The 29th Kaamos Symposium Abstract Booklet

3rd and 4th December 2025
University of Oulu

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

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10:50-11:20 Medium talk, online: **Clément Massé**, CARNIVORE CONSERVATION WITHOUT NUMBERS: How Indigenous knowledge can inform wolverine-reindeer herding coexistence and conflict management in Sápmi/Northern Finland

11:20-11:40 Short talk: **Wille-Pekka Lepo**, Benthic biodiversity in subarctic stream networks - headwaters as upholders of variation through space and time

11:40-12:00 Short talk: **Nicolina Johanson**, Arctic plant-pollinator network changes under grazing pressure and soil nutrient enrichment

12:00-12:20 Short talk: **Shreya Pandey**, Comparison of Illumina and Nanopore sequencing technologies from Environmental DNA metabarcoding method for biodiversity monitoring from ancient archive coniferous litterfall samples

12:20-13:00 Lunch break

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Chair: **Stefan Prost**

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14:00-14:30 Medium talk: **Seppo Vainio**, From Gemmules to Exosomes: A New Paradigm of Biological Connectedness

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Talks

Morning session, 3rd December

Keynote: Richard Johnson, Forested buffers mitigate land-use effects on aquatic invertebrate and terrestrial spider communities in stream-riparian meta-ecosystems

Our understanding of how stream-riparian meta-ecosystems respond to environmental impacts and management interventions is limited by studies that simultaneously quantify the drivers of aquatic and terrestrial biodiversity. Our early work on aquatic and riparian assemblages in four forested and four agricultural streams showed spatial and temporal patterns of riparian assemblages (beetles and spiders) correlated with local habitat (vegetation type, soil characteristics), while stream assemblages correlated more with catchment scale variables (land cover). Together with riparian habitat variables, abundances of aquatic insects (dipterans, EPT) were strong predictors of riparian arthropods, especially spiders.

Using a paired-reach approach, with upstream disturbed (unbuffered) and downstream forest-buffered reaches to mimic riparian rehabilitation, we studied the effects of forested buffers on instream macroinvertebrates, emerging aquatic insects and riparian spider assemblages in six streams situated in an agricultural catchment. Forest-buffered reaches had higher abundances of emerging insects, especially insects with strong dispersal abilities such as EPT, while unbuffered reaches had higher abundances of non-insects and weaker flying insects (e.g. chironomid midges). Abundances of emerging insects differed seasonally, largely due to higher abundances of Diptera (mainly chironomid midges) in spring, Ephemeroptera (mainly Baetidae) in summer and Trichoptera (mainly Limnephilidae) in summer and autumn. Correlation revealed that riparian spider abundances and guilds were associated with between-reach differences in habitat (e.g. higher abundances of web-building spiders in forest-buffered and free-living spiders in unbuffered reaches) and with abundances of emerging insects (e.g. mayflies, caddisflies). Constrained ordination and variation partitioning confirmed that riparian habitat and emerging insects independently explained significant variability of spider families and guilds.

Molecular methods (fatty acids and metabarcoding of spider guts) were used to quantify the importance of forested buffers for maintaining key linkages in stream-riparian meta-ecosystems. Total PUFA concentrations of emerging insects and spiders differed (main effects) among taxa and seasons and between reaches. However, for total PUFA of emerging insects only the interaction between taxa x season was significant, while for spiders both taxa x reach and taxa x season were significant. Notably, nine of the top 10 individual PUFA that characterised seasonal variability in emerging insects and spiders were identical. The highest concentrations of aquatic-derived ω-3 PUFA were found in emerging insects in summer and in spiders in autumn. While web-building spiders had high concentrations of ω-3 EPA in spring as predicted, indicating feeding on aquatic insects, they had lower ratios of EPA+DHA:ω-6 PUFA than the free-living spiders, indicating that they are also feeding on PUFA-poor aquatic insects and/or consuming proportionately more terrestrial food resources. DNA gut contents of the web-building linyphiid showed that diets indeed consisted of relatively high abundances (70%) of nutritionally poor terrestrial insects (e.g. dipterans, hemipterans, collembola). In summary, this work has shown the importance of riparian buffers for instream and riparian assemblages and for maintaining the cross-habitat resource flows that underpin biodiversity and function in stream-riparian meta-ecosystems.

Presenter: Richard Johnson, Swedish University of Agricultural Sciences, Sweden

Aino Juutinen, The effects of brownification on benthic diatom communities in boreal streams

Brownification is currently one of the main environmental concerns of northern freshwaters. In brownification increased humic substances, dissolved organic carbon and iron are decreasing water transparency and changing the water color. The mechanisms behind browning are complex, but it seems to be accelerated by land-use actions, especially forest drainage. The changes in light environment by decreased water transparency is expected to influence benthic primary producers, in rivers mainly epilithic algae, which are dependent on light. Here we combined data from field surveys in northern Finland and an mesocosm experiment to study the effects of brownification on diatom communities. The field survey showed that diatom community composition was mainly affected by water pH, but water color and nutrient availability were important as well. As changes in these key variables may be intertwined in forestry actions, we conducted an mesocosm experiment concentrating on the role of light environment by manipulating water color while keeping the water chemistry otherwise similar. The diatom communities differed significantly between the three brownification treatments and in addition, it decreased alfa diversity (Shannon). The results from the experiment combined with the field survey data underline the individual importance of water color as a factor that is part of the ecological changes occurring in freshwaters under brownification trend. As epilithic diatoms are the key primary producers in lotic ecosystems further effects in the food webs can be expected.

