predators and their prey get out of synchrony. I will give an overview of these mismatches, the evolutionary consequences and the population consequences using data from our long-term study (1955-present) on a small song bird, the great tit (*Parus major*). I will present data of birds, caterpillars and trees to show that to understand patterns of selection on the phenology of the birds we need to take the phenology of the entire food chain into account. Next, I will switch gears and focus on the potential for genetic change in response to selection on phenology in great tits. We have been studying the genetics and physiology underlying phenology by creating selection lines of early and late reproducing great tits, using genomic rather than phenotypic selection. We breed great tits of these selection lines under controlled conditions and look at their lay dates as well as at RNA expression. As a final step we introduced selection line eggs into our wild population to measure their fitness depending on their phenology. In the last part of the talk, I will present data on how phenological mismatches have knock-on effect at the population level.

**2. Calving site selection criteria of wild forest reindeer (*Rangifer tarandus fennicus*) in
Kainuu, Finland – Implications for habitat conservation**

Puoskari Viivi, Rytönen Seppo, Paasivaara Antti

3. Fox hunting for conservation? Grouse, red fox populations and the effects of predator control

Jim-Lino Kämmerle

Although not threatened at a global scale, many Central-European grouse populations are red-listed. Declining reproductive success and fragmented habitats have been linked to grouse population declines. Predators of eggs and chicks, especially generalist predators that often benefit from landscape fragmentation, have been implicated in this development. Lethal control of predators is thus often an integral part of grouse management, employed with the goal to increase grouse population parameters. While intensive control of predator abundance can generally improve prey population parameters, in practice the effectiveness of predator control is rarely quantified, contesting the appropriateness of predator removal as a conservation measure. Our current research focusses on this topic, zooming in on a declining remnant population of capercaillie (*Tetrao urogallus*) in the Black Forest, Germany. We first assessed how range contractions of capercaillie in the area may be linked to landscape configuration and predator abundance before looking at potential pathways, the suitability of predator removal as a conservation tool and the effectiveness of the currently applied spatially-restricted removal of red foxes (*Vulpes vulpes*) in lowering fox abundance and predation pressure by foxes.

4. Skeletal malformations and inbred wolf (*Canis lupus*) populations

Jannikke Rääkkönen

5. Fungal decomposer assemblages in stream bioassessment: a cross-taxon comparison

Jussi Jyväsjärvi, Kaisa Lehosmaa, Jukka Aroviita, Heikki Mykrä, Jarno Turunen, Timo Muotka

We used predictive modeling (RIVPACS) to assess the relative performance of aquatic fungi in comparison to diatoms and benthic macroinvertebrates, in detecting the effects of anthropogenic stressors on stream communities based on a multiple-stressor design, focusing on nutrient enrichment, sedimentation and pH, and their interactions. Our data came from 67 reference streams and 45 variously impacted streams in western and central Finland. At each site, we also measured alder leaf decomposition rate in a 28-d experiment. The predictive models of all three biological groups clearly outperformed a corresponding null model in terms of model precision and accuracy. Based on deviation of observed number of taxa from that of expected by the models (i.e. O/E ratios), we showed that fungi clearly outperformed the other two groups in detecting the effects of all three stressors, as well as their interactions. Macroinvertebrates performed almost equally well in detecting acidification whereas diatoms were only effective at detecting nutrient enrichment, and even then they were outperformed by fungi. However, performance of fungi depended on taxonomic resolution used: OTUs based on DNA sequence-similarity (97% threshold) were much more sensitive in detecting human disturbance than genus-level (BLAST) data. Leaf decomposition was faster in nutrient-enriched than in reference streams but was greatly reduced by other stressors, resulting in breakdown rates not differing from reference under multiple-stressor situations. As sequencing techniques are becoming more effective and less costly, use of fungal assemblages may provide an efficient method for future stream bioassessment.

