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Abstract book

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Browning alters food-webs and leads to biodiversity loss riverine in riverine ecosystems

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Concentrations of terrestrial-derived dissolved organic carbon (DOC) in freshwater ecosystems have increased consistently, causing freshwater browning. The mechanisms behind browning are complex, but in forestry-intensive regions browning is accelerated by land drainage. Here, I will introduce the results of our recent studies, which are based on both well-replicated manipulative browning experiments and extensive field data encompassing a wide browning gradient. Based on experimental and field observations, browning reduced dramatically the periphytic algal biomass, suppressed the availability of nutritionally essential polyunsaturated fatty acids, but increased the availability of terrestrial-derived and nutritionally poor-quality long-chain saturated fatty acids (LSAFA). The ongoing browning process is inevitably inducing a dramatic reduction in the nutritional quality of the stream biofilm, potentially causing biological degradation in algal-consuming communities, such as benthic macroinvertebrates. The field data from boreal forests streams suggest that invertebrate assemblages in brownified streams are less diverse and compositionally altered compared to those in non-humic, clear-water streams. A distinct invertebrate community change along the browning gradient was observed at around 12-13 mg DOC L-1. Only four taxa increased along the gradient, while 13 taxa showed a decreasing response. Our findings of both a gradual biodiversity loss and an abrupt biodiversity change along a browning gradient provide a benchmark against which forthcoming changes to stream biodiversity relative to the predicted browning trend can be gauged. With DOC levels in boreal freshwaters set to increase further in the future, the loss of invertebrate biodiversity in boreal streams seems inevitable. Restoration of drained peatlands as a means of reducing terrestrial biodiversity loss has shown some promise but responses of freshwater biodiversity and ecosystem functions to restoration of adjacent peatlands remain largely unknown.

DOC Transport Processes in a subarctic headwater stream revealed by multi-year high-resolution measurements

Danny Croghan

Dissolved Organic Carbon (DOC) is critically important to streams as an energy resource and contributes to a range of abiotic and biotic processes. Headwater stream catchments are particularly important contributor to carbon cycle fluxes. Currently, DOC dynamics in subarctic catchments are undergoing drastic shifts due to climate change. However, a lack of long-term high-resolution measurements of DOC in subarctic streams has hindered process-based understanding of these systems. To address this, we sought to better understand seasonal and inter-annual variation in DOC transport processes using a long-term high-resolution dataset of DOC to improve mechanistic understanding of DOC processes in the Pallas catchment. We collected a 4-year dataset of continuous in-stream DOC measurements alongside a range of hydrometeorological parameters for the Pallas Lompolonjänkä catchment. A range of high-frequency data analysis were undertaken. Spectral density plots across the study period were produced for DOC concentration and load to identify key periods of DOC mobilization, and to assess the extent of inter-annual variability. Concentration-Discharge analysis was then used to classify the relationship between discharge and DOC to reveal shifts in DOC mobilization between seasons and years. Breakpoint analysis was also undertaken to identify shifts in the breakpoint of the C-Q relationship, which provided information of how the system changes from chemodynamic to chemostatic in differing months. Hysteresis analysis was used to assess the response of DOC to different flow events throughout the study period, which improved understanding of whether near-stream sources or distal sources were the main contributors to stream DOC, while this also provided evidence of how the sources of DOC altered throughout the study. Finally, a statistical model to identify the controlling hydrometeorological parameters of DOC was developed, which allowed the shifts in controls on DOC between seasons and years to be observed. The study provides crucial information about annual and seasonal variability in transport processes of DOC in the Pallas catchment, which is crucial for improving understanding of how DOC dynamics in headwater subarctic catchments will continue to evolve in the rapidly changing climate.

