2019 KAAMOS Symposium

Abstract booklet of the 23rd Kaamos Symposium, 11th and
12th of December 2019, University of Oulu

UNIVERSITY OF OULU

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18:00 – 23:00 Evening party and poster session at the University of Oulu Botanical Gardens

1. The Phylogeographic Structure of Tropical Plant Communities and Populations

Olivier Hardy[1]

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The phylogeographic structure refers to the way phylogenetically related species or populations are distributed across spatio-environmental gradients. These patterns are studied in the frameworks of community ecology (inter-specific level) and population genetics (intra-specific level) but usually using different data analysis tools. However, it is possible to use a common descriptive framework at the two levels and attempt a comparison. Here, I will use examples from tropical African forests to illustrate how the phylogeographic structures can inform on population or community processes. At the inter-specific level, from local to continental scales, phylogenetic turnover appears well correlated to the ecological distance between plant communities, independently of their geographical distance, while species turnover depends both of spatial and ecological distances. Species turnover and lineage turnover can therefore provide complementary information to decipher biogeographic isolation and ecological differentiation. At the intra-specific level, the phylogeographical structures observed in African tree species seem to result essentially from (past) biogeographic isolation, possibly driven by Quaternary climate changes (forest refuge hypothesis). However, molecular dating indicates that these phylogeographical structures established early, sometimes during the Pliocene, and while they might have been reinforced during subsequent glacial–interglacial cycles, interglacial phases did not lead to genetic homogenization. Therefore, interpreting phylogeographical patterns of African trees must account for a much deeper past than previously assumed, and cannot be limited to the last glacial period, reflecting a slow dynamic.

2. Genomics of Conifer Reproductive System Peculiarities

Tanja Pyhäjärvi[1]

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3. Phylogenetic Relatedness Predict Disease Pressure

Yingying Wang[1]

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Biodiversity is declining dramatically. Meanwhile, disease risk of infectious disease in human, wildlife and livestock is undergoing an increase. Several studies showed that a change in biodiversity can impact disease risk. The objective of this thesis is to advance the understanding of the relationships between disease risk and biodiversity. My results give new insights into these relationships. My findings suggest that the commonly used species richness is not a good indicator of disease risk, and phylogenetic diversity are more important than species richness in affecting disease risk. My results highlight the role of phylogenetic relatedness in the relationships between disease risk and biodiversity and showed that if the species in an assemblage are closely related, especially among competent host species, the assemblage is expected to have a higher disease risk. My study suggests that future studies should look beyond species richness when studying relationships between biodiversity and disease risk.

4. Dispersal – Genetics Detection and Fitness Consequences

Dilan Saatoglu[1], Alina K. Niskanen[1,2], Markku Kuismin, Thomas Kvalnes[1], Yimen Araya-Ajoy[1], Peter S. Ranke[1], Hannah Froy[1], Håkon Holand[1], Henrik Pärn[1], Bernt Rønning[1], Ingerid J. Hagen[1,5], Sigbjørn Lien[6], Thor Harald Ringsby[1], Bernt-Erik Sæther[1], Arild Husby[1,7], Mikko J. Sillanpää[3,4], Henrik Jensen[1]

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Dispersal, the permanent movement of individuals between populations, has profound consequences to individual fitness, population dynamics and population genetics. To study the multiple effects of dispersal, dispersers and their offspring need to be identified reliably. Genetic methods aid in both purposes and thus help in understanding the causes and consequences of dispersal, which can be used in conservation and management of wild populations. We studied dispersal and its fitness consequences in a house sparrow (Passer domesticus) metapopulation in Norwegian archipelago using long-term data. We genotyped 2745 adult house sparrows for over 180 000 single nucleotide polymorphisms (SNPs) distributed across the genome. We used this genomic data to improve previous observational dispersal data using a newly developed genetic assignment method BONE. We found that both female and male immigrants produced more recruiting offspring during their lifetime than resident birds. However, immigrant females had slightly lower survival probability than resident females. These results differ from previous results on observational data and show the importance of genetic data in ecological studies. The results will be used as a basis of more detailed studies of dispersal and its eco-evolutionary consequences.