Katri Ruottinen, Diminishing snow cover has accelerated the range expansion of an alien ungulate species

Invasive species spreading is one of the main causes of biodiversity decline and is further exacerbated by climate change, which may alter local conditions towards a favourable direction for the invaders. Such has presumably been the case with the white-tailed deer in Finland. The species was originally introduced from the United States in the 1930s as a potential future game species but is invasive and now the most abundant ungulate species in Finland. The population has grown from just five to over 100 000 individuals, and its effects on agri- and horticulture, understorey plant communities and forest regeneration, and native deer species are a topic of heated discussions. We integrated time series data on climatic variables and white-tailed deer distributions from 1964 to 2019 to study not only the spatial spread and range expansion of the species, but also whether specific climate conditions have affected the rapid spread of the species. We used change in land surface area occupied by the deer as the response variable and tailored variables of climate (snowy days, temperature, precipitation), number of hunters, and the North-Atlantic Oscillation (NAO) index as the explanatory variables in linear modelling. Our results suggest that the range expansion was further aided by lack of snow and hindered by hot summer temperatures. More specifically, the number of days when the snow cover depth exceeded 20 cm limited the range. The Finnish climate, especially winter, has warmed faster than the global average, resulting in diminishing snow covers in the core parts of the deer range. This suggests that the future climate may further aid the spread and range expansion of this alien species, which underlines the need to study their interactions and effects with the surrounding ecosystems.

Gerrit Wehrenberg, Conservation Genomics for Threatened Wildlife - from the field to the lab and back again

We find ourselves in turbulent times, facing upheavals across all aspects of our lives. The biodiversity crisis, which includes species extinction and the loss of genetic diversity, might be one of the biggest challenges for our own species. This anthropogenic crisis will not only define our human future but could lead to the sixth mass extinction in the entire history of life on our planet. But what can we do? Here, I want to focus on how state-of-the-art molecular technologies can aid conservation practice. Conservation genetics is a relatively young, applied research field with rapidly developing methods to tackle these issues effectively. But we often fail to translate our powerful results into real conservation implementation. How can we achieve the jump from a fully academic field to truly applied research? This is a brief insight into how conservation genomics could better find its way into effective species conservation along my research on the Siberian flying squirrel, the cheetah, and the European bison.

Habibollah Mohammad Parast Tabas, Role of endosymbiotic bacteria (*Pseudomonas synxantha* DSM13080) in growth and stress adaptation of host plants in boreal and arctic climates

Endophytes are microorganisms residing with in the host plant. Microorganism and host cells interact and the close relationship between the mother plant and endophytes is good for both. Endophytes improve biometric qualities, crop output, pathogenic repulsion and plant development, bioremediation, synthesis of bioactive compounds, notably from medicinal herbs and induced systemic resistance. These microorganisms enhance plant development, function as biological control agent and exhibit resilience to a wide array of biotic and abiotic pressures. They are widely distributed in the natural habitats and demonstrate intricate relationships with the plant encompassing mutualistic, antagonistic, and infrequently parasitic interactions. Because of their unique ecological niches, endophytes inside plants may have more direct and positive impact on plant than microorganisms. They form symbiotic relationship with plants, inhabiting spaces such as roots, stems, leaves, flowers, fruits and seeds. Endophytes can contribute to overall soil health by promoting beneficial soil microbiota and improving soil structure. These include improved nutrient acquisition through nitrogen cycling and phosphate solubilisation, production of siderophore and phytohormone, detoxification of heavy metals and organic pollutants and enhanced tolerance to both abiotic and biotic stresses. In additional, endophytes stimulate the production of essential plant hormones, including indoleacetic acid (IAA), cytokinin, and gibberellic acid (GA), and are beneficial in promoting plant growth. The pseudomonads are a class of bacteria having members with important environmental functions, such as plant growth promotion. In addition, pseudomonads are considered ubiquitous; they play a key role in nutrient cycling and are a major component of the soil microbial communities. Many pseudomonades live in a symbiotic relationship with plants, utilizing nutrients and exudates from plant surfaces and surviving environmental stress by occupying protected sites provided by plants architecture. Bacteria in the genus *Pseudomonas* have an exceptional capacity to produce a wide variety of metabolites, including antibiotics that are toxic to plant pathogens. We have identified an endosymbiotic bacterium, *Pseudomonas synxantha* DSM13080, from buds of Scots pine. *P. synxantha* DSM13080 promotes host growth and development without the production of known plant growth -stimulating hormones. In this study, I study plant- endosymbiont interaction in Scots pine and the model species *Arabidopsis thaliana*. I inoculated seedlings of pine and *A. thaliana* with *P. synxantha* DSM13080 and studied the effect on growth and levels of nutrients and secondary metabolites in pine and Arabidopsis seedlings compared to controls.

