The 28th Kaamos Symposium
Abstract Booklet

4th and 5th December 2024
University of Oulu

GRADUATE SCHOOL
UNIVERSITY OF OULU

BIODIVERSE ANTHROPOCENES
UNIVERSITY OF OULU

FACULTY OF SCIENCE
UNIVERSITY OF OULU

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There will be computer exercises done in groups as part of the workshop so please bring a laptop or group up with someone with a laptop.

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18:00-24:00 Poster Session and Botanical Garden Party simultaneously

Talks

Morning session, 4th December

Keynote: Mikkel Pedersen Ancient Environmental DNA - A window into million-year-old ecosystems

Ancient environmental DNA (eDNA) analysis has emerged as a powerful tool for reconstructing past biodiversity, offering unprecedented insights into the biological compositions of ancient ecosystems. Recent breakthroughs have demonstrated that eDNA can be preserved in geological deposits over 2 million years old (Kjær et al. 2022), significantly extending the temporal range of this method. This advance provides a unique window into deep-time ecosystems, even in deposits where fossils are absent. However, deep-time geological deposits are sparse and represent isolated snapshots of past environments. This raises critical questions about the broader applicability of such data: How well do these snapshots capture the complexity of ancient ecosystems? And what are their limitations in reconstructing long-term evolutionary and ecological dynamics using ancient environmental DNA? Questions that might refine our understanding of the potential and boundaries of ancient eDNA as a tool for studying Earth's deep past.

Johanna Honka Deciphering origins and caretaking of Northern horses

The early evolutionary history of the modern domestic horses (*Equus caballus/E. ferus caballus*), named as DOM2 lineage, is quite well documented due to numerous archaeological and ancient DNA (aDNA) studies. Based on current knowledge, the domestication process that led to modern horses began somewhere within the Pontic-Caspian steppe between ~4500-3200 BCE (before common era), resulting in a domestication bottleneck and reproductive control ~2700-2200 BCE, coincidental with dispersal of DOM2 horses. However, how and when these domestic horses arrived into Northern Europe, as well as the specifics of their care, remain poorly understood. In this study, we reviewed the current knowledge of horse domestication, with a focus on Nordic regions, and analysed prehistoric and historic horses from Finland, Estonia, Lithuania and Western Russia to assess the extent of human supplementary feeding practices, compare regional differences in horse diets, and investigate maternal genetic diversity. We used radiocarbon dating, stable isotope analysis of carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) to infer long-term diet and mitochondrial DNA variation obtained from ancient DNA in archaeological bone and tooth samples. We also compared our stable isotope data to published isotope data of other horses and animals. Our aim was to better understand the extent of supplementary feeding by humans, regional dietary differences, and maternal genetic diversity in these horse populations. We identified three wild horses in our dataset, along with one dating back to the period of horse domestication/dispersal, with most samples representing domestic horses from the 400-1400 CE. Stable isotopes of carbon and nitrogen revealed a west-east gradient in carbon isotope ratios, implying regional dietary differences related to climate and vegetation. Additionally, we observed high nitrogen stable isotope ratios in some horses, indicating that they were likely fed more intensively on manure-fertilized agricultural plants. Mitochondrial DNA diversity was high, revealing multiple maternal lineages.

Presenter: Johanna Honka

Authors: Johanna Honka, Daniela Salazar, Igor V. Askeyev, Dilyara N. Shaymuratova, Oleg V. Askeyev, Arthur O. Askeyev, Gulshat Sh. Asylgaraeva, Renat R. Valiev, Kristiina Mannermaa, Giedrė Piličiauskienė, Suvi Olli, Markku Niskanen, Jouni Aspi and Laura Kvist

Niina Kiljunen Gall midge diversity in the light of DNA

Species living on Earth have been under taxonomic research for over 260 years, yet fewer than 2 million species have been scientifically described. This number represents only a small fraction of the estimated total number of species, which is at least 10 million and likely much more. Despite the admirable work by taxonomists, the vast majority of species still remain undiscovered. Concurrently, we are facing a human-induced biodiversity loss and high extinction rates. Efficient DNA-based tools are needed to accelerate species identification, but also discovery and description of the unknown species, in order for us to study world's biodiversity more comprehensively in this urgent crisis. The yet unknown species often belong to hyperdiverse groups, are typically tiny-bodied and abundant, resemble alike, and sometimes lack or have very few distinct external or internal morphological characteristics, making their morphological examination challenging and impractical. These species are often referred to as *dark taxa*. Gall midges (Cecidomyiidae) provide an excellent example of such. Less than 7,000 species of gall midges have been described, but based on DNA barcoding, they are estimated to comprise 1.8 million species globally. In Finland, gall midges are a poorly studied taxon and only 385 species are reported. Based on DNA barcoding analysis of over 9,000 gall midge specimens, we suggest there occur several thousand of gall midge species in the country. To gain a clearer understanding of Barcode Index Numbers (BINs) reliability as species proxies on gall midges, 3 nuclear markers were sequenced in a preliminary study for small set of gall midge specimens. Preliminary insights will be shared in the presentation.