6. The Evolutionary dilemma of ant supercolonies

Heikki Helanterä

Ant supercolonies are the largest known cooperative units in the world. They consist of networks of interconnected nests, each with numerous queens that cover large areas and are ecologically dominant. Despite their enormous ecological success, as seen for example their success as invasive pests, or their dominance in their native ecosystems, ant supercolonies are an evolutionary dilemma. This is because each supercolony consists of individuals only distantly related to each other. In such cases kin selection, the fundament of evolutionarily stable altruism in social insects, stops working. Consequently, the supercolonies are potential evolutionary dead ends, as they can be predicted to collapse due to internal conflicts and selfishness, or mutation accumulation due to diminished efficacy of selection on workers. I will present work describing supercolonies of *Formica* ants, and looking for signs of such collapse, using behavioural and ecological methods and population genetic and transcriptomic data.

7. Over a thousand years of evolutionary history of domestic geese from Russian archaeological sites, analysed using ancient DNA

Johanna Honka, Matti T. Heino, Laura Kvist, Igor V. Askeyev, Dilyara N. Shaymuratova, Oleg V. Askeyev, Arthur O. Askeyev, Marja E. Heikkinen, Jeremy B. Searle, Jouni Aspi

The European domestic goose is a widely farmed species known to have descended from the wild greylag goose (*Anser anser*). However, the evolutionary history of this domesticate is still poorly known. Ancient DNA studies have been useful for many species, but there has been little such work on geese. We have studied temporal genetic variation among domestic goose specimens excavated from Russian archaeological sites (4th–18th centuries) using a 204 base pair fragment of the mitochondrial control region. Specimens fell into three different genetic clades: the domestic D-haplogroup, the F-haplogroup that includes both wild and domestic geese, and a clade comprising another species, the taiga bean goose. Most of the subfossil geese carried typical domestic D-haplotypes. The domestication status of the geese carrying F-haplotypes is less certain, as the haplotypes identified were not present among modern domestic geese and could represent wild geese (misclassified as domestics), introgression from wild geese, or local domestication events. The bones of taiga bean goose were most probably misidentified as domestic goose but the domestication of bean goose or hybridization with domestic goose is also possible. Samples from the 4th to 10th century were clearly differentiated from the later time periods due to a haplotype that was found only in this early period, but otherwise no temporal or geographical variation in haplotype frequencies was apparent.

8. Ancient DNA provides insights into the population history of the reindeer

Matti Heino, Tom van der Valk, Patricia Pečnerová, Jørgen Rosvold, Michael D. Martin, Mietje Germonpré, Kjersti Kvie, Igor V. Askeyev, Dilyara N. Shaymuratova, Oleg V. Askeyev, Eleftheria Palkopoulou, John Stewart, Rebecca Miller, Knut Røed, Juha Kantanen, Friederike Johansson, Mihály Gasparik, Alfréd Dulai, Pedro Castaños Ugarte, Jone Castaños de la Fuente, Erik Ersmark, Øystein Flagstad, Eline Lorenzen, Tatiana Krakhmalnaya, Lumi Viljakainen, Linda Wickström, Erika Rosengren, Ronnie Liljegren, Jonas Ekström, Maria Mostadius, Glenn Yannic, Laura Kvist, Love Dalén, Jouni Aspi

Ice Ages and warmer periods between them, interglacials, have shaped the distributions of many species. The distributions of cold-adapted species have generally expanded during the Ice Ages and contracted during the interglacials. More temporal fluctuations in the climate during the Ice Ages have also had an impact on the distribution of species. One cold-adapted species is the reindeer, which maximum distribution during the last Ice Age reached all the way from Spain and British Isles across Siberia to North America. We have studied the demography of the reindeer by analyzing mitochondrial DNA from remains dating to the last Ice Age and the Holocene. The results reveal a dynamic population history. A local European reindeer population has been at least once partly or totally been replaced by a population likely coming from the east. The results also shed light on the colonization history of Fennoscandia.