Svitlana Sytnyk, Physiological Responses of black locust to Infestation by Invasive Leaf Miners

Black locust (*Robinia pseudoacacia* L.) despite its controversial reputation as an invasive species, is among the most widespread tree species in forestry within the Ukrainian steppe zone. Its rapid growth and ability to thrive on nutrient-poor soils make black locust a valuable component of plantations for phytoremediation purposes. However, in recent decades, the invasion of two North American leaf miners, *Parectopa robiniella* and *Macrosaccus robiniella* (Lepidoptera: Gracillariidae), has become a serious threat to this species throughout Europe. These endophagous insects feed within the mesophyll tissue, causing extensive damage to the photosynthetic apparatus. This study examined the impact of leaf miners' infestation on the photosynthetic performance of *R. pseudoacacia* trees of different ages. Chlorophyll fluorescence parameter – background, stationary, maximum, and variable fluorescence were measured in infested and uninfested leaves to evaluate photochemical efficiency and stress responses. Infested leaves exhibited a significant decline in fluorescence values, indicating impaired photosystem II activity and reduced photosynthetic efficiency. The effect was particularly pronounced in younger trees (<15 years), suggesting that juvenile individuals are more sensitive to herbivore-induced stress, likely due to higher metabolic activity and lower investment in structural or chemical defenses. In contrast, older trees showed a more stable fluorescence response, implying greater physiological buffering capacity and possibly enhanced resistance mechanisms. These findings highlight that the photosynthetic responses of *R. pseudoacacia* to herbivory are age-dependent and reflect a shift in defensive strategies throughout tree ontogeny. Overall, this study contributes to our understanding of how black locust adapts physiologically to invasive leaf miners and provides insight into the mechanisms underlying age-related variation in tolerance to herbivore pressure in long-lived woody species.

Presenter: Svitlana Sytnyk[1]

Authors: Svitlana Sytnyk[1], Kyrylo Holoborodko[1]

1. Dnipro State Agrarian and Economic University, Dnipro, Ukraine

Afternoon session, 3rd December

Keynote: Caroline Isaksson, Urban air pollution and its impact on birds and bumble bees

Urban habitats and landscapes are markedly different from non-urban "natural" habitats. One key difference is the higher levels of air pollution in cities. Air pollution is a major threat to health for all living organisms – from plants to humans. There are many different types of air pollutants but particle matter with aerodynamic diameter less than 2.5 µm ($PM_{2.5}$), nitrogen oxides (NO_x), volatile organic compounds (VOC) and tropospheric ozone are the pollutants of greatest concern in urban areas. Most of these air pollutants come either directly or indirectly from incomplete combustion of fossil fuels, hence directly linked to traffic-load. Up to date, most knowledge stems from research on humans and laboratory rodents. However, birds and bumble bees that are common residents in urban environments possess completely different respiratory systems to mammals, hence studies of these taxonomic groups are of great ecological importance. Using both experimental and descriptive approaches of wild birds and bumble bees, I will summarize our findings about the impacts of air pollution on these animal groups.

Presenter: Caroline Isaksson, Lund University, Sweden

Suvi Olli, Ancient DNA and stable isotopes unravel the history and past diet of the Baltic Sea region's chickens and the continuity of landrace lineages

Very little is known about the origins and breed history of domestic chickens (*Gallus gallus domesticus*) in northern Europe due to limited written records and the absence of ancient DNA evidence. To address this, we analysed archaeological chicken bones from Finland, Estonia, and Lithuania using ancient DNA, stable isotope analysis, and radiocarbon dating. We sequenced a 201 bp fragment of the mitochondrial control region and SNPs from the *thyroid-stimulating hormone receptor* (*TSHR*) and *β-carotene dioxygenase 2* (*BCDO2*) genes, comparing the findings with modern Finnish and Estonian landrace chickens and other ancient and modern chickens. Our results show genetic differences between ancient Finnish and Baltic chickens, particularly in *TSHR* and *BCDO2* allele frequencies, despite geographical proximity. Chickens from the Finnish Åland Islands were especially distinct, also possessing a unique mitochondrial haplogroup not seen in other ancient European samples. Northern European chickens also differed from central and southern European chickens from the same periods. Modern Estonian landrace chickens are genetically closer to ancient ones than modern Finnish landrace chickens, suggesting more recent genetic mixing in Finland. Both Finnish and Estonian landraces differ from modern production breeds. Stable isotope analysis revealed regional dietary differences and some chickens with differing diets. Based on stable isotope analysis, differing chicken-keeping practices were revealed as the results indicated the presence of free-roaming individuals and individuals with differing levels of supplementary feeding with manure-fertilised crops and animal protein.