Robert Kesälahti Genomic Imprinting in Scots pine (*Pinus sylvestris*)

Scots pine has an excellent ability to adapt to local environments, proven by its wide distribution across Eurasia. Genomic imprinting, an epigenetic phenomenon where the expression level of a gene depends on the parental origin, could be a factor behind this adaptability. Genomic imprinting is caused by epigenetic modifications ("imprints") made to genes, regulatory regions, and histones. Imprints can completely silence the expression of a gene or repress it. Imprinted genes have been found in multiple angiosperm, mammal, insect species and recently in *Marchantia polymorpha*, a large thalloid liverwort.

Numerous theories have been presented for the origin of this phenomenon, but none of them has been widely accepted. According to the popular kinship theory, genomic imprinting is caused by competition between the parents for the allocation of resources to the development of offspring. This competition mainly takes place in the tissues in charge of resource allocation for the developing offspring: endosperm in angiosperms and placenta in mammals.

We investigate whether genomic imprinting also exists in conifers using Scots pine as our model species. Conifers have a haploid, maternally inherited megagametophyte (endosperm analog). The parental conflict, described in the kinship theory, cannot take place in the haploid megagametophyte. Alternative theories for the origin of genomic imprinting do not require parental conflict, as imprinting could exist in systems where coadapted maternal-offspring traits have large fitness effects. Seed dispersal in conifers is usually limited around the mother tree, so it would be beneficial for offspring to resemble their mothers. Imprinted genes have also been found in embryos in both angiosperms and mammals, also hinting at the possibility of another reason behind it.

Reciprocal crosses are required to differentiate genomic imprinting from allele-specific expression. We have performed reciprocal crosses for selected Scots pine pairs and collected seeds resulting from these crosses. We have performed RNA-sequencing for the diploid embryos and exome captures for the haploid megagametophytes of the seeds. Exome capture data from megagametophytes allows the identification of maternal and paternal alleles. We can then compare the expression levels of a gene when it has been inherited both paternally and maternally. Previous results of allele-specific expression in Scots pine indicate abundant allele-specific expression in embryos. This ongoing study aims to provide information on whether genomic imprinting has evolved convergently or has a shared history.

Presenter: Robert Kesälahti

Authors: Robert Kesälahti, Sandra Cervantes, Alina Niskanen and Tanja Pyhäjärvi

Maria Khan Addressing Challenges in Species Delimitation: Genomic Solutions for Cases of Barcode Sharing

Introduction: This talk sheds light on two long-standing issues of taxa under complex evolutionary circumstances specifically a pair of sibling species of Small Emperor moth *Saturnia pavonia* and *S. pavoniella*. The two species show a parapatric model of distribution, i.e., their distributions meet but do not overlap. They appear nearly identical in their external morphology, and they are shown to hybridize readily in the laboratory. This suggests that they have speciated but have not isolated ecologically. The second case focuses similarly on a pair of species with virtually identical appearance and problematic taxonomy: Burnished Brass *Diachrysia chrysitis* and *D. stenochrysis* and/or *D. tutti*. However, the ranges of the two putative species largely overlap, and their females are shown to release chemically different sexual pheromones to attract males. Individuals cannot be reliably separated by morphology. Within the domain of DNA barcoding, the occurrence of barcode sharing poses a formidable obstacle, complicating species delineation and impeding accurate identification efforts. Both these cases present notable instances of barcode sharing. These cases have long confounded researchers, hindering progress in biodiversity studies and taxonomic classification.

Methods: Advanced genomic techniques were utilized to overcome these obstacles, employing a standardized set of nuclear markers through the target-enrichment method and sequencing with the Illumina NovaSeq platform. Through rigorous analysis and comparative studies, we have endeavored to untangle the intricate genetic dynamics inherent to these taxa. Our research sheds light on the evolutionary relationships and genetic differentiation among these species, providing valuable insights necessary for resolving taxonomic ambiguities.