From thaw till fall: interacting hydrology, greenhouse gas fluxes and carbon cycle in Arctic stream-lake continuum

Kaisa-Riikka Mustonen, Hannu Marttila, Kaisa Lehosmaa, Iina Koivunen, Jeffrey Welker, Mika Korkiakoski, Annalea Lohila, Jussi Jyväsjärvi

Carbon -water interactions are critical components of Arctic freshwater ecosystems. Dissolved organic matter (DOM) is the basis for in stream biological processes and is the foundation of biogeochemical linkages between terrestrial and aquatic landscapes and between the river bodies and the atmosphere via outgassing. Quantity and quality of DOM is strongly related to the microbial communities, as microbes play an important role in the freshwaters biochemical cycle converting DOM into nutrients, and mineralizing carbon into carbon dioxide (CO_2) and methane (CH_4). Despite the importance of streams in carbon cycle, Arctic streams are under-represented in global atmospheric GHG emission estimates owing to a lack of measurements in Arctic conditions. In this study we used combination of multiscale measurements to quantify carbon availability (DOC/DIC concentrations) and quality (water absorbance, $SUVA_{254}$ index), water sources (stable H_2O isotope proxies), microbial community structure (rRNA sequencing), and CO_2 and CH_4 fluxes and concentrations. Our study site is a typical groundwater influenced peatland dominated second order watershed located at Pallas-Yllästunturi National Park. Sampling was conducted three times during summer 2019 at 21 locations along the stream gradient. Results show that the water source of our study stream differed temporally and spatially along the stream continuum, and these differences were strongly related to the carbon amount and quality. At all sampling occasions our sites were constant sources of CO_2 and CH_4 to the atmosphere. Methane concentrations showed stronger spatial variation, whereas differences in CO_2 concentrations were also related to sampling occasion. Methane concentration was the most important environmental variable explaining the differences in microbial community structure, overdriving the influence of temporally varying DOC amount and quality. In addition, high abundance of methanotrophic taxa was highlighting the importance of methane as a carbon source in our study stream, further emphasizing the importance of the methanotrophic groups on the CH_4/CO_2 balance of northern catchments. Catchment wide studies conducted in Arctic and Boreal regions including interactions between aquatic and terrestrial ecosystems are especially needed today as northern areas are experiencing unprecedented extreme warming, precipitation changes and shifting snow depths.

Geodiversity in biodiversity research and conservation

Maija Toivanen

Geodiversity is an integral part of natural diversity – the abiotic counterpart to biodiversity. Geodiversity consists of the variation in geology, soils, topography, geomorphology, and hydrology.

Here, I represent the concept of geodiversity and some ways to measure it, focusing on geodiversity–biodiversity relationship. Linking abiotic and biotic nature is not particularly a new idea, but by acknowledging the full diversity of abiotic nature as geodiversity should advance our understanding of the relationships between living and non-living environment. By acknowledging geodiversity, we can achieve a more holistic understanding of the diversity of nature. And further, integrate geodiversity in conservation assessments across scales.

Where we, as humans, might sometimes have a very material-oriented view on geodiversity, other species live and thrive in the settings that geodiversity creates. Geodiversity can be seen as the stage of nature where species are the actors. Thus, geodiversity has wide potential in biodiversity research and conservation, and more.

Microbial rarity in stream networks: biodiversity patterns and types of rarity

Jacqueline Malazarte, Timo Muotka, Jussi Jyväsjärvi, Kaisa Lehosmaa, Kaisa-Leena Huttunen

Microbial communities are typically dominated by rare species that represent the majority of biodiversity and perform vital ecological functions. We explored this ‘rare biosphere’ using data on bacterioplankton communities at 13 sites of a boreal stream network across three years, with five temporal replicates each year. Using the relative mean abundance of 0.01 as the rarity cutoff, we observed 565 abundant and 10 657 rare taxa. Bacterial communities consisted mainly of permanently (35 %) or transiently (60%) rare species. Conditionally rare (mostly rare, occasionally abundant) taxa only consisted 3% of all bacterial taxa. Both common and rare taxa exhibited a reduction in species richness along the flow path, but significantly so only for rare taxa. Both rare and abundant subcommunities differed strongly between the upmost headwaters and downstream sites. Rare taxa were mainly assembled by homogenizing selection whereas the common biosphere was driven by dispersal-related stochasticity or undominated processes. Our data show that the rare and common bacterial biosphere in streams display similar spatial and temporal patterns but are controlled by different ecological processes.