Presenter: Suvi Olli (1)

Authors: Suvi Olli (1), Rudolf Gustavsson (2), Hanna Kivikero (3), Lembi Lõugas (4), Kristiina Mannermaa (5), Giedrė Piličiauskienė (6), Eve Rannamäe (7), Jeremy B. Searle (8), Laura Kvist (1), Johanna Honka (1)

1. Ecology and Genetics Research Unit, University of Oulu
2. Stiftelsen kulturmiljövård
3. Department of Philosophy, History, and Art Studies, University of Helsinki
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5. Department of Cultures, Archaeology, University of Helsinki
6. Faculty of History, Department of Archaeology, Vilnius University
7. Institute of History and Archaeology, University of Tartu
8. Department of Ecology and Evolutionary Biology, Cornell University

Kristóf Zsolt Tóth, The recombination landscape and sex-specific patterns of recombination in three families of great reed warblers

Recombination shapes genome evolution by creating novel haplotypes and breaking down linkage, thereby modulating the efficacy of selection. Using a three-generation pedigree of the great reed warbler (*Acrocephalus arundinaceus*; 11 F_0, 6 F_1, 17 F_2), we generated high-coverage whole-genome data and localised crossovers (COs) at a fine scale. We identified more than 700 autosomal COs and found a pronounced sub-telomeric concentration along chromosome arms. This bias was evident in both sexes but significantly stronger (two-sample Kolmogorov–Smirnov test, $p=7.47 \times 10^{-6}$) in male meioses, with paternal COs occurring closer to chromosome ends than maternal COs. Despite this positional dimorphism, recombination rates did not differ between the sexes.

Crossovers were strongly enriched within genes relative to intergenic regions and, within genes, occurred more often in exons compared with introns. We did not detect significant skew between coding sequence (CDS) and untranslated regions (UTR). Median distances from COs to the nearest gene were markedly smaller than expected under random placement, indicating that recombination preferentially targets gene-proximal sequence. CpG islands were also enriched for COs, with a notably stronger enrichment in paternal than in maternal meiosis (two-sided label-permutation test, $p = 0.0016$).

To quantify the evolutionary impact of these patterns, we estimated genome-wide genetic shuffling ($\bar{r}$). Across analyses, the intra-chromosomal component of $\bar{r}$ that results from COs was higher in females compared to males. Together, our results reveal a highly structured recombination landscape in great reed warbler. Crossovers are telomere-focused and gene-associated, with subtle but consequential sex differences in their localisation along chromosomes. Our results underscore the value of chromosome-wide, sex-partitioned analyses for interpreting the genomic and evolutionary consequences of recombination.

Aino Erkinaro, Dinner is served: decomposition and release of nutrients from decaying pink salmon carcasses

Pink salmon (*Oncorhynchus gorbuscha*), an alien species in northern Europe, has over the past few years experienced dramatic growth in numbers and in distribution. The 2-year lifecycle of pink salmon ends in mass death of all spawning individuals. Nutrients and other resources provided by decaying pink salmon carcasses are expected to have various direct and indirect ecological effects in its non-native distribution area. So far little is known about the rate of carcass decomposition in northern Europe, and the consequent release, concentrations, and storage of nutrients, all partly affected by decomposer community compositions. In 2023 we monitored pink salmon carcass decomposition and nutrient release for 9 weeks in six Barents Sea catchment rivers in an experimental set-up mimicking hotspots of carcass accumulation sites. While pink salmon carcasses on shore disappeared in a few days, carcasses in stream were decomposed notably slowly, still present and releasing nutrients even after 9 weeks. Decomposing carcasses had no significant effects on water chemistry in free-flowing stream water compared to control areas. However, in hyporheic zone water, nutrients accumulated into the sediment in considerable amounts, and on average we observed 18 times higher nitrogen and 25 times higher phosphorous values in carcass compared to control areas, although there seemed to be high among- and within-sites variation. Biofilm bacterial community composition changed through the decomposition process from mostly aerobic to mostly anaerobic communities, indicating a formation of a local oxygen depletion around the carcasses. These results indicate that pink salmon carcasses have potential to affect nutrient availability and benthic communities in invaded areas, but the effects may be habitat-specific.

Presenter: Aino Erkinaro

Authors: Aino Erkinaro, Hannu Marttila, Sami Kivelä, Timo Muotka, Kaisa-Leena Huttunen

Lena Huovinen, Temporal dispersal via seed banks in grassland plant metacommunities

Soil seed banks are hidden biodiversity reservoirs storing species, genetic and functional diversity. The delayed germination of seeds that form soil seed banks can buffer environmental variation and promote species coexistence in plant communities, which has implications for restoration and conservation efforts. Seed bank dynamics are driven by temporal variation, e.g. grazing creates small-scale disturbances that promote both the input of seed into the seed bank and the germination of seeds out of the seed bank. Spatial factors, such as habitat area and connectivity, might influence the relative importance of temporal dispersal. In habitats where the local species pool is limited, namely in small or isolated areas, temporal dispersal could provide an important additional source of diversity. We studied the interactive effects of the spatial factors habitat area and connectivity, and large mammalian herbivory as determinants of seed bank diversity and seed trait composition in a grassland plant metacommunity system in Åland, Southwest Finland. We combined seed bank species composition data with dormancy-related functional seed trait data. Our results show that grazing increased seed bank diversity and CWM seed coat thickness in the seed bank. Seed bank diversity decreased with habitat connectivity independently of the presence of grazing and seeds were more spherical in more isolated seed bank communities. The results could suggest that seed bank diversity and trait composition respond to both spatial and temporal variation.