9. Discovering genetic diversity and molecular basis of local adaptation of Scots pine

Jaakko Tyrmi, Outi Savolainen, Tanja Pyhäjärvi

Scots pine is a keystone species in many Eurasian ecosystems with a huge distribution range, spanning from mountain ranges of southern Spain to taigas of eastern Siberia. Decades of forestry research indicates it is locally adapted to the various environmental conditions found within its range. Yet, little is known about the molecular basis of this adaptation and detailed characteristics of the species population structure remains poorly characterized at the genome-wide level, as the massive size and repetitive nature of conifer genomes has prevented contemporary genomic surveys. We have now generated a genome-wide dataset using targeted sequencing approach and uncovered population structure with previously unseen differentiation between western and eastern parts of the distribution. To detect putative signs of local adaptation our sampling was performed along two latitudinal gradients, enabling us to contrast allele frequencies to environmental variables. In addition, we have applied traditional F_{st} -based outlier detection methods to uncover signs of local adaptation. Survey of genome-wide linkage disequilibrium patterns also revealed a large haplotype structure, suggesting a presence of a huge inversion in the Scots pine genome. Better characterization of the genomic variation will also contribute to breeding and genetic resource management.

10. Variable DNA methylation and gene expression in Scots pine adaptation

Emmi Alakärppä, Heikki M. Salo, Luis Valledor, Maria Jesús Cañal, Hely Häggman, Jaana Vuosku

As long-lived sessile species, conifers depend on phenotypic plasticity, which enables adaptation to environmental change. Recent findings suggest that epigenetic regulation, including DNA methylation, plays an important role in plasticity. Epigenetic modifications can lead to changes in gene expression, which affects the phenotype of plants. We investigated variations in the expression of 19 adaptation-related circadian clock genes and 6 Scots pine DNA methyltransferase (DNMT) genes between three Scots pine (*Pinus sylvestris* L.) populations located in northern and southern Finland. The Scots pine DNMT genes were identified in this study. Moreover, we compared the global DNA methylation levels between the populations. As a material, we used mature seeds, from which diploid embryos and haploid megagametophytes were studied separately. We observed between-population variation in the expression levels of 11 adaptation-related genes in megagametophytes and 8 genes in embryos. For DNMT genes, the expression levels varied in embryos in 3 genes, which participate in maintaining DNA methylation. Altogether, our results suggest that differential DNA methylation and gene expression contribute to local adaptation in Scots pine populations and may enhance the fitness of trees under rapidly changing climatic conditions.

11. Toolbox for studying microbial metaphenomics

Marja Tirola

High-throughput sequencing of microbial communities has enabled tremendous expansion of the sequencing data. Still, it has to be admitted that one-dimensional sequencing only gives genetic potential, the function of which has to be proven. A new term, metaphenomics, was recently launched (Jansson & Hofmockel 2018)) to emphasize the need of studying phenotypic diversity and activities of microbial communities in each environmental context. In this lecture I will present the development of molecular microbiology tools that supplement sequencing results with a functional dimension. First approaches used stable isotope and radioisotope labeling to study actively multiplying organisms, based on DNA, RNA or fatty acids as bulk measures or with spatial resolution. Many of the recently developed tools include droplet-based microfluidic approaches to reveal connected gene pairs, single-cell transcriptomics or other single-cell features. One potential approach is to use Raman microscopy to sort cells based on their phenotypic characteristics or growth (Berry et al. 2015). When combined with efficient sequencing technologies, the new tools create a powerful toolbox to study the physiology of millions of microbes at the same time.

Jansson, J.K. and Hofmockel, K.S. (2018) The soil microbiome-from metagenomics to metaphenomics. *Curr. Opin. Microbiol.* 43:162-168.