Towards sawfly-literacy: A book and DNA reference library for North European sawflies

Marko Mutanen, Marko Prous, Andrew Liston, Niina Kiljunen, Mikk Heidemaa, Andreas Taeger, Matti Viitasaari, Veli Vikberg, Tommi Nyman

To be able to efficiently understand biological diversity, monitor changes in it and conserve it, we must speed up taxonomic workflows and find better ways to identify specimens as species play a central role in all biodiversity research and conservation. In many taxa, we remain largely illiterate with regards to species diversity. Sometimes this is because species are numerous and difficult to tell apart from each other. Many times, up-to-date literature is not available. In the worst case, even the taxonomic framework itself is deficient, meaning that many species remain taxonomically un-delimited and undescribed. Sawflies of northern Europe represent a group with relatively comprehensive taxonomic framework, although species boundaries in many groups remain unclear. Another problem is that sawfly species are often extremely difficult to identify morphologically as useful literature is lacking. Supported by the Putte funding by the Finnish Ministry of Environment, our team is preparing a book of North European sawflies with about 800 species represented. The book will include not only high-quality photographs of adult specimens and larvae but will also provide DNA barcodes and other genetic markers that make their identification much more straightforward than before. One important goal of the book project is to motivate new people to come passionate of sawflies and that this way knowledge of them would start accumulating rapidly so that in the future all groups of them could be included in the assessments of endangered species.

Evolutionary history of European *Agriades*: Implications for taxonomy and conservation

Nok Ting Lam, Vladislav Ivanov, Leonardo Dapporto, Roger Vila, Marko Mutanen, Vlad Dincă

A good knowledge of the evolutionary history of organisms and an accurate taxonomic framework are keys for efficient biodiversity conservation measures. This is particularly relevant for European butterflies, which include numerous model species for research and are often used as bioindicator organisms and umbrella species for conservation. The Holarctic genus *Agriades* includes seven arctic-alpine species in Europe of which several have a debated taxonomic status. They are localized and allopatric and at least two of them are of high conservation value, namely *A. aquilo* (Habitats Directive) and *A. zullichi* (endemic to southern Spain). In the last decades, from two to four species have been recognized in the European *glandon* and *pyrenaicus* species-groups. Despite this taxonomic uncertainty and conservation value, detailed molecular studies on these taxa are lacking and most molecular data is limited to DNA barcodes. We investigated the evolutionary history and species delimitation of these species-groups using high-throughput double-digest RAD sequencing (ddRADseq). While delimiting allopatric species is challenging due to the gradual nature of speciation, various analyses using genomic ddRAD data (phylogenetic inference, STRUCTURE, PCA, SNAPP) suggested the presence of one species in the *glandon* species-group and one or two in the *pyrenaicus* species-group. The differentiation within the *glandon* species-group (i.e. *glandon, aquilo, zullichi*) appears to be relatively recent, although *aquilo* and *zullichi* may still be regarded as evolutionary significant units (ESUs). Notable geographic structure was found within the *pyrenaicus* species-group, with four allopatric ESUs detected. Genomic data revealed the evolutionary trajectory of European Agriades and suggested some tendency of taxonomic oversplitting within this genus. These findings may aid conservation efforts by providing information to prioritize regions and organisms. While species are arguably still the most used units in conservation, considering ESUs as relevant units may represent a beneficial update in terms of efficiency and flexibility.