Results: Both cases displayed sharing of barcodes between the sister species, Saturnia being more intermixed as compared to Diachrysia where a few samples shared barcodes with the other species. In both of the cases, nuclear markers were instrumental in the delimitation of the species and presented a very clear picture when subjected to phylogeny and the true species model. A series of population genomic and species delimitation analyses showed past introgression events that could be attributed to the mitonuclear discordance found in these taxa.

Conclusion: Our study underscores the complexity of species delimitation in the context of barcode sharing, while also highlighting the effectiveness of genomic solutions in elucidating such complex biological phenomena. Especially species under complex evolutionary circumstances in this case *Saturnia* and *Diachrysia*, but which also might be the case of similar taxa under complex evolutionary circumstances. By leveraging genomic technologies, significant strides have been made in surmounting the limitations of conventional DNA barcoding approaches. While barcode sharing can be looked upon as a challenge in species delimitation, it provided us with insights into mitochondrial discordance and past introgression events between the species further leading us to make assumptions on the evolutuionary history of both taxa. We invite participants to engage in a discussion on the intricacies of species identification and explore innovative strategies for addressing the challenges posed by barcode sharing in biodiversity research.

Soile Jokipii-Lukkari Novel heartwood formation associated *NAC*

The Scots pine (*Pinus sylvestris*) wood can be divided to the physiologically active outer part of the stem, sapwood (SW), and the innermost part called heartwood (HW) that contains no living cells. HW formation takes place in the transition zone (TZ) where the reserve materials of sapwood are converted to HW extractives. From the extractives, especially the concentrations of the stilbenes pinosylvin and its monomethylether have a strong negative correlation with the mass loss of HW caused by wood-decaying fungi. Until now, the factors initiating and controlling HW formation have remained obscure, but it has been described as an active, controlled process of senescence, the form of programmed cell death (PCD). PCD occurs both as an integral part of development and as a reaction to biotic and abiotic challenges. *BIFUNCTIONAL NUCLEASE 1* (*BFN1*) has been identified as one of the core genes associated with several types of developmental PCD. We have previously examined the dynamics of transcriptome modulation during heartwood formation in Scots pine. The expression of specific transcription factor gene *NAC* was found to correlate strongly with the stilbene synthase pathway indicating a putative role in heartwood formation. Here we present multiple lines of evidence showing that this *NAC* binds directly to the promoter of Scots pine *BFN1*. Because the content of stilbenes has large total variance and high heritability, it is assumed that breeding could increase the HW durability of Scots pine. It will be interesting to explore if the studied *NAC* could be utilized as a marker to predict HW properties in the future.

Presenter: Soile Jokipii-Lukkari

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Afternoon session, 4th December

Keynote: Sujeet Singh Conservation genetics of threatened vertebrates in India

Vertebrates are facing threats such as hunting, climate change, and habitat loss due to human activities like deforestation and encroachment. These factors can lead to population decline and isolation, which can reduce genetic diversity and increase the risk of extinction. To address these issues, it is crucial to study population genetics and landscape connectivity to develop effective conservation strategies. India, a biodiversity hotspot, is home to several threatened vertebrate species, including tigers, brown bears, snow leopards, red pandas, Siberian ibex, and various primates. These species are further threatened by anthropogenic activities and climate change. This paper will address several studies in the fields of conservation genetics, landscape genetics, and metagenomics, with a special focus on the Bengal tiger, Himalayan brown bear, snow leopard, red panda, and Siberian ibex. Briefly, STR analysis of Bengal tiger populations in the peninsular, Terai Arc, and Sundarbans tiger landscapes has been conducted to evaluate conservation units in the Sundarbans landscape. Himalayan brown bear populations distributed in the western Himalayas have been studied using landscape genetic approaches to evaluate the functionality of predicted bear corridors. This analysis identified geographic distance and resource availability (food) as the primary drivers of genetic differentiation. Genetic analysis of red panda pellets in the Kanchenjunga Landscape (KL) has shown that red pandas occur in a meta-population framework in KL-India. We will also discuss the utility of advanced genomics tools to understand historical bottlenecks in Siberian ibex populations and the gut microbial diversity of primate species.

Tamara Hiltunen Beyond the Eye: What Atoms and Satellites Reveal About Reindeer foraging patterns.