Berry, D. et al. (2015) Tracking heavy water (D₂O) incorporation for identifying and sorting active microbial cells. *Proc. Natl. Acad. Sci. U. S. A.* 112: E194-E203

12. Arctic plants and microbes in purification processes

Kaisa Lehosmaa, Piippa Wäli, Anna Liisa Ruotsalainen, Anna Maria Pirttilä, Annamari Markkola

Human-induced processes, inter alia mining, agriculture and forestry have led to nitrogen and/or heavy metal loads to recipient water bodies and soils. Often it is not cost-effective to build active treatment units for these operations, therefore passive treatment solutions are urgently needed. Plants and microbes, as well as their combinations, have no need for external energy, being such passive treatment solutions. Plants uptake nutrients from soil and water, microbes degrade organic compounds and pollutants and effectively bind heavy metals, while microbial symbionts help plants to adapt to extreme environmental conditions. The potential role of plants, microbes and plant-associated microbes in bioremediation is a relatively unexplored field of research. Ongoing HybArkt- project aims to plan, construct, and test hybrid passive water treatment systems that allow year-round removal of nitrogen and heavy metals from waters in arctic conditions. The presentation focuses on introducing this project but also presents research on mechanisms of floating hook-moss (*Warnstorfia fluitans*) and microbial symbionts accumulating heavy metals and nitrogen in cold climate conditions. Overall, waste management solutions can be local, but the challenge is to find suitable environmental conditions to stimulate growth of target organisms.

13. Little helpers – Microorganisms in the passive treatment of mining-affected waters in Northern peatlands

Katharina Kujala

Mining operations produce large amounts of wastewaters, which contain a variety of contaminants stemming e.g. from the ore beneficiation process and thus have to be purified before they can be safely released into downstream water bodies. In Northern Finland, peatlands are used in the purification of mining-affected waters. Wastewaters at the site contain high concentrations of nitrogen compounds, sulfate, metals and metalloids. Two treatment peatlands (TPs) have been in use for ~10 years to treat mine process and drainage wastewaters and have removed contaminants from mining-affected waters with varying efficiency. Microorganisms and the reactions catalyzed by them play a substantial role in the removal of contaminants from mining-affected waters in TPs. E.g., sulfate reducers can reduce sulfate to sulfide, allowing for the precipitation of metals as metal sulfides in the anoxic layers of the peat, while nitrifying and denitrifying microorganism play a key role in the removal of nitrogen compounds by coupled nitrification-denitrification in peat soil. The talk will address some of the most important microbial groups involved in wastewater purification in the two studied TPs and show results from > 7 years of field and laboratory work from the TPs.

14. Transcriptional changes during bilberry (*Vaccinium myrtillus* L.) fruit ripening – focus in analyses of the high throughput sequencing data

Nga Nguyen, Marko Suokas, Katja Karppinen, Jaana Vuosku, Laura Jaakola, Hely Häggman

Bilberry (*Vaccinium myrtillus* L.) is economically the most important wild berry species of genus *Vaccinium* in Northern Europe. This is due to high content of health-beneficial compounds such as anthocyanins, carotenoids, vitamins, minerals and fibers. Berry development and ripening processes are regulated at transcriptional and growth regulator level followed by modifications both in physiology and morphology (e.g anthocyanin accumulation). At the ripening stage, many studies have also reported the impacts of the genetic and environmental factors on the anthocyanin biosynthesis in bilberry fruit. However whole genome sequencing data for the species is still absent. In the present study, we provide an overview on bilberry transcriptome-level data at two developmental stages, unripe green and ripening. Toward this end, we exploited the high throughput next-generation sequencing technology, RNA sequencing (RNA-seq) for the wild non-model plant species bilberry. As a result, we identified putative ripening-related regulatory genes in bilberry, which were analyzed by qPCR at five fruit developmental stages. In addition, the transcriptome dataset enabled us to discover interesting bioactive compounds synthesized during fruit ripening. Thus, we present here the first data for wild *Vaccinium* species acquired by RNA-seq. The *de novo* transcriptome database of wild bilberry provides novel insights into fruit development and ripening process in bilberry.

