21st Kaamos symposium, 12-13 Dec 2017

UNIVERSITY OF OULU

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Cover photo: wild forest reindeer killed by wolves (Johanna Suutarinen)

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Darwin – my hero and anti-hero

Anders Pape Møller

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All biologists are aware of the unique contributions of Charles Darwin to modern evolutionary thinking, but most are unaware of the ethics involved in the emergence of the theory of natural selection, adaptive radiations and speciation. I give a brief overview of these events to illustrate the ethical dilemmas that Charles Darwin faced. Furthermore, I present a number of case stories of ethics dilemmas from real life. Finally, I present an ethics statement for a modern university department that I have helped develop.

Keywords: Alfred Wallace; Charles Darwin; ethics; ethics statement; John Gould.

Selective social information use in solitary bees

Olli Loukola

Animals from social insects to apes learn from each other about foraging options, predation threat, or whom to mate with. While social learning is largely studied between conspecifics, useful information can also traverse species boundaries. Some bird species extract crucial information about the suitability of nesting sites from members of other species. However, little is known about social information use by other non-social animals. Using electronic monitoring of field nesting sites, we show that solitary megachilid bees use the nesting success (nest is parasitized or not) of heterospecific mason bee (*Osmia bicornis*) in determining the quality of the observed nest and use it as a basis of decision making. We show that bees copied or rejected a novel nest site feature preference of *O. bicornis* experimentally manipulated to exhibit successful or unsuccessful nesting, respectively. We conclude that in contrast with current theories of species coexistence, niche overlap between species may dynamically change depending on the observed success of surrounding individuals.

Female sexual signalling in capital breeders

Gautier Baudry, Juhani Hopkins, Anna-Maria Borshagovski, Phillip Watts, Arja Kaitala

The use of sexual signals by females to attract males is poorly studied. Optimizing signalling effort is important for successful reproduction in capital breeding females, as they have a limited amount of resources that must be shared between fecundity, maintenance and signalling. We investigated sexual signalling pattern of unmated female capital breeder and the effect of intra-sexual competition on their sexual signalling. We used the common glow-worm *Lampyris noctiluca*, where adults do not feed, and flightless females glow at night to attract flying males. We found that 1) signalling duration decreased with time spent unmated while signalling intensity did not show conclusive trend; 2) competition did not affect sexual signalling, but time spent unmated does. We suggest that because they have a finite amount of resources to reproduce, the costs of delayed mating shapes sexual signalling pattern in female capital breeders.

Steer clear of beauty: Female sexual signaling and female-female competition in the common glow-worm

Anna-Maria Borshagovski, Juhani Hopkins, Gautier Baudry, Ulrika Candolin and Arja Kaitala

Sexual competition between females is common but not well understood. High investment into offspring is thought to restrict female competition for mates. In cases where females compete in mate attraction, less attractive females may develop strategies to avoid competition. In the common glow-worm (*Lampyris noctiluca*; Lampyridae), wingless females glow to attract flying males, which prefer the brightest females. Adult glow-worms do not eat, so they have limited energy for eggs, maintenance and glowing. Females are in a hurry to mate because they lose more eggs the longer it takes to attract a male. Especially small, less attractive females have a high risk of complete mating failure if they do not attract a mate soon. We tested experimentally how females react to a competitor by using green light-emitting diodes (LEDs) simulating bright females. We predicted that they either parasitize the light of a better competitor in order to get a mate (that is, they move close to the LEDs not glowing), or they glow and move away from the LEDs to hinder males' ability to compare them. We found that females increased the distance to the LEDs and glowed. Thus it is possible that moving away might increase female's relative attractiveness to flying males. Spatial distribution and distances to competitors may play a crucial role in mate attraction and sexual competition, suggesting that the scattered distribution of glowing females in nature may be a result of female-female competition.

Competitors location disrupts accuracy of signal-based mate choice

Juhani Hopkins, Veijo Kaitala, Arja Kaitala

Mate choice is often based on comparison of sexual signals with larger or stronger signals attracting more mates. However how signals are perceived depends on distance to the signaller. Increasing distance between a signaller and the potential mate it’s attracting will reduce the perceived signal strength making accurate comparison of potential mates difficult. This may greatly affect how effective sexual signals are and reduce their effectiveness in some situations. It may also provide a way for weak competitors to cope in sexual competition: if they are very close to a mate, their signals will appear stronger. We describe a model studying optimal distance from stronger competitors for sexual signallers. We test our models predictions using the common glow-worm (Lampyris noctiluca), a species where females glow to attract males. The model and experiment reveal two potential strategies for sexual signallers. Weak signallers should attempt to position themselves between potential mates and competitors or move far from competitors to make accurate comparison harder. Strong signallers should move close to weak signallers to reduce the weaker signaller’s chance of appearing stronger. This reveals unexpected spatial competition between strong and weak signallers. The conclusion is that while signal strength is important in sexual selection, the physics involved in animal senses also have to be considered when studying mate choice.