Mykyta Peregrym, Floristic discoveries in a temperate flora: trends and drivers from three decades of vascular plant records in Ukraine

Floristic discoveries remain possible even in regions with a long history of botanical research. We analyzed 330 vascular plant discoveries in Ukraine (1997–2024), including 56 taxa newly described to science, to identify key drivers of floristic recording in a temperate flora. Each record was assessed

by taxonomic group, habitat, seasonality, data source, and the role of herbarium specimens and citizen science platforms.

Synanthropic habitats accounted for most discoveries, followed by grasslands, woodlands, and rocky outcrops, while mountainous areas were major centers of new taxa and hybrids. Most new records came from spring and summer field surveys, though historical herbarium specimens remained vital for describing new species. Citizen science platforms, though not yet used for formal descriptions, have helped reveal new national records.

These findings show that floristic knowledge remains incomplete even in well-studied temperate regions and highlight the value of integrating historical collections, underexplored habitats, and public participation to enhance biodiversity documentation and conservation.

Presenter: Mykyta Peregrym[1,2]

Authors: Mykyta Peregrym[1,2], Ihor Olshanskyi[3] & Svitlana Zhygalova[4]

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Morning session, 4th December

Keynote: Pekka Niittynen, Changing winter and snow conditions as key drivers of northern ecosystem shifts

Winter and snow are fundamental regulators of northern ecosystems, shaping biodiversity, species distributions, and ecological processes across high-latitude and alpine environments. As climate change accelerates, shifts in snow cover duration, depth, and seasonal timing are disrupting plant communities, altering animal behaviour, and transforming habitat availability from snowbed hotspots to whole tundra landscapes. The complex climate-snow-topography relationships can cause nonlinear microclimatic responses to overall warming, and even the local rates of realized climate change may be effectively different across and within tundra landscapes. These changes ripple through food webs, influencing everything from soil microbes to large herbivores, and challenge our ability to predict future ecosystem responses. This presentation explores how evolving winter and snow conditions drive ecological shifts in northern regions, emphasizing the interconnected impacts on both plants and animals in a rapidly warming world.

Presenter: Pekka Niittynen, University of Jyväskylä, Finland

Kaisa-Riikka Mustonen, Climate Impacts on Northern Stream Ecosystems: An Extreme Winter Thaw Case Study

The changing Arctic water cycle is disrupting the variable yet highly predictable hydrological regime of northern catchments. These shifts alter the timing and magnitude of discharge, which in turn can influence stream ecosystem processes by modifying the amount and quality of carbon and nutrients. Especially the winters of snow-dominated landscapes are changing tremendously via processes related to the Arctic water cycle, such as increased rainfall and extreme temperature fluctuations. Yet, winter remains the most understudied season across the northern latitudes, despite its growing importance in the context of rapid warming of the north.

We present evidence of a panarctic climate-driven winter event that triggered biological activity in a typical subarctic stream at the Pallas-Yllästunturi national park in northern Finland. By using simultaneous high-frequency measurements of water vapor, precipitation, and stream water isotopes, along with water chemistry, discharge, and stream bacterial community attributes, we captured an exceptionally warm Atlantic air intrusion event in early winter 2020–2021. This event led to complete snowpack melt and a high discharge and dissolved organic carbon pulse, which further activated the aquatic bacterial community despite the cold and dark conditions.

Our findings reveal how large-scale climate anomalies can abruptly disrupt local-scale hydrology and trigger biological activity in wintering stream ecosystems, highlighting the sensitivity of aquatic ecosystems and biogeochemical processes to shifting seasonality patterns. Capturing this event underscores the need for continuous high-frequency measurements across all seasons. Overall, this study underlines winter as a critical season for stream ecological research and highlights the responsiveness of northern stream ecosystems to climate-driven change.

Presenter: Kaisa-Riikka Mustonen1

Authors: Kaisa-Riikka Mustonen1, Hannah Bailey2, Danny Croghan2, Kaisa Lehosmaa1, Jonna Tauriainen1, Pertti Ala-Aho2, Valtteri Hyöky2, Jeffrey Welker1,3

(1) Ecology and Genetics Research Unit, University of Oulu; (2) Water, Energy and Environmental Engineering, University of Oulu; (3) Department of Biological Sciences, University of Alaska Anchorage, USA

Clément Massé, CARNIVORE CONSERVATION WITHOUT NUMBERS: How Indigenous knowledge can inform wolverine-reindeer herding coexistence and conflict management in Sápmi/Northern Finland

Human-carnivore interactions are influenced by local socio-ecological dynamics, yet conservation policies still overlook the potential of Indigenous and Local Ecological Knowledge for mitigating conflicts. In Arctic Europe, large carnivore predation on semi-domestic reindeer is a major source of conflict: In the Sámi homeland especially, where the wolverine (*Gulo gulo*) is the primary predator of reindeer, current research gaps hinder both conflict resolution and carnivore conservation. But a research gap is not always a knowledge gap. Frequent interactions between reindeer and wolverines have provided herders with extensive knowledge of e.g. predation timing, wolverine hunting behavior, movement, etc.; a knowledge that quantitative methods have struggled to capture.