In-situ biodiversity research using miniaturized laboratory equipment and its potential for local capacity building

Stefan Prost

We live in an era of unprecedented global change, disrupting the integrity of ecosystems worldwide. Human-mediated environmental and climate change is depleting biodiversity faster than it can be characterized, while invasive species cause agricultural damage, threaten human health and disrupt native habitats. Conservation and biosurveillance-focused groups are faced with the immense task of characterizing baseline biodiversity data, documenting community change or genetic diversity and health of threatened species, as well as detecting harmful invasive pests and pathogens. The advent of high-throughput sequencing (HTS) technologies, coupled with the development of standardized DNA marker systems and a significant reduction in whole-genome sequencing costs have greatly facilitated large-scale monitoring of biodiversity and species diversity in the last decade. However, many biodiversity hotspots are located in regions that lack readily available access to molecular laboratories or the necessary research funding. Thus, the ability to sequence biological samples within the country of origin with portable, inexpensive laboratory equipment can bring major benefits for biodiversity monitoring and explorations, while simultaneously creating opportunities for developing local scientific capacity. In this presentation I will outline the present state of in situ miniaturized laboratory equipment-based biodiversity research.

Population genetics of Eurasian golden eagles

Ekaterina Karabanina, Gerhardus Lansink, Suvi Ponnikas, Laura Kvist

Golden eagle (*Aquila chrysaetos*) is one of the most known raptor species whose distribution range spans across the Northern Hemisphere. Being apex predators, golden eagles had been seen as pest predators of livestock and game animals and, therefore, were heavily persecuted for centuries. As a result of shooting a poisoning, the species dramatically declined and disappeared from many parts of its distribution during the 19 th -20 th centuries. Legal protection and conservation programs in the last decades allowed the population to start recovering, but golden eagles are still endangered on national levels across the Palearctic and in Mexico. In order to improve the conservation effort, information on population structure and the level of genetic diversity are important. While European, Japanese, and North American golden eagles have been well-studied, little is known about the populations in Russia and most of Asia. In this project we used a combination of mitochondrial (mtDNA control region) and nuclear (microsatellites) genetic markers to study large-scale phylogeography of golden eagles in the Northern Hemisphere, with a focus on Eurasia. We estimated basic genetic diversity parameters and checked for the presence of genetic structure, using museum samples of previously unstudied areas of the species' distribution such as Russia and central Asia. First, we analyzed differentiation between two previously discovered mitochondrial lineages (Mediterranean and Holarctic). Then, we checked for geographical variation and structure. Finally, we took an insight into temporal variation of golden eagles from the times of during and after the population bottleneck of the end 19 th -beginning of the 20 th centuries.

Modelling golden eagle (*Aquila chrysaetos*) and white-tailed eagle (*Haliaeetus albicilla*) habitat selection and flight activity for safer wind farm planning

Hannu Tikkanen

White tailed eagle (WTE) and golden eagle (GE) are most vulnerable avian species to wind power parks in Finland. Resource selection functions can be used to model the occurrence and movements of endangered species within a landscape, and thereby forecast how the planned land use or development may impact them. We used GPS monitoring data to model habitat use of a) flying white-tailed eagles at the Finnish coast and b) flying golden eagles nesting in Northern Finland and we modelled the flying times and collision risks at these areas. By using the models it is possible to find areas suited for wind power parks.

The movements of white tailed eagles (WTE, n=14) and golden eagles (GE, n=9) were studied by using satellite transmitters We developed a Resource Selection Function (with generalized linear mixed effect models and spatial data) to model habitat use of flying sub-adult WTE at Finnish coast and nesting GE in North Finland, in relation to different environmental factors in the landscape. We found out the average flight times of eagles by gps-data. We compared the risks of different wind power areas to WTE according to how the areas are located in areas favored by eagles.