Genomic response to life within the Chernobyl exclusion zone

Phillip Watts

On April 26, 1986, a fire and explosion in Reactor 4 of the former nuclear power plant at Chernobyl (CNPP), Ukraine, released more than 9 million terabecquerels (TBq) of radionuclides over much (>200,000 km2) of Europe and eastern Russia. The Chernobyl Exclusion Zone (CEZ) was established at about a 30 km radius around the accident site to limit human exposure to radioactive fallout. The CEZ contains elevated levels of radioisotopes, notably Strontium-90 and Cesium-137 that have half-lives of about 29 and 30 years, respectively. Wildlife inhabiting the CEZ provide clear models of the biological consequences of exposure to environmental radionuclides, and there are frequent reports of, for example, developmental instability, genetic damage and mutation rate associated with inhabiting areas contaminated by radionuclides. In this presentation I will present an overview of some of the genomic consequences of exposure to environmental radionuclides exhibited by wildlife (the bank vole, *Myodes glareolus*).

Environmental radiation affects gut microbiome of small mammals from Chernobyl

Anton Lavrinienko[1], Tapio Mappes[2], Eugene Tukalenko[2,3], Timothy A. Mousseau[4], Anders P. Møller[5], Rob Knight[6,7,8], James T. Morton[6,7], Luke R. Thompson[9,10], Phillip C. Watts[1]

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Gut microbiota composition depends on many factors, although the impact of environmental contaminants is largely unknown. We used amplicon sequencing of bacterial 16S rRNA genes to quantify whether anthropogenic radionuclides at Chernobyl (Ukraine) impact the gut microbiome of the bank vole Myodes glareolus. Exposure to elevated levels of environmental radionuclides had no detectable effect on the gut community richness but was associated with an almost two-fold increase in the Firmicutes:Bacteroidetes ratio. Animals inhabiting uncontaminated areas had remarkably similar gut communities irrespective of their proximity to the nuclear power plant. Hence, samples could be classified to high-radiation or low-radiation sites based solely on microbial community with >90% accuracy. Radiation-associated bacteria had distinct inferred functional profiles, including pathways involved in degradation, assimilation and transport of carbohydrates, xenobiotics biodegradation, and DNA repair. Our results suggest that exposure to environmental radionuclides significantly alters vertebrate gut microbiota.

Differential gene expression of the bank vole (*Myodes glareolus*) exposed to low-dose radiation environment of Chernobyl exclusion zone

Jenni Kesäniemi, Toni Jernfors, Anton Lavrinienko, Eugene Tukalenko, Tapio Mappes, Phillip Watts

Leaked radioactive particles from mining activity and nuclear disasters project their effects on the environment for decades. Ionizing radiation causes genomic and oxidative stress in organisms, but genome wide gene expression studies on species exposed to chronic low-dose ionizing radiation (LDIR) are scarce. We conducted *de novo* RNA sequencing on liver and spleen tissue of bank voles (*Myodes glareolus*) caught from two separate areas within the Chernobyl exclusion zone where background radiation levels exceed 10 µSv/h, as well as from two control areas near Kiev. Chernobyl voles show a metabolic switch to increased fatty acid oxidation. Key differentially expressed metabolic genes in the liver include *Cpt1, Pdk4, Fgf21* and *Scd1*. Moreover, innate immune system seems to be compromised in Chernobyl voles. Both liver and spleen show wide downregulation in interferon-induced genes and several genes belonging to the antiviral MHC class I system. Spleen tissue shows upregulation of inflammation pathways and mast cell activation, suggesting parasite or bacterial infection. Surprisingly, we did not find differentially expressed genes involved in enzymatic antioxidant systems, however, genes involving vitamin A, B5 and C metabolism (having antioxidative properties) were upregulated in the liver. Finally, upregulation of DNA damage-inducible protein *Gadd45a* and activating transcription factor *Atf5* in the liver provide evidence for response to environmental stress. Metabolic switch towards fatty acid oxidation is known to be linked with a more stable genome state. Further studies are required to determine whether changes in gene expression are caused directly by LDIR, or as a result of differences in habitat quality.