In this study, we investigate the potential and possibilities of integrating Indigenous Knowledge and their knowledge-holders into wolverine conservation science and management. Using a co-creation process and semi-structured interviews with herders and policymakers, 1) we document the extent of herders' Indigenous Knowledge about wolverine-reindeer interaction in areas most affected by predation, 2) we assess the possibilities and obstacles for integrating this knowledge into policymaking, 3) we suggest strategies for improving conservation action and conflict management in the study area.

Our results showcase the extensive herder's knowledge on wolverine-reindeer interactions, offering insights that surpass those of scientific knowledge (e.g. on predation, scavenging, denning, movement, behaviors links with terrain and snow conditions, or coping herding strategies). We pinpoint the barriers policymakers' face for recognizing and integrating this knowledge, and we outline key strategies to overcome these challenges, and bridge Western science with the deep-rooted experiential knowledge of herders. Our findings reveal how Indigenous knowledge can enhance conservation strategies while fostering more effective human-wolverine coexistence. We confirm how Indigenous knowledge and Western science can, together, offer novel insights into elusive carnivore ecology, and offer pathways toward knowledge co-production and management models beyond conflict narratives.

Could the future of Arctic carnivore conservation lie in recognizing herders not just as stakeholders, but as knowledge-holders in their own right? This research invites a paradigm shift, where valuing local and Indigenous contributions to knowledge production forms the basis for sustainable coexistence with carnivores, in the Sámi homeland and beyond.

Wille-Pekka Lepo, Benthic biodiversity in subarctic stream networks - headwaters as upholders of variation through space and time

The "small but mighty" headwaters often contribute disproportionally to network-scale benthic biodiversity as differences in community composition between separate headwater branches can be high; headwaters harbour high variation between local communities, even though their local (alpha) diversity may be quite low. In spatially isolated headwaters, environment is the main driver of community composition, whereas in mainstream dispersal rates are high and so called "mass effect" swamps any effects of local environmental factors on metacommunity structure. This stream network position (SNP) hypothesis has become a major framework in metacommunity dynamics of stream ecosystems.

Temporal community variation, on the other hand, has not been studied extensively from the SNP perspective. In our study, we studied both spatial and temporal variation of benthic macroinvertebrate communities in boreal stream networks, at same time in the same area: we sampled five similar-size catchments in NE Finland, and one of them was also sampled annually from 2016 to 2020. We found that headwater and mainstem communities differed significantly from each other, both having strong indicator taxa. Headwater communities had higher environmental and biological variation between sampling sites (spatial beta diversity) and higher temporal community turnover between annual sampling occasions (temporal beta diversity) compared to their mainstem counterparts. However, we found strong "variation in variation" in headwater communities, some being exceptionally stable and some highly variable through time. The decreasing pattern of beta diversity from headwaters to mainstem also seemed to be quite consistent across years; however, some years did not fit into this frame, indicating that a single year may not give all encompassing picture of stream community dynamics, and inter-annual monitoring is required to gain full understanding of the functioning of stream ecosystems.

Nicolina Johanson, Arctic plant-pollinator network changes under grazing pressure and soil nutrient enrichment

Pollination is essential for the reproduction of most flowering plants and the functioning of terrestrial ecosystems. Yet both plants and their pollinators are declining globally due to anthropogenic changes such as habitat loss, climate change, nutrient enrichment and land-use intensification. These pressures can alter not only species abundance and diversity, but also the structure of plant-pollinator networks, with consequences for ecosystem stability. In high-latitude grasslands, short growing seasons, low nutrient availability and rapid environmental change may amplify the impacts of drivers such as nutrient enrichment and grazing, but their combined effects on plant-pollinator networks remain poorly understood.

Here we investigate how factorial manipulations of nutrient addition and grazing exclusion influence the abundance, diversity and composition of flower-visiting insects, and how these responses are reflected in the structure of plant-pollinator networks. We conducted flower visitation surveys in tundra and montane grasslands in NW Finnish Lapland using a long-term Nutrient Network experiment with crossed grazing exclusion and nutrient addition treatments.

Nutrient addition and grazing exclusion altered pollinator abundance, diversity and community composition, but their effects differed between the sites. In the nutrient-poor tundra, both treatments, individually and combined, increased visitation and reshaped flower-visitor communities, indicating sensitivity to bottom-up and top-down drivers. In the more productive montane site, grazing exclusion increased visitation while nutrient addition had weak effects, suggesting top-down control plays a stronger role in regulating visitation. Tundra networks had very low complexity, limiting the range of metrics that could be reliably compared, whereas the montane networks showed detectable changes, particularly under the combined NPK x Fence treatments. Overall, the impacts of nutrients and grazing on plant-pollinator interactions depended on site with the low-productive system showing highest vulnerability to treatments.

Presenter: Nicolina Johanson

Authors: Johanson, N., Andrzejak, M., Olde Venterink, H., Carvalheiro, L.G., Eskelinen, A. & Virtanen, R.