Ecosystems in the Arctic and northern Finland are experiencing significant shifts due to climate change. These changes have both direct and indirect impacts on the behaviours, lifecycles, and fitness of the region's wild and semi-domesticated reindeer (*Rangifer* sp. L.). Notably, the impacts vary across regions and between seasons and years, creating complex and inconsistent patterns. Reindeer demonstrate niche and behavioural plasticity, which may enable them to adapt to the effects of long-term and seasonal shifts in conditions. This plasticity is attributed to their well-studied foraging ecology, which can be broadly categorised into two areas: movement patterns and dietary choices. However, given the substantial environmental changes since many of these studies were conducted, understanding whether and how reindeer diets and movements have evolved over various temporal and spatial scales is increasingly critical. Furthermore, directly linking movement, diet, and habitat use is essential to understanding whether reindeer and their foraging resources are adapting to climate-driven changes.

Technological advances in GPS telemetry and dietary analysis have improved the availability of fine-scale data on animal movements and diets. Techniques, such as DNA metabarcoding or microhistology of stomach contents or faeces, provide detailed snapshots of diet composition at the time of sampling. In contrast, stable isotope analysis (SIA) of carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) offers a broader perspective, capturing trophic niches and dietary patterns over varying temporal and spatial scales with a single sampling event. By combining stable isotope measurements ($\delta^{13}C$, $\delta^{15}N$) and/ or DNA metabarcoding-derived diets with GPS tracking data, valuable insights into the relationships between diet, habitat selection, and foraging locations can be achieved. However, such direct integration remains underutilised in ungulate and reindeer research.

This presentation explores reindeer foraging behaviour across different temporal and spatial scales, focusing on wild reindeer in Svalbard and semi-domesticated reindeer in northern Finland. It highlights how the combined use of datasets from multiple methods enhances understanding of reindeer foraging ecology amidst environmental changes. Additionally, it demonstrates how these integrative approaches can address methodological challenges and provide a more comprehensive perspective on reindeer movement, diet, and habitat selection.

Presenter: Tamara Hiltunen

Authors: Tamara A. Hiltunen[1], Maria Väisänen[1,2], Audun Stien[3], Erik Ropstad[4], Jouni Aspi[1], Sami Kivelä[1], Jouko Kumpula[5], Stefaniya Kamenova[6,7,8], Steve D. Albon[9], Jordi Bartolomé[10], Leif Egil

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Erika Sininärhi Physiology of personality: Prenatal androgen exposure is connected to social rank and boldness in the banded mongoose (*Mungos mungo*)

Consistent behaviour, aka personality, predicts individual tendency of certain behavioural patterns and has implications for natural populations. Personality is known to have partly genetic basis and be related to fitness, thus if natural selection targets certain personality traits, populations may change rapidly and drastically as a result. Preservation of diversity in personality may in turn improve population resilience as a whole, to survive in a constantly changing environment. However, how variation in personality traits arises as a combination of genetic and environmental factors, and how it links with other traits of individuals is still poorly understood. For instance, maternal effects have been linked to behaviour of offspring, but only few studies have been done in wild populations. Here, we investigated whether mother's social rank influences personality (boldness) of offspring through prenatal androgen exposure in the banded mongoose (*Mungos mungo*). Study was done in a wild population located in Mweya, Uganda. We used digit ratio (2D:4D) and anogenital distance (AGD) as indicators of prenatal androgen exposure and mother's chronological age as a proxy of social rank due to age-based dominance system of the species. Individual personality was estimated as an index based on voluntary participation in field weighing events, which serves as a measure of boldness in the human context in these free-living mammals. We discovered that both digit ratio and AGD were connected with mother's social rank and personality of offspring, making androgen exposure a potential mediator between these traits. Measured by digit ratio, offspring of older females had higher androgen exposure, which in turn predicted bolder behaviour in offspring. In contrast, the effects of AGD were sex-specific: as with AGD; the female offspring of dominant mothers had more prenatal androgen exposure, but only males with higher AGD were bolder. Our results imply that dominant mothers may prime their offspring for competition through prenatal androgen exposure, and they help us to understand the underlying mechanisms that generate individual variation in personality and behaviour in wild mammals.