A life history perspective to climate change driven elevational shifts among boreal nocturnal lepidoptera

Netta Keret[1], Juhani Itämies[1,2], Marko Mutanen[1], Markku Orell[1], and Panu Välimäki[1]

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Climate warming has shifted species geographical ranges northwards or to higher elevations in mountains. These changes has been generally connected only to temperature rise. For ectotherms in seasonal environments, however, life history theory relies largely on the length of summer, which varies somewhat independently of ambient temperature per se. Prolongation of summer reduces seasonal time constrains and enables species to establish in new areas, because over-wintering stage can be reached in time. Reduction in time constrains are also predicted to prolong organisms breeding season when reproductive potential is under selection.

We studied temporal change in the summer length and its effect on species' performance by combining long-term data on the occurrence and abundance of nocturnal moths and weather conditions in boreal region (Värriötunturi fell). We found that summers have lengthened on average five days per decade, which profoundly delay the onset of winters. The summer length in the previous season determines moth abundance in the following year. The elevational "center-of-gravity" has increased for most of the species studied. Moth assemblages in low elevation pine heath forest and middle elevation mountain birch forest have become inseparable. Yet, the flight periods have remained unchanged, which underpins condition-dependence of ectotherm performance. We conclude, that climate change driven changes in the season length has potential to affect species' ranges and affect the structure insect assemblages, which may reflect to ecosystem level processes.

The bioarchaeology of human-horse interaction

Markku Niskanen

This presentation focuses on the study of the human-horse interaction in the light of bioarchaeological evidence. The bioarchaeological research community (BARC) studies the complex interaction of behavior (including cultural), environment, morphology and genetic inheritance in past and present human and animal populations, temporal and geographic trends, as well as the human-animal interaction (e.g. domestication, artificial selection, etc.). As a biological anthropologist, I have personally focused on human skeletal variation and adaptation for all of my academic years. It is now time to pay attention to horses, which is an extremely fascinating and important animal species. Horses were domesticated at least 5500 years ago. This domestication was one of the most significant events in prehistory. It revolutionized transportation and warfare, resulted in major social and political changes, and shaped our genetic and linguistic landscape. In addition, selective breeding has influenced the horse biology since their domestication. Due to horses' enormous importance, the history of a many horse breed (e.g. the Finnhorse) cannot be entirely separated from the history of a particular nation (e.g. the Finns). There are thus officially recognized "national" breeds. For example, the Finnhorse has been the official national horse breed of Finland since 2007. It is now possible to focus on the genetic history of this breed due to a research grant from the Finnish Cultural Foundation to Docent Laura Kvist and her research group.

“Most beautiful favorite reindeer” – Osteobiographies of two reindeer offered at a Saami offering site

Anna-Kaisa Salmi

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Telling the stories, or osteobiographies as they are called, of humans, is standard fare in current archaeological research. The analysis of osteobiographies of human skeletons through a range of archaeological techniques provides information on age, gender and ethnic identities, life courses of people, illness, and disability, as well as on how the abovementioned things were understood in specific historical contexts and societies. Analysis of skeletal remains of animals can similarly be used to reconstruct their osteobiographies and the social roles they had in human as well as animal societies. This presentation will present the stories of two reindeer that were offered at a Saami offering site. Animal offerings made at various sacred sites were an integral part of the ethnic religion of the Sami from ca. 800 AD onwards. In this presentation, I will focus on two individuals offered at the Paddusas offering site in Northern Sweden in ca. 1170–1280 AD and 1445–1635 AD, respectively. I will tell their osteobiographies as they unfold by looking at age, sex, and size of the individuals, the stable isotope composition of their teeth and bones, and the offering site context where their bones were deposited. I will discuss how the lives of these reindeer were tangled with those of humans and other animals against a backdrop of changing social and economic environment, colonial contact between the Saami and Scandinavian state powers, and reindeer domestication.

Willow tree wetlands in polishing phase of sewage water treatment in cold climate

Heini Postila

Willow tree wetlands has successfully used for sewage water purification eg. in few wastewater treatment plant in Sweden. In Finland, willow tree wetland has little bit used to water purification in southern and central part. The aim of this study is clarify, how well willow tree wetland can working in water purification purposes in northern condition and which species can be most suitable (survival in cold conditions, biomass production). As part of HuJa (Enhancing the treatment of nutrient and metal containing storm water and wastewater with biomaterials - European Regional Development Found) project a pilot scale treatment wetland was constructed nearby the Toranki wastewater treatment facility in Kuusamo, Finland during 2015- 2016. In June 2016 there has planted about 1700 willow trees, mainly 4 different species: three cold resistant willow (Salix spp. Karin, Gudrun and Klara) hybrid varieties and one local variety. During ground frost-free period, 2016 and 2017 has followed eg. the water purification by water sampling. The biomass growth was evaluated based on measurements in autumn 2017. The long-term purification efficiency of willow tree wetland is not possible to say yet, but based on first two summer, there is total nitrogen removal about 80% and total phosphorus about 60-85%. In biomass growth and survival has been clear difference between species. Based on preliminary results, willow tree wetland is suitable for nitrogen and phosphorus removal also in northern conditions.