Territorial GE preferred the vicinity of their nest, steep slopes, clear cuts, forests with low canopy cover and peat bog edges. They avoided human settlement, water and wide, open peat bogs. Model accuracy was 85% (cross validation with AUC). The average yearly flying time was 1150 h/pair. Flying times per specific areas in home ranges from both female ja male varied from less than 0,01 to more than 10 h / 1,5 ha square. 27 % of GE flew in the risk zone formed by wind turbine rotors (100-300 meter height) Migrating WTE preferred the vicinity of the coast, scattered archipelago and the vicinity to their natal nest, and avoided human facilities like urban areas and industries, as well as open sea. Model accuracy was 83% (cross validation with AUC). The average yearly flying time for WTEs was 610 h. The median flight height was 81 m above land and 20 m above the sea. The difference in collision risk differs hundredfold between the assessed grids (2,5*2,5 km).

Resource selection functions showed that eagles use some areas disproportionately more than other areas. By modeling eagle movements and flight volumes, we can approximate collision risks for the eagles in different areas. By considering these when planning areas for wind farms, collision risks can be minimized. Models minimize the need for laborious field work, smoothens decision making, and promotes the use of renewable energy.

Life-history dependent phenotypic plasticity in growth and human-induced selection

Nico Alioravainen, Tuomas Leinonen, Teuvo Niva

Individual size is a commonly used proxy for the survival probability in nature as it tends to correlate e.g., with fast growth, better feeding ability and predator avoidance. Therefore, it has been obtained widely into stocking practises, even though the individual growth rates can be context dependent. Here, we compared hatchery and riverine growth of juvenile brown trout (*Salmo trutta*) from three different genetically distinct population from the rivers that discharge to the Lake Inari. We built von Bertalanffy growth model to estimate growth curves of stocked brown trout based on 20 years of fisheries catch statistics. We show that these three populations have a plastic, environment-dependent response in growth, but also have different life-histories. The life-histories not only diverged in growth reaction norms between environments, but their catchability differed between active and passive fishing methods. Our results show that the management practices favouring a large size at the stocking do not result in a large sized individuals in catch. We also demonstrate that fishing methods selects life-history strategies differently generating a potential for fisheries-induced evolution.

Extended phenotypes as mediators of transfer of relational concepts between species

Reetta Hämäläinen

Conceptualization requires cognitive abilities because it enables extrapolating previous experiences into new situations, and it has long been considered to be a privilege of primate brains. However, recent evidence shows that many animal species (e.g., rats, pigeons, and bees) are capable of conceptualization, but the extent of species and situations where conceptualization is displayed is not yet fully understood. We tested whether pied flycatchers can form relational concepts (smaller/bigger rule) when using experimentally manipulated (clutch size) information that is based on extended phenotype from great tits. First flycatchers observed a tit demonstrator that apparently had preferred either large or small symbol when choosing a nest box and were then enforced to choose between two empty nest boxes with symbols of different shape and size but preserved the relational rule (smaller/bigger). The results suggest that the interaction of the great tit females' physical size and clutch size (high/low) has a significant effect on the symbol size choice of pied flycatcher.

Effects of forest management on the spatial distribution of the willow tit (*Poecile montanus*)

Satu Kumpula, Emma Vatka, Markku Orell, Seppo Rytkönen

Modification, fragmentation and loss of boreal forest habitats has been intensive during the last century due to forestry practises and land use. This has been related to population declines of several forest species, including the willow tit that was once the 4th most common bird species in Finland and is nowadays endangered. In this study we searched for the mechanisms of how the forest management methods could explain the decline of the willow tit population. We used long-term breeding data of the willow tit nestings collected in Oulu, Northern Finland. This data was combined with accurate spatial forest management and habitat quality data using Geographic Information Systems (GIS) methods. The data was analysed with linear mixed models. The clear-cuttings were found to affect the willow tit dispersal and nearest neighbour distances more than thinnings. Both clear-cuttings and thinnings increased the nearest neighbour distances. The natal and breeding dispersal distances were lengthened by increasing proportions of clear-cuttings. 65 % of the breeding density decrease was explained by forest management. The habitat loss caused by clear-cuttings and the decrease in habitat quality caused by thinnings has had a major role in the decline of the willow tit population. The effects of forest management were witnessed in a cumulative 0-30-year period meaning that forest management causes long-term habitat degradation and loss. Availability of deciduous snags in the forests can compensate the habitat loss to some extent by providing better breeding opportunities for the willow tits.