5. Streamside Forests: Importance, Pressures and Conservation

Mari J. Tolkkinen[1], Jani Heino[1], Saija H.K. Ahonen[2], Kaisa Lehosmaa[2], Heikki Mykrä[1,2]

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Headwater streams and streamside forests are tightly interconnected. These streamside forests are also called “riparian forests” or “riparia”. Although the knowledge about stream-riparian interactions has increased considerably recently, in practice riparian zones are still mainly seen as means for protecting stream water quality. However, recent research has shown that riparian forests disproportionately foster forest biodiversity and are in a key role in maintaining stream functions and diversity. Unfortunately, multiple pressures are threatening biodiversity and ecosystem processes of streams and riparian forests and they are threatened in Finland and worldwide. In this presentation I focus on explaining 1) what are the key characters of riparian forests, i.e. how are streams and riparia interconnected, 2) why are riparian forests so important to biodiversity and 3) how can they be protected against intensive land-use, particularly forestry. The presentation is based on our review-article (manuscript) “The inseparable two: headwater streams and riparian forests depend on each other”, financially supported by Maj & Tor Nessling Foundation.

6. Why Is Understanding Biodiversity– Geodiversity Relationship Important? Evidence from Freshwaters

Maija Toivanen[1]

[1]Geography Research Unit, University of Oulu, Oulu, Finland

7. Arctic Water Cycle Forensics Forensics – Case of Northern Freshwater Ecosystems

Kaisa-Riikka Mustonen[1], *Kaisa Lehosmaa*[1], *Aino Erkinaro*[1], *Hannah Bailey*[1], *Hannu Marttila*[2], *Pertti Ala-Aho*[2], *Jeffrey Welker*[1,3]

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Arctic freshwaters are changing rapidly in response to more pronounced warming of Arctic areas. Rapid warming can shift precipitation phases from snow to rain and change the amount and location of frozen ground, which can further affect the availability, timing or quality of freshwater resources (i.e. hydrological processes). To truly understand what is driving the change of Arctic freshwaters, we need to understand the interactive components involved in Arctic water cycle, such as sea ice patterns, atmospheric dynamics, and hydrological processes which are all rapidly shifting due to climate change. Stable water isotopes of oxygen and hydrogen (O^{18} and H^2) are a very powerful and widely used tool to study the global water cycle. The isotopic composition of water can be regarded as a "fingerprint" of a water molecule which varies depending on its source and transport processes. Water transport through Arctic water cycle is controlling the ecosystem processes within watersheds, as water is carrying organic and inorganic carbon as dead and decaying organic matter (DOM) through different phases of water cycle. Quantity and quality of DOM is further affecting the vital biochemical processes of aquatic ecosystems, as it is strongly related to the abundance, activity and composition of microbial communities. There is an urgent need for a holistic perspective of the freshwater cycle that quantifies the interactive nature of these abiotic and biotic components of Arctic freshwater systems.

8. Contrasting Body-Size Shifts in Urban Communities

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Urbanisation involves a cocktail of human-induced rapid environmental changes. Following increased metabolic rates caused by the urban-heat-island effect, and associated costs for a given body size, we predicted that urbanisation would drive shifts to smaller body size. However, urban settings are also characterised by pronounced habitat fragmentation, which could select for dispersal phenotypes. Via a replicated, nested sampling design across ten terrestrial and aquatic animal taxa, covering urbanisation gradients at local and landscape scales, we assess imposed selection pressures and we show that urban communities consist of smaller species (or with smaller extended phenotypes) in six taxa, while three taxa displayed size increases. Only within these three taxa is body size positively associated with dispersal ability, a trait linked to mitigating low connectivity of ecological resources. Our results thus show that the general trend towards communities consisting of smaller-sized species is overruled by filtering for larger species when size positively covaries with dispersal ability. We thus demonstrate that the urban-heat-island effect and urban habitat fragmentation are associated with contrasting community-level body-size shifts that critically depend on the association between body size and dispersal. As we show that urbanisation-driven body-size shifts occur interspecifically too, we discuss the mechanisms (environmental filtering, phenotypic plasticity, genotypic change) behind these community- and population-level shifts in body-size distribution. Since body size is key to inter-specific relationships, the resulting shifts in body size may impact urban ecosystem functioning, while our findings also indicate that such impacts may be mitigated via multi-scale implementation of urban blue/green infrastructure.