Legacy effects of logging on forest understorey in decadal time scales

Lauralotta Muurinen[1], Jari Oksanen[1], Ilkka Vanha-Majamaa[2], Risto Virtanen[1,3]

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Changes in boreal forest understory communities lead to changes in ecosystem processes, affect other biota and alter ecosystem services. Since 1950's intensive forestry practices have been the main factor altering forest communities in Finland and threatening of many forest dwelling organisms. Based on biological understanding there is a clear need to shift from clear-cut based forestry on more sustainable use of forests. Many studies have shown immediate effects of forest management on forest understory plant communities, whereas the persistence of these effects in the longer term is less well known. In this study we tested how multiple forest loggings altered understory plant communities and affected their succession over 60 years by resampling permanent experimental plots with varying logging treatment history from Northern Finland. Logging treatments were found to have negligible effects on understory communities during the earlier successional stages (years 1961, 1986), whereas the effects of logging were clear in the latest successional stage (year 2013). Logged plots had few species related to old-growth forests and had significantly lower amount of coarse woody debris. On one hand forestry practices based on light and multiple forest logging would better maintain natural like forest understory and thus better maintain natural like functioning and properties of boreal forests also over long time periods. However, on the other hand the results underline the lack of ability of forest management to maintain natural like late successional forests and emphasize that even moderate forest logging in the past has legacy effects influencing the key features for forest biodiversity and endangered species. Thus there is a clear need for conservation on natural and old growth forests and development of alternative cost efficient but sustainable forest management methods.

Biomonitoring 2.0: Metagenomic analysis of macroinvertebrates along El Llobregat, NE Iberian Peninsula

Leif O.S. Väisänen, Cesc Múrria, Owen S. Wangensteen, Simona Somma, Miquel À. Arnedo, Narcís Prat

Massive parallel sequencing technologies which utilises DNA barcoding for automated species identification for a community. Cost effective and time efficient application with scalable taxonomic resolution, when applied with biological monitoring indices (EU Water Framework Directive) to determine ecosystem health. Comparison of ecological status using traditional morphotaxonomy against high throughput DNA sequencing: [1] eDNA; [2] invertebrate bulk sampling; and [3] drift net sampling. Field work: water collection (eDNA) and filtration in situ of 1.5l river water; drift net sampling; bulk sampling i.e. kicknet method and sample sprting. DNA extraction: PowerWater DNA isolation kit (MolBio) for eDNA and soil DNA isolation kit (Norgen) for drift net and bulk sample extraction. CO1 amplification Miseq sequencing. DNA extraction, PCR production and purification. Illuminia Mseq v3 2x250bp 25 M initial reads. Bioinformatic pipeline: quality control with sequence alignment and chimera removal. Clustering delimitation of molecular taxonomic units with comparison with reference data and taxonomic assignment (Ecotag). Morphological and bulk sample revealed similar patterns suggesting high accuracy of this method. B-diversity-nMDS high consistency across replicates and coherent similarities across sites using different methods. Genomic differences in community composition indication high sensitivity to DNA concentrations and bias on PCR amplification by primer affinity. Fish and terrestrial ecosystems were incorporated in eDNA results. Coherent results using IBMWP metrics with drift lest optimal method. Taxonomic resolution potential at species level but gaps in library prevent this even at genus level. Fast and efficient, cost effective biomonitoring tool requires more research before routine application.

Arctic Science with Attitude

Jeff Welker, UArctic Research Chair

Today, the Arctic is a region that is exhibiting changes that are unprecedented. There are a cascading set of consequences ranging from transportation, fisheries, atmospheric processes, sea ice- & landscape climate feedbacks, food web ecology and consequences for the communities that occupy these regions or that rely on resources derived from the north. This presentation will provide an overview of the Arctic System and highlight some of the observational data, experimental findings and attempt to connect-the-dots regarding social behavior, climate and Arctic consequences.