Species delimitation in a Parapatric pair of Saturnia moths as revealed by Target Enrichment.

Maria Khan

My study focused on understanding the evolutionary relationships and delimiting widely distributed parapatric pair of Saturnia moth species in Europe ,namely *Saturnia pavonia* and *Saturnia pavoniella*. For this purpose, Target enrichment approach alongside mtDNA sequencing was utilized to resolve the issues that come with parapatric taxa, such as admixture, geneflow, hybridization, and introgression. The dataset involved members of both the taxa along with two hybrids and one outgroup, *Saturnia josephinae*. Based on the target enrichment genomic dataset results, both *S. pavonia* and *S. pavoniella* were recovered as two widely separated and strongly supported monophyletic groups with the hybrids grouping together, being intermediate, and separating from both the species. The ML tree generated from mtDNA sequencing data gave a different picture and showed both the taxa to be admixed. This inconsistency can be attributed to mitonuclear discordance, which can be caused either by biological factors (e.g., introgressive hybridization or incomplete lineage sorting) or operational factors (e.g., misidentification or incorrect species delimitation. This study showed the target enrichment approach was very efficient in inferring the phylogenetic relationship and demonstrated a clear scenario about the taxonomic and phylogenetic relationships between these species. This study can serve as a template for further dedicated studies to delimit species under complex evolutionary circumstances, such as parapatry.

Nitrogen addition and warming modulate the pathogen impact on plant biomass

Xuebin Yan

The ongoing global changes are interacting with pathogens to influence plant biomass, but experimental test of their interactions is scarce. We conducted a 4-year field experiment in a Tibetan alpine meadow to examine the interactive effects of nitrogen addition, warming and foliar pathogens (via fungicide application) on plant biomass. We also measured plant functional traits, species richness and abundance to test the possible mechanisms underlying these interactions. Our results showed that foliar fungal pathogens reduced plant community biomass under nitrogen addition, which in turn weakened the positive nitrogen effect on community biomass. Mechanistically, nitrogen addition shifted the plant communities towards fast-growing traits; this happened predominantly because of changes in within-species trait values. Moreover, the reduction in species richness amplified the pathogen effect under nitrogen addition due to the increased density and susceptibility of the most dominant species (i.e. *Kobresia capillifolia*). Furthermore, warming did not interact with pathogens and nitrogen addition to influence plant community biomass, but their three-way interaction modified the biomass of *K. capillifolia*. Our study highlights the importance of considering foliar fungal pathogens when assessing ecosystem responses to multiple global change factors.

Meristem-colonizing endosymbiont bacteria promoting host plat growth

Habibollah Mohammad Parast Tabas

The meristem-colonizing endosymbionts were first described in Scots pine by us and so far, no other group is studying them on a global scale. The published research data suggest that bacterial endosymbionts of meristematic cells are not restricted to Scots pine but exist in many plant species. This research is revealing a completely new mechanism of endosymbiosis in plants. Also, many pathogens of both plants and animals invade the host cell interior. However, the most common microbial tools, such as rhizospheric bacteria of the soil, and endophytes that typically colonize plant root apoplast, have demonstrated inconsistent field. 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 pseudomonds live in a symbiotic relationship with plants, utilizing nutrients and exudates from plant surface 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 earlier 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 will study plant- endosymbiont interaction in Scots pine and the model species Arabidopsis thaliana. I will inoculate seedlings of pine and A. thaliana with *P. synxantha* DSM13080 and study the effect on growth and levels of nutrients and secondary metabolites in pine and Arabidopsis seedlings compared to controls. I will also analyze the genome of *P. synxantha* DSM13080 for genes responsible for plant growth promotion and having similarity with rhizobial symbiosis. Lastly, I will study involvement of small RNA species (sRNAs) or micro-RNAs (miRNA) in the interaction between Scots pine and another endosymbiont, *Methylorubrum extorquens* DSM13060.