9. Comparative Analysis of Larval Growth in Lepidoptera Reveals Instar-Level Constraints

Sami M. Kivelä[1], Robert B. Davis[2], Toomas Esperk[2], Karl Gotthard[3], Marko Mutanen[1], Daniel Valdma[2], Toomas Tammaru[2]

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Selective pressures on age and size at maturity affect the evolution of juvenile growth trajectories within the limits set by developmental constraints. In insects, maintenance of efficient growth likely necessitates periodic renewal of certain surfaces by moulting, because surface area to volume ratio of a larva decreases during growth and many surfaces are crucial for physiological functionality. Therefore, the moulting cycle is a major source of constraints on larval growth trajectories. A null hypothesis of isometry would mean that the relative measures of growth remain constant across moults and instars. Here, we used the phylogenetic comparative approach and studied ontogenetic changes and allometry in instar-specific characteristics of larval growth in 30 lepidopteran species. Relative instar-specific mass increments (RMI) typically, but not invariably, decreased across instars. Ontogenetic change in RMI varied among families, but there was only little within-family variation. End-of-instar growth deceleration (GD) became stronger with increasing body size across instars, and across-instar change in GD was conserved across taxa. Ontogenetic allometry was generally non-isometric both in RMI and GD. Results indicate that multiple species must be rigorously studied for generalizations concerning growth trajectory evolution. Developmental and physiological constraints affecting growth trajectory evolution must also be taken into account in analyses of age and size at maturation.

10. Svalbard Reindeer Winter Diets: Interannual Variation and Long-Term Changes

Tamara Hiltunen[1]*, Jouni Aspi*[1]*, Audun Stien*[2]*, Jeffrey M. Welker*[3]

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Svalbard reindeer (*Rangifer tarandus platyrhynchus*) are found on an archipelago in the High Arctic, a region that is undergoing significant changes in winter and summer climates. These changes range from adverse effects on winter foraging such as ice locked pastures due to rain on snow (ROS) events to the positive effects of warmer summers and higher forage productivity. These complex interactions between stochastic climatic events and vegetation dynamics impact reindeer population dynamics. The winter diets of these herbivores are still uncertain as are any changes associated in response to climate change. The $\delta^{13}C$ and $\delta^{15}N$ values were determined for serum samples collected from adult, female reindeer at the end of winter between 1995 and 2012. Linear mixed models were utilised to determine the effects of environmental and physiological parameters on the reindeer $\delta^{13}C$ and $\delta^{15}N$ values. Forage and serum isotope values were used in Bayesian mixing models to ascertain the winter diets. Over the entirety of the study, there was significant enrichment in the $\delta^{15}N$ values and depletion in $\delta^{13}C$ values. These concurrent changes indicate that the winter diets have shifted to include a greater proportion of graminoids. This diet shift in conjunction with vegetation community composition changes in the interior of Svalbard may be a means by which Svalbard reindeer may partially tolerate increases in the frequency and duration of ROS.

11. How to Make More Out of Community Data with Joint Species Distribution Modelling?

Otso Ovaskainen[1]

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A central aim community ecology is to understand the processes that determine the assembly and dynamics of species communities at different spatiotemporal scales. To facilitate the integration between conceptual and statistical approaches in community ecology, we have developed Hierarchical Modelling of Species Communities (HMSC) as a general, flexible framework for modern analysis of community data. HMSC belongs to the class of joint species distribution models, and it makes it possible to derive simultaneously species- and community level inference from data on species occurrences, environmental covariates, species traits, and phylogenetic relationships. HMSC applies to a wide variety of study designs, including hierarchical data, spatial data, temporal data, and spatio-temporal data. I describe the general HMSC framework and discuss its applicability with case studies that include both macro-organisms and microbiota. The R-package Hmsc is available in CRAN.

12. Interaction Between Scots Pine and Endosymbiotic Bacterium: Benefits for Human?

Anna Maria Pirttilä[1]

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In general, microbes are found in every tissue of plants, and they are largely unstudied. Compared to human microbial counterparts, the plant-associated microbes have diverse and important roles for the host, extending the host phenotypic plasticity. We are studying interactions between the plant and the microbe and apply the results to benefit humankind. Specifically, we have identified a new facultative endosymbiosis in meristematic tissue of pine buds, where Methylorubrum spp. live in host cells as the dominant species. The endosymbionts aggregate around the nucleus of living host cell and carry genomes encoding nucleomodulins, eukaryotic transcription factors, which may interfere with host transcription and metabolism. We are currently elucidating mechanisms of manipulating host cells by the endosymbionts with prospects to identify new targets for intracellular pathogens. Earlier we have shown that polyhydroxybutyrate (PHB) produced by *M. extorquens* is important for the interaction. PHB is synthesized by the endosymbiont and degraded upon infection to produce antioxidants, oligomers of 3-hydroxybutyrate, enabling survival in host tissue. This is a new defence mechanism discovered in bacteria towards oxidative stress. We are developing the compounds isolated and identified from plant microbes as drugs against human diseases.