Shreya Pandey, Comparison of Illumina and Nanopore sequencing technologies from Environmental DNA metabarcoding method for biodiversity monitoring from ancient archive coniferous litterfall samples

Biodiversity is essential for ecosystem stability, productivity, and resilience but is increasingly threatened by anthropogenic pressures, including habitat destruction, climate change, pollution, and invasive species. Traditional biodiversity assessments based on morphological species identification are time-consuming, labor-intensive, and prone to misidentification, limiting their effectiveness for large-scale monitoring and historical reconstructions. Environmental DNA (eDNA) metabarcoding offers a non-invasive, high-throughput alternative, detecting species through genetic material shed into the environment. This project applies eDNA metabarcoding to historical environmental archive specimens, specifically conifer-litterfall samples, to reconstruct past biodiversity, assess long-term ecological changes, and evaluate shifts in arthropod and fungal communities over several decades. This study focuses on conifer litter samples collected between 1962 and 1998 by the Natural Resources Institute, LUKE, Finland.

Illumina sequencing is a well-established, high-accuracy platform offering deep sequencing and reliable performance across biodiversity studies. In contrast, Oxford Nanopore Technologies (ONT) provides key advantages, such as it is inexpensive, portable, and capable of real-time, in-field sequencing. Its accessibility and minimal infrastructure requirements make it suitable for remote fieldwork and for use in low-income countries. These features position ONT as an appealing complement or alternative to Illumina, despite its historically higher per-read error rates. Although ONT has historically shown higher error rates than Illumina (~0.0001% vs. ~0.02%), its accuracy is rapidly improving with new chemistries and basecalling models, closing the gap at a fast pace.

While, Illumina and Nanopore sequencing produced broadly similar genera from the historical eDNA samples. Both platforms recovered comparable numbers of species and genera, with most differences limited to rare, low-read taxa. Common taxa showed strong overlap. OTU richness and alpha diversity were consistent across platforms, and testing four Nanopore clustering modes in Apscale revealed only one significant deviation: the ESValpha1 metric differed significantly from Illumina. Overall, Nanopore performed similarly to Illumina, with meaningful differences confined to the rarest taxa.

Afternoon session, 4th December

Keynote: Simone I. Lang, Climate change effects on terrestrial ecosystems in High Arctic Svalbard

High Arctic terrestrial ecosystems on Svalbard are under increasing climate pressure, with changes occurring four times faster compared to any other region on Earth. The University Centre of Svalbard used its year-round presence to conduct research in this crucial field. Changes can be seen during summer but also during winter months when warming can lead to rain-on-snow events. Climate change is expected to alter tundra ecosystems, with shifts in plant diversity and abundance. These changes can be expected to lead to a shift in ecosystem functioning. Changes in vegetation may include for instance subsequent implications for permafrost insulation. In the INSULATE project, we aim to study the effects of climate change, both biotic and abiotic factors, on permafrost insulation on a year-round basis in the Arctic.

Presenter: Simone I. Lang, University Centre in Svalbard, Norway

Seppo Vainio, From Gemmules to Exosomes: A New Paradigm of Biological Connectedness

Recent discoveries across plant, microbiome and animal biology reveal that cells universally employ a conserved system for packaging and exporting molecular information through secretory nano- and microscale droplets, commonly termed collectively here for simplicity as exosomes. These exosomes, abundant in berries, fruits, plant sap, and all major body fluids, including excreted ones, contain the same classes of biomolecules long recognized as central to physiological homeostasis: lipids, proteins, metabolites, and diverse coding and non-coding RNAs including DNA. Mounting evidence shows that these molecular exosomes are not confined within species boundaries. Instead, they can traverse biological barriers such as the gut epithelium, the blood–brain interface, the placenta, and germline in mammals, and even the leaf and root systems of plants. Such findings imply the existence of a trans-species molecular communication network woven into the fabric of life.

As much of the information that modulates genome dynamics originates from non-coding sequences, now known to be selectively exported via EVs, these insights a re-evaluation of long-held assumptions about biological individuality, inheritance, and the limits of communication among organisms. Intriguingly, this emerging understanding resonates with Charles Darwin’s 19th-century pangenesis hypothesis, which proposed that all cells emit tiny “gemmules” capable of influencing the germline. More than two centuries later, modern research shows that exosomes and related vesicles function remarkably like the gemmules Darwin imagined, carrying molecular signatures of cellular experience outward into tissues, organisms, and ecosystems.

Taken together, these discoveries invite a broad rethinking of the biological interactome and secretome as foundational dimensions of life, potentially reshaping our concepts of evolution, adaptation, and interspecies connectedness.