Presenter: Erika Sininärhi

Authors: Erika Sininärhi, Aura Palonen, Henna Pääkkö, Hazel Nichols, Harry Marshall, Francis Mwanguhya, Solomon Kyabulima, Robert Businge, Michael Cant and Emma Vitikainen

Antti Pöllänen Seasonal and regional variation in Finnish forest reindeer survival: Impacts of predation and winter weather

The survival of Finnish forest reindeer (*Rangifer tarandus fennicus*) varies seasonally, and this variation is mainly caused by predation. In a study of 305 GPS-tagged females across two Finnish subpopulations, Suomenselkä and Kainuu (2010–2022), survival patterns differed by region and season. Results showed higher survival rates in Suomenselkä (mean 0.90, increasing trend) than in Kainuu (mean 0.84, declining trend). Seasonal survival varied by region, with the lowest rates in Kainuu during winter and in Suomenselkä during autumn migration. Predation was the primary cause of mortality, with wolves (*Canis lupus*) responsible for 58% of predation cases and predation rates two times higher in Kainuu, where wolf density is higher. This study provides the first survival estimates for this reindeer subspecies, highlighting the influence of site-specific factors on seasonal survival. To elaborate on factors affecting winter survival, future research will examine the impact of snow characteristics and harsh weather (particularly severe rain-on-snow events) on wolf predation rates for Finnish forest reindeer. Reduced foraging ability can enhance reindeer movement, increasing vulnerability to wolves, especially in Kainuu

Keywords: Population Ecology; Predation; Rain-on-snow; Finnish forest reindeer

Lucy Cotgrove Exploring Thermal Physiology and Aerobic Scope in Salmon Juveniles Amidst Heatwaves

Aquatic ectotherms become more vulnerable during heatwaves due to increased energy needs and reduced oxygen in warmer waters. Understanding thermal physiology is critical for population shifts. Heatwave risk assessments often focus on immediate effects, disregarding long-term physiological constraints and fitness impacts. The age at which organisms mature is genetically linked to their ability to use oxygen, a key factor in energy distribution, and responds strongly to environmental temperatures. By measuring how salmon juveniles manage energy at temperatures ranging 16 - 23°C, we bridge the gap between physiological heatwave effects, life history and fitness of salmon. Relating thermal performance to genetic differences in maturation timing, we show how energy distribution changes between life strategies at different temperatures. These findings provide better understanding how evolution responds to climate change and in developing conservation strategies for Atlantic Salmon.

Presenter: Lucy Cotgrove

Authors: Lucy Cotgrove, Evan Sala and Jenni Prokkola

Alina Niskanen Inbreeding genomics and inbreeding depression in the Finnish grey wolf

Inbreeding is a common problem in small and closed populations. It can cause lowered fitness by increasing the homozygosity of harmful alleles, i.e., by unmasking mutational load. The Finnish wolf population went through a severe population bottleneck in the 19th century, and the population size started to increase in the 1990s. In the 21st century, the population size has fluctuated between 150 and 300 individuals. However, the number of breeding individuals is considerably lower, and dispersal from the neighbouring Russian population seems relatively low. Here, we first use genome data from Finnish wolves to study the realized inbreeding levels between 1994–2016 and the timing of past inbreeding events, and then use this inbreeding information to examine whether there is inbreeding depression in the probability of acquiring an alpha status or being infected by *Trichinella* or *Echinococcus* parasites.

We estimated genomic inbreeding using runs of homozygosity (F_{ROH}) and realized genetic load by estimating the proportion of homozygous deleterious loci of all loci. We found that genomic inbreeding has mildly increased over time, but the mean level of inbreeding is still low. A few individuals showed clear evidence of recent inbreeding based on the length of homozygous-by-descent segments. Our preliminary results suggest that the fitness of inbred individuals may be reduced, as we found some evidence that more inbred individuals are less likely to become breeding alpha individuals than less inbred individuals. However, we did not find strong evidence of inbreeding depression in parasite prevalence or abundance.

Presenter: Alina Niskanen

Authors: Alina K. Niskanen[1], Suvi Ponnikas[1], Linnéa Smeds[2], Hans Ellegren[2], Ilpo Kojola[3], Mia Valtonen[3], Helena Johansson[3], Marja Isomursu[4], Laura Kvist[1] and Jouni Aspi[1]

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Morning session, 5th December

Keynote: Elisabetta Versace Soft ideas: from physics to evolution and development

While human neonates come to this world as dependent creatures, with immature sensory and motor systems, other species are able to move around autonomously and have well developed perception of the world soon after birth. These precocial animals, such as domestic chicks and tortoise hatchlings, provide a unique opportunity to investigate ideas that are present at the beginning of life and that do not depend on learning and experience but constitute the building blocks of mental life. We recently discovered that ideas present at the very beginning of life reflect important aspects of the physical and social environment, such as gravity and the presence of animate objects. Interestingly though, these early ideas are not stereotyped and fixed. We will discuss the evolutionary reasons why early ideas and expectations are soft and plastic.