Berry cuticular wax: Composition, morphology, biosynthesis and effect of environmental factors

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The outer surface of plants is covered by a layer of cuticular wax. The cuticular wax is a component of the cuticle, which forms barrier between the plant and the environment. It also plays a role in non-stomatal water loss, protection from UV rays and in plant defense. We aim to analyze the composition and morphology of cuticular wax in bilberry (*Vaccinium myrtillus L.*) and lingonberry (*V. vitis-idaea* L.) fruits with a focus on bioactive compounds. Composition analysis will be done using GC-MS and morphology will be studied microscopically by using SEM. Biosynthetic route for wax components in berries will also be studied by using the recently created transcriptome data from ripening bilberry fruits. Also the effect of environmental conditions such as temperature, water deficit and light conditions on the wax morphology and biosynthesis will be evaluated in this study. Our study will bring new information on the potential industrial applications of berry wax. The fruit industry produces large volume of berry waste as side streams after processing. Berry waste can potentially be utilized to extract natural cuticular wax, which has demand in food and pharmaceutical products as well as cosmetics.

Genomics of local adaptation under asymmetric gene flow in *Arabidopsis lyrata*

Tuomas Hämälä, Tiina M. Mattila, Outi Savolainen

Short scale local adaptation is a complex process involving selection, migration and drift. The expected effects on the genome are well grounded in theory, but to examine these on an empirical level has proven difficult, as it requires information about local selection, demographic history and recombination rate variation. Here, we use locally adapted and phenotypically differentiated *Arabidopsis lyrata* populations from two altitudinal gradients in Norway to test these expectations on a whole-genome level. Demography modelling indicated that populations within the gradients diverged less than 2 kya and that the sites are connected by gene flow. The gene flow estimates were, however, highly asymmetric with migration from high to low altitudes being several times more frequent than vice versa. To detect signatures of selection for local adaptation, we estimated patterns of lineage specific differentiation among four populations. Concordant with theory, adaptive loci in the low-altitude populations were concentrated in areas of lower recombination rates than in the high-altitude populations. Although most selected loci showed patterns of conditional neutrality, we found a strong case of allelic trade-off between one low- and high-altitude pair, indicating antagonistic pleiotropy. These results provide novel insights into genomic architectures and evolutionary processes driving local adaptation under gene flow.

Reindeer grazing and climate warming changes fungal communities in the tundra

Saija Ahonen[1], Henni Ylänne[1], Kati Saravesi[1], Anna-Liisa Ruotsalainen[1], Marko Suokas[1], Minna Männistö[2], Annamari Markkola[1], Sari Stark[3]

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Fungi play important role in carbon and nutrient cycling in Arctic ecosystems. Mycorrhizal fungi transport recently fixed carbon belowground and in soils with low pH, decomposition is mainly driven by saprophytic fungi. Soil fungal communities are tightly linked with aboveground vegetation, but also aboveground herbivory can have direct and indirect effects on soil fungi. As temperatures in the Arctic are continuing to increase due to climate change, the activity and composition of soil fungal communities may change. This can decrease the vast carbon stores in tundra soils, if decomposition is enhanced more than plant photosynthesis. In this study, we investigated whether different decadal history of reindeer grazing shapes the response of fungal communities to warming and fertilization. By assessing soil fungal communities with high-throughput sequencing of the ITS2 rRNA gene area, we found that the difference in reindeer grazing pressure had caused a clear shift in soil fungal communities. We suggest that this is linked to the grazing-induced vegetation differences. We also found that several fungal taxonomic and functional groups reacted to the warming and fertilization treatments. Yet, the direction of the change depended on the grazing pressures. Thus, our results indicate a key role of grazers in shaping the responses of fungal communities to climate change.

Illegal killing regulates the legally harvested wolf population in Finland

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Illegal killing of wildlife is a global issue. It is the major threat to recolonizing wolf (*Canis lupus*) populations. In Northern Europe poaching is focused on wolves because of escalated carnivore conflict. Poaching is largely cryptic, i.e. hidden criminality and difficult to measure. Wolf population in Finland has fluctuated between 100-300 wolves during the past 20 years without known reason. We examined the role of poaching on wolf population changes. We created different scenarios to detect the effect of poaching on population level. Data consisted data of 130 tagged wolves from the period 1998-2014. Illegal killing and legal hunting were the most common causes of mortality, respectively. Social status of the animal had a significant relation to their fate. Breeding individuals had the highest risk to die illegally. Poaching risk had clear seasonal trend and survival dropped steeply in midwinter. Poaching rate varied considerably between the years. According to results poaching has regulated Finnish wolf population which is simultaneously legally harvested. Legal hunting seems to decrease poaching in short run but does not increase the tolerance as such as legal harvesting has been present throughout the study years. Our results offer usable scientific knowledge for conservation, management and law enforcement.