15. Rest in pee: corpse management of the invasive Argentine ant inhibits growth of pathogenic fungi

Kesäniemi Jenni, Koskimäki Janne, Jurvansuu Jaana

16. Plant biodiversity losses in the Anthropocene: evidence for underlying mechanisms

Risto Virtanen

Plant biodiversity and its maintenance is widely recognized crucial for multiple ecosystem functions and services. Many anthropogenic threats on plant diversity are intensifying, including increases of nutrient deposition. Consequent increases in plant available nutrients has led to changes in community compositions and losses of species especially in grasslands of densely human-populated areas. The mechanisms underlying these plant community biodiversity losses and other changes are poorly known. The main hypotheses tested are 1) that nutrient resource additions increase plant biomass production, and this reduces light availability near ground and consequently poor light-competitors (small plants) are eliminated (standard resource competition). 2) however, under biomass consumption e.g. due to grazing biomass accumulation is reduced and thus light competition becomes mitigated, and species loss rates decrease, 3) resource additions have primarily direct impacts on species loss (sensitivity) and thus light competition and grazing do not effectively mitigate impacts of increased nutrient availability. These hypotheses were tested using 5-year experimental data on grassland bryophytes subjected to factorial nutrient (NPK) and grazing exclusion experiment. Nutrient additions had both indirect vascular plant light-competition mediated negative effects on bryophyte richness but also primarily negative direct species specific nutrients effects. The roles of different mechanisms affecting bryophyte loss can vary during transient dynamics and predictions on the roles of direct nutrient effects vs. indirect light-limitation effects based on short- vs. medium term experiments may differ.

17. Parental care in the context of intra- and interspecific interactions

Topi Lehtonen

When present, parental care is often a key life cycle stage, influencing the success of both parents and their offspring. Yet, impacts of parental care on interactions between parents and other individuals in the community are often overlooked. I will present a series of studies, conducted on Australian, Finnish and Nicaraguan fish, showing how parental care can affect selection due to both within (e.g. sexual selection) and between (e.g. parental aggression) species interactions.

18. How to treat a daughter who refuses to leave the nest?

Sanja Hakala, Rosanna Lindgren, Heikki Helanterä

The correlation between poor dispersal and complex societies in ants is well documented. Especially supercolonial ant species that live in the biggest societies with lowest relatedness, tend to show poor dispersal. However, the underlying causal mechanisms of this pattern are not clear.

We studied the dispersal behavior of young *Formica aquilonia* queens. The young queens of this supercolonial ant species often drop their wings in their natal colonies, which indicates their reluctance to disperse. This can be seen as selfish behavior caused by the low relatedness within their societies. According to our pilot study the workers actively kill a proportion of these young queens – behavior that has been reported in other supercolonial species but not in *Formica*.

In a follow-up study we confirmed the queen execution behavior in a more controlled setup. It seems that the workers detect the selfish behavior of the young queens and answer it by limiting the number of queens they allow to stay in the colony. Such a costly behavior implies that there is an unresolved conflict over dispersal in these societies.

19. The tolerant chimpanzee - quantifying costs and benefits of sociality in wild female bonobos (*Pan paniscus*).

Niina O. Nurmi, Gottfried Hohmann, Tobias Deschner, Oliver Schülke

Access to food resources is a key determinant of reproductive success in mammalian females. Contest competition over defensible, high quality food leads to dominance rank effects on food intake and net energy intake. We tested predictions from three hypotheses that link high gregariousness and social tolerance of female bonobos to their food resource characteristics. We quantified feeding behavior using a modified Focal Tree protocol, and assessed energy balances via urinary C-peptide of insulin in 14 wild female bonobos at LuiKotale, DRC. We found that food intake rate moderately increased while feeding effort decreased with female dominance rank, indicating that females engaged in contest competition in high-quality food resources. However, these rank effects did not translate into variation in energy balance, as measured from urinary C-peptide levels. Instead, energy balance varied independently of female rank with the monthly proportion of fruits in the diet. In combination with the observation that females join forces with other females in conflicts against males, our results support the hypothesis predicting that females trade off feeding opportunities for safety against male aggression.

20. Diving into murky waters – studying brownification effects on communities in headwater streams

Maria Rajakallio

21. Fisheries-induced selection on brown trout behaviour

Nico Alioravainen

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