Temporal changes in boreal vegetation under 70 years of conservation

Tuija Maliniemi, Karoliina Huusko, Lauralotta Muurinen, John-Arvid Grytnes, Helena Tukiainen, Risto Virtanen & Janne Alahuhta

Conservation through protected areas is often relying on the idea that biodiversity is relatively static. This assumption is increasingly questioned as species and entire communities shift their distributions in response to rapidly changing environmental conditions. Empirical evidence on the performance of protected areas spanning decades is still sparse or lacking from several environments, even though it is needed to understand species dynamics, to support the modelling of protected area performance and to assist protected area management. By using vegetation resurvey data from Rokua National Park in Finland, we provide rare empirical evidence of vegetation changes in five boreal habitat types that have taken place under 70 years of conservation and in the absence of disturbances (fires and reindeer grazing) typical to boreal biome. We show that successional changes have led to increased compositional similarity between the habitat types, and this may lead to declines in biodiversity and the original conservation objectives.

Summer habitats of wild forest reindeer (*Rangifer tarandus fennicus*) in Finland – a preliminary predictive model

Antti Paasivaara, Salla Kaartinen, Viivi Puoskari, Seppo Rytkönen, Jyrki Pusenius

Resource selection functions (RSF) are valuable tools for estimating the relative probability of an animal utilizing an area and predicting where they may occur. Our objective was to develop a preliminary model and a nationwide map for the probability of occurrence of breeding in wild forest reindeer (WFR). Large scale knowledge of the potential habitats of WFR is needed for regional scale conservation and management planning. WFR females were fitted with remote sensing collars during 2008 - 2014 in the Kainuu and Suomenselkä regions. GPS locations of females were obtained via GSM or Iridium networks. We estimated 50% fixed-kernel summer home ranges for females from 15 th May to 31 th July (n = 77 home ranges, ca. 10 000 GPS fixes). RSFs contrasted observed and random home ranges, with random home ranges (n = 77) drawn from a uniform distribution within the known range of two Finnish WFR populations in addition to a 50 km buffer zone. The predictor variables for the analysis were selected a priori based on earlier literature and field experience and calculated from National Forest Inventory 2011 remote sensing data. Compositional analyses and variation inflation factor procedures were employed to control the highly correlated predictors. Information theoretic approach was used for model selection. The performance of the final model was validated with k-fold cross-validation, which was visualized by receiver operating curves. The occurrence of WFR during summer increased with the area of open peatland and the area of forest with a rich field layer of twigs and shoots. We extrapolated the model to all available areas for WFR in Finland (10x10 km grid map), which indicate that only few areas from total area outside the Finnish reindeer management region were estimated to have a high probability (from 0.5 to 1) of being used by WFR in summer.

Boreal moth biomass is either stable or increasing in time depending on key life-history traits

M. Yazdanian, T. Kankaanpää, J Itämies, T. Merckx, J. Pöyry, P. Sihvonen, A. Suuronen, P. Välimäki, S. Kivelä

Dramatic insect declines and their consequences for ecosystems globally have received considerable attention recently. Yet, it remains poorly known which traits explain declines and whether the decline in insects expands to high latitudes. We adopted a trait- and biomass-based approach to estimate temporal changes in moth communities in Finland in 1993-2019. We analysed spatial and spatiotemporal variation in moth functional groups' abundances with Joint Dynamic Species Distribution Models and accounted for environmental conditions. We did not detect any declining trends in the biomass of moth functional groups, but most groups were stable over time. Moreover, the biomasses of species using coniferous trees, lichens, and mushrooms as hosts, multivoltine species, as well as monophagous and oligophagous species feeding on trees have increased. We found that growing season and winter climatic conditions as well as habitat structures partially explained variation in moth biomass. Although the boreal moth communities are rapidly changing, in terms of total moth biomass they seem to perform better than expected on the grounds of global trends across several key functional groups.