Presenter: Seppo Vainio, Kvantum Institute, Laboratory of Developmental Biology, Disease Networks Research Unit, Oulu university

Stephen Venn, Resilience and Ecology

Concepts are devices we use to help us understand and communicate about complex phenomena. Ecology is full of concepts, which are often difficult to comprehend at first glance. The Zoologist Charles Elton published the book *Animal Ecology* in 1927, which was fundamental to the subsequent development of ecology as a scientific discipline. The book covered such topics as community ecology, food chains, population cycles and ecosystems, which enable us to understand what is happening to populations of species. There have subsequently been a number of paradigm changes that have revolutionized how we interpret changes in species populations and the factors that drive those changes. Another major development has been the introduction of the concept of biodiversity, which arose from the work of E.O. Wilson in the 1980s, which has revolutionized our perception of the effects of anthropogenic activities on nature. The concept of biodiversity has helped biologists to develop a deep understanding of the negative effects we are having on nature, but it is a difficult concept for non-biologists to grasp, and despite four decades of talking about biodiversity loss, we are still struggling to generate effective policies for the conservation of biodiversity. Recent decades have brought a number of novel concepts, such as Ecosystem Services and Nature-based Solutions, that are intended to be more accessible to and convincing for non-biologists. Sustainability, planetary health and resilience are all frameworks that facilitate the development of strategies that are not explicitly biocentric but give more attention to the well-being of nature and the environment. Ecological resistance refers to the capacity of an ecosystem to withstand perturbations, and thereby helps us to consider which ecosystems and populations are particularly vulnerable and require attention to ensure their persistence.

Presenter: Stephen Venn[1,2]

1. Frontiers of Arctic and Global Resilience (FRONT), Pentti Kaiteran katu 1, PO Box 8000, FI-90014 University of Oulu, Finland
2. Department of Invertebrate Zoology & Hydrobiology, Faculty of Biology & Environmental Protection, University of Lodz, Banacha 12/16, 90-237 Lódz, Poland

Zsófia Fekete, Hybridization between brown hares and mountain hares and its implications

The range of distribution and the habitats of the brown hare (*Lepus europaeus*) and mountain hare (*Lepus timidus*) overlap in Finland, where the brown hare is a relatively recent arrival. With the help of climate change, the temperate climate-adapted brown hare is rapidly expanding its range northward. At the same time, this means pressure on the cold-adapted mountain hare, whose range is contracting. Besides the influence of climate change, the brown hare is also possibly outbreeding the mountain hare.

These two, closely related species hybridize freely in their contact zone, producing fertile offspring. The gene flow between them is heavily imbalanced in the direction from the mountain hares towards the brown hares, but the factors causing this directionality and its consequences are yet to be understood.

Our aim was to investigate the genomic background and consequences of the hybridization of the two species. For this, we generated ddRAD sequencing data in collaboration with researchers from the

CIBIO, Portugal. In our study, we included over 300 ddRAD-sequenced samples of brown hares and mountain hares. We included samples of both species from Finland, of brown hares from Western Europe, and of mountain hares from Siberia. We have previously also generated chromosome level genome assemblies for both hare species involved. High quality reference genomes enable detailed genomic analysis and help us identify the genomic regions and genes involved in the ongoing evolutionary and selective processes more precisely.

Understanding the evolutionary processes of local adaptation may also provide valuable insight for informed conservation efforts of the mountain hare.

Mauno Konu, RNA viruses in different types of ant societies

Ants are ecologically very significant species, and they can be found almost everywhere in the world. Yet their viruses are rather poorly studied. From around 17,000 known ant species, only 187 virus species have been characterized.

The social structure of ant colonies creates an ideal environment for pathogens to spread: the nests have a stable climate, and genetically homogeneous ants constantly interact with each other and the environment. On the other hand, ants exhibit specific behaviors to mitigate this risk: they groom and clean one another and carry sick and dead individuals out of the nest.

In this study, I have characterized viruses from 15 ant species that represent two different colony structures observed in ants: monogynous and polygynous. In monogynous species, the new queens leave the nest to start a new colony alone, while in polygynous species, new queens are allowed to remain and reproduce in their home colony. This difference in social structure between species offers an opportunity to study the abundance and diversity of viruses in different ant societies.

From these 15 studied ant species, I have found in total of 168 virus species, out of which 152 were new to science, almost doubling the number of known ant viruses. In addition, I will compare how the virus abundance differs between the ant species representing the monogynous and polygynous social structures.

Anu Halonen, Behavioral type variability and dispersal in *Formixa exssecta*

We investigated personality traits, behavioral predictability, and dispersal tendencies in *Formica exsecta* queens. Nest fragments were collected from multiple populations, and queens were reared under controlled laboratory conditions. We also sampled fragments containing older, established queens to compare age groups. Behavioral assays quantified activity, exploration, and boldness for all queens, and dispersal tendency for young queens. Contrary to many previous studies, dispersal was not associated with activity, exploration, or boldness. Activity and exploration were correlated, but boldness was independent of both. Bolder individuals tended to show greater temporal plasticity in defensive behavior. Young queens were more active than older queens, but no other age-related differences emerged. These findings suggest that while personality structure encompasses plasticity and predictability, personality traits may not influence dispersal in this species.

Posters

Kaisa Lehosmaa, Endophytic microorganisms of aquatic moss precipitate elements intracellularly in metal-rich water

Niina Kiljunen, Searching *Fellow Feelings* through a Multidisciplinary Approach: Exploring Dark Taxa with Young Citizens

Shreya Pandey, Comparison of Illumina and Nanopore sequencing technologies from Environmental DNA metabarcoding method for biodiversity monitoring from ancient archive coniferous litterfall samples

More posters may be available (but not necessarily presented).