Justus Reunanen Maternal microbiota communicates with the fetus through bacterial extracellular vesicles

Dr. Reunanen will present his group´s latest research on bacterial extracellular vesicles (EVs) during healthy pregnancies. Their study found these vesicles in amniotic fluid, similar to those from the maternal gut microbiota, and demonstrated that they can cross biological barriers to reach the fetus. This discovery highlights a new form of communication between the maternal microbiota and the fetus, which may play a role in preparing the fetal immune system for gut colonization after birth. The implications of this finding of a novel layer in communication between eukaryotes and prokaryotes in relation e.g. to EVs produced by plant endophytic bacterial microbiomes and present knowledge about plant EVs are discussed.

Elisa Heilmann Microbiome of the common reed in relation to metal accumulation

Utilizing the ability of plants to bind harmful substances from their environment, called phytoremediation, has been researched globally. Plants are capable of binding heavy metals as well as other environmentally harmful substances into their structures, and thus aid in the remediation of polluted land areas and water bodies. Along with plants, bacteria and fungi are also utilized in this context. Such microbes have multiple biochemical pathways for transforming and binding different toxins and metals. Plants have a wide variety of microbes living on their surfaces, epiphytes, and inside them, endophytes, which likely contribute to the bioremediation potential of plants. The common reed (Phragmites australis) is a plant with a notably wide distribution, ranging from the arctic to the tropics. It is a wetland species that typically grows on the shores of different water bodies, as well as in other wetland environments. The capacity of common reed for binding harmful substances from water has shown promise in the southern latitudes due to its tolerance of heavy metals and large biomass production. It is also especially effective in binding nitrogen, phosphorus, as well as other organic compounds from water. However, in the northern climates, studies on common reed in phytoremediation are still limited. We studied the fungal and bacterial microbiome of the common reed, as well as copper (Cu) and zinc (Zn) concentrations inside the plant tissue, at four sites with variable distances to a mining site, using amplicon sequencing and metal analysis measured with ICP-MS. The samples were analyzed specific to each plant organ; rhizome, root, shoot and inflorescence, to estimate where common reed stores metals and to find interactions with associated microorganisms. Our results indicate that bacterial taxa associated with metal-rich conditions are more abundant in the common reed near a mining site, potentially contributing to the plant's tolerance and accumulation of heavy metals. Cu and Zn concentrations were the highest in the roots of the plant.

Jelena Belojevic Moving, but not prospering: Breeding dispersal in southern dunlins (*Calidris alpina schinzii*)

The global decline of shorebird species results from the combined impacts of human activities and climate change. The key factor contributing to the observed adverse trend is the deterioration of essential staging and breeding grounds for long-distance migratory waders, attributed to agricultural practices and land abandonment. Coastal grasslands along the Baltic Sea provide vital habitats for shorebirds during migration and for reproduction. Over the past two decades, there has been a notable increase in the restoration of Baltic coastal meadows, primarily through extensive cattle grazing. However, grazing carries the potential for negative side effects. Cattle may inadvertently trample nests and broods, and inadequate grazing practices can exacerbate the predation risk. Additionally, weather conditions in the Baltic are altering because of climate change, with a particular increase in wind-driven floods that can wash away nests and young broods. To assess the impacts of these threats and adapt current management practices accordingly, we investigate breeding dispersal in response to nest failure of one of the most endangered waders in Europe – the southern dunlin (*Calidris alpina schinzii*). Using a long-term data set on their life history, we investigate 1) if nesting success predicts the dispersal distance and direction in relation to previous nesting attempts and 2) nest survival probability relative to the dispersal distance and nest fate. Our study on dispersal behavior in southern dunlins provides insights into whether and how threatened bird populations can deal with the ramifications of environmental change and provides fundamental data to assess the viability of those populations.

Oona Leppiniemi Statistical modelling of palsas and peat plateaus across the Northern Hemisphere

Palsas and peat plateaus are unique permafrost landforms found in northern peatlands that contribute to northern biodiversity and global carbon storage. However, these landforms are under severe threat from anthropogenic climate change, with rapid permafrost degradation occurring across the Northern Hemisphere. This thesis examines the environmental characteristics, spatial distribution, and morpho-ecological state of palsas and peat plateaus to assess the impacts of climate change on these vulnerable landforms at both local and circumpolar scales. Statistical modeling, ordination methods, and high-resolution geospatial data will be used to identify environmental drivers critical to the persistence of palsa peatlands. The first study compares environmental drivers of palsa occurrence in different regions (Hudson Bay, Iceland, Northern Fennoscandia, and Western Siberia), revealing both common and regionally distinct environmental characteristics. The second study models changes in the distribution of suitable environments for palsa and peat plateaus under three different emission scenarios (RCP2.6, RCP4.5, RCP8.5) and predicts an almost complete loss of suitable environments by the end of the century. The third study assesses the morpho-ecological state of palsa mires in Finnish Lapland, showing a strong degradation over the last 50 years and a generally poor condition of the landforms. Together, these studies improve our understanding of the distribution and climate sensitivity of palsas and peat plateaus, with important implications for future carbon dynamics and conservation strategies in permafrost landscapes.

Afternoon session, 5th December

Keynote: Autun Purser Deep Sea Life under permanent ice cover

Deep sea life can be found across the world ocean, though often the distribution of fauna are related to surface productivity. In some areas, surface productivity is difficult to gauge and production regimes complicated by thick ice cover, in some regions virtually permanent cover, perhaps transported by occasionally wind dominated surface transport or under ice currents.

In this presentation two contrasting ecosystems are presented; deep in the central Arctic below permanent sea ice, and deep below the Weddell Sea ice, Antarctica. In these contrasting regions seafloor coverage by megafauna can be very high, with 100 % coverage not uncommon in some hotspot locations. With videos and images, the functioning of newly discovered giant, crawling sponge ecosystems of the Arctic are contrasted with extensive icefish brooding colonies of Antarctica – all below near permanent ice cover and discovered with AWI towed camera systems during the last decade.

Virpi Pajunen Biogeography of small things – diatoms under environmental change

The Earth is facing a rapid environmental change, comprising climate change, ecosystem degradation and biodiversity loss, and this will influence all the living: whether big or small. Traditionally, very small creatures, such as micro-organisms, has thought to be ubiquitous and highly adaptive to change due to their fast reproduction rates and high dispersal abilities. Diatoms, unicellular aquatic algae, have these qualities. However, a growing number of studies indicate that these important primary producers may have similar biogeography patterns as larger species, suggesting that also microorganisms can have climatic preferences and physical dispersal barriers. Amongst freshwater diatoms, some species occur or thrive merely in restricted areas, such as in cold and harsh conditions or in islands; and have adapted to these unique environments. The changes in environmental conditions will modify the habitat conditions to that extent that some species may perish. Thus, we are running against the biodiversity loss to find habitats with distinctive communities, identify the driving processes of ecosystem resilience, and hopefully, save something precious on the way.

Sami Kivelä Evolution in urban environments in Lepidoptera

Urban environments are characterized by higher temperatures and consequently longer growing seasons than surrounding rural areas due to the urban heat island (UHI) effect. Another typical characteristic of urban environments is widespread artificial light at night (ALAN). UHI is likely to affect the evolution of thermal tolerance, whereas both UHI and ALAN are expected to affect seasonal phenology and life-cycle regulation of insects because the UHI facilitates an extended activity period in urban environments, whereas ALAN may affect the perceived photoperiod. Photoperiod is a key environmental cue for life-cycle regulation. We studied urban evolution of heat tolerance and seasonal life-history plasticity in Lepidoptera. Adults of the moth *Chiasmia clathrata*, but not larvae, from urban populations were more heat tolerant than those from rural populations. Long-term field observations in and around six cities in Finland and Sweden showed that flight seasons of the butterfly *Pieris napi* and *C. clathrata* are longer and end later in most of the studied cities, suggesting a difference in timing of diapause induction. We also measured the photoperiodic reaction norms for diapause in these two lepdiopterans in two cities. There was a genetic shift in the reaction norms so that urban populations had a lower day length threshold for direct development than rural ones, which is consistent with reaction norm adaptation to the UHI and not to ALAN. By using *C. clathrata* from Mid-European and North-European urban and rural populations, we experimentally tested whether dim ALAN affects diapause induction and if urban populations show adaptations to ALAN. Dim ALAN prevented diapause induction in all populations, this response being stronger in Mid-European populations and indicating no urban adaptation to ALAN. Finally, we studied the dynamics of urban evolution in the butterfly *Coenonympha pamphilus* and *C. clathrata* by using a population genomic approach. Genetic population structure was strong in *C. pamphilus* and practically absent in *C. clathrata* that showed a signature of recent population expansion. It is plausible in both species that urban adaptations have multiple origins. These studies suggest that heat tolerance and seasonal life-cycle regulation readily evolve in urban insect populations in relation to the UHI. ALAN seems to create a developmental trap, which may contribute to insect declines especially at mid-latitudes. The phylogeographic context seems important for understanding urban evolution at a large spatial scale.

Paula Palanco Lopez Human-microbial relationships in alternative agriculture: context, processes and dynamics

Against a backdrop of growing concerns after situating antimicrobial resistance (AMR) among the top ten global causes of death (Murray et al., 2022), agricultural use is considered one of the main drivers of AMR. This use is only increasing, despite the continuous surveillance and control efforts of global health institutions. In my research, I look into those cases in which farming is done without relying on antimicrobial use, this is, ‘alternative’ farms. Concretely, I am interested in what kind of relationships alternative farmers develop with microbial communities, what processes and dynamics are established between them, what are the perspectives that motivates this kind of farming, and, importantly, what kind of (social, economic, ecological) context makes it possible. I investigate these questions using qualitative methods such as interviews and participant observation, and so far I have carried out fieldwork in eight Finnish alternative farms. Ultimately, I am wondering which lessons can be learned from alternative farming that can inform better agricultural AMR policies?

Tracy Hruska Lessons for Surviving (and even Leading) Multidisciplinary and Multi-Partner Research Projects

My presentation will share lessons learned from my own recent experiences with consortium research projects and European funding mechanisms. Aimed at PhD students and other early career researchers, I will offer observations, strategies, and cautionary tales for participating in (and leading) multinational research teams and for collaborating in interdisciplinary research more generally.

In late May 2024, I moved from the United States to start my current position as a Postdoctoral Researcher in Cultural Anthropology at Oulu. My position is part of a large research project called MOTIVATE – "Monitoring Of Terrestrial habitats by Integrating Vegetation Archive Time series in Europe." Funding comes from Biodiversa+, a European co-funded program focused on transnational biodiversity research. Typical of the program, MOTIVATE includes teams from six European countries who have promised to play nicely together and to build on each other's work to produce interdisciplinary and transdisciplinary scholarship that will advance science and contribute to biodiversity conservation action and policy. The Finnish team – Roger Norum and I – comprise the only social scientists on the project, with everyone else spread between botany, plant ecology, and remote sensing.[1] Progress in the project thus far has offered insights into implementation of European Union environmental policy and complex network of European environmental research institutions, projects, and partners.

In November of this year, with nearly six months of MOTIVATE experience under my belt, I led – as PI – the writing of a funding application for a large consortium project for the (7 funded partners, 1 unfunded partner) to the 2024 Biodiversa+ Transformations grant call, and also took part in the development of a Work Package for another Biodiversa+ funding application (6 funded partners, 3 unfunded partners) led by a Czech team.[2]

In addition to my direct encounters with Biodiversa+, I have also taken part in various conference events and workshops, including one explicitly interdisciplinary workshop on biodiversity. I am also part of leading two new networks, one at Oulu (for early career researchers interested in interdisciplinary environmental research) and one spread across Europe (made up of social science and humanities researchers in primarily natural science Biodiversa+ projects).[3] Efforts such as these exemplify both that the need for interdisciplinary research in environmental conservation is widely recognized and that there is interest in learning how to do it better.

Collectively, these experiences have reiterated for me that effective interdisciplinary – and even just multidisciplinary – research is difficult, logistically, organizationally, and sometimes emotionally. But it is also worth doing, as it is offers both a) promise for tackling real-world problems in all their muddled complexity; and b) important ways to build a career in academic research. My talk is premised on the notion that effective, collaborative research across disciplines is enabled much more through *process* than brilliance. The bar is surprisingly low for getting involved in (and invited to be part of) exciting research projects. And being a good collaborator is a learnable skill. In my talk, I will provide concrete tips to help early career researchers be not just better research collaborators but also collaborative leaders.

[1] – ominous music in background

[2] – sound of me tooting my own horn

[3] – sound of marching

Posters

Hanna Virpiranta REWET: REstoration of WETlands to minimise emissions and maximise carbon uptake – Introduction of Open Lab 3, Ylpässuo, Kiuruvesi, Finland

Kamonwan Khanthong Screening of microbial species isolated from PFAS contaminated area for bioremediation purposes

Martin Grethlein Environmental Genomics in times of global change: the bay mussel (Mytilus trossulus) as an indicator species

Mauno Konu Screening of microbial species isolated from PFAS contaminated area for bioremediation purposes

Nicolina Johanson The effects of long-term fertilization and grazing exclusion on flower abundance, community composition and diversity in high-latitude grasslands