13. Scalable Nonparametric Pre-screening Method for Searching Higher-Order Genetic Interactions Underlying Quantitative Traits

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In genomic association studies, phenotypically important gene-by-gene interactions are typically identified via exhaustive search by enumerating all possible interaction terms. An immediate problem is that the number of higher-order interaction terms grows rapidly infeasible imposing a serious computational challenge for typical applications with high-throughput sequencing datasets. Ideally the dimension of a feature space consisting of all genes could be reduced before enumeration based on strong marginal gene-phenotype associations producing fewer interaction terms to be considered in an exhaustive search. However, individual genes contributing multiplicatively to the phenotypic variation may not be identifiable by linear pre-screening methods since a phenotype may exhibit strong gene-by-gene interaction effects in the presence of negligible linear marginal effects. The only way of identifying determinants of phenotypically important gene-by-gene interactions from the marginal gene-phenotype associations is therefore to use nonparametric/nonlinear methods. The Gaussian process (GP) based automatic relevance determination (ARD) is known to be theoretically among the best alternatives for such purpose. However, the estimation of GP models is feasible only for low-dimensional datasets (~200 genes) which severely prevents the GP-based ARD method to be applied for high-throughput sequencing data. We have developed a nonparametric pre-screening method which reduces the GP-based ARD method into a linear similarity regression problem. The proposed method preserves all the major benefits of the GP-based ARD and extends its scalability to high-dimensional datasets with tens of thousands of genes. We present several examples to show that the proposed method compares superiorly with existing methods suitable for higher-order interaction search.

14. Quantitative Genetics of Lodgepole Pine Wood Quality Traits

Haleh Hayatgheibi[1,2], Anders Fries[2], Johan Kroon[3], Harry X. Wu[2,4]

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[4] CSIRO NRCA, Black Mountain Laboratory, Canberra, Australia

Stem bending, breakage, and general instability of lodgepole pine (*Pinus contorta Dougl. ex Loud. var. latifolia Engelm.*) has been a major problem in northern Sweden due to low stem stiffness. The overall aim of this study was to evaluate the potential incorporation of wood quality traits into lodgepole pine advanced breeding programs. To achieve this, 823 increment cores were sampled from 207 half-sib families at two progeny trials of lodgepole pine and genetic variations in wood density, microfibril angle (MFA), modulus of elasticity (clearwood stiffness; MOEs), and fibre traits were characterized. To evaluate genetic gains in selection for an early MFA transition from juvenile to mature wood, six different regression functions were fitted to the MFA profile of each tree to delineate the age variation in MFA transition. Results of this study indicate that simultaneous improvement of DBH and stiffness is achievable when an optimal selection index combining both traits is implemented. Additionally, it is possible to select for an earlier MFA transition from juvenile to mature wood, and thus, decreasing the proportion of the log containing juvenile wood in lodgepole pine selective breeding programs.

15. Predation by Wolves on Wild Forest Reindeer in Multi-Prey System

Ilpo Kojola[1]

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Predation by a generalist predator may have a greater effect on the population of secondary than primary prey species owing to apparent competition between the prey species. Boreal and mountain caribou (*Rangifer tarandus caribou*) in North America have been coming increasingly endangered. Experimental reductions of primary prey e.g. moose might stop decreases in caribou populations but not lead to recovery. Controlling grey wolf (*Canis lupus*) for reduction of predation has usually not resulted in caribou recovery either. Because habitat fragmentation due to forestry favors moose and consequently, a predator dependent on moose, habitat restoration would enhance recovery but is a slow process. We examined relationships between populations of grey wolves' (*Canis lupus*) primary prey, moose (*Alces alces*), the secondary prey, wild forest reindeer (*R. t. fennicus*) and wolves, during 1996-2017, within the 6 000 km2 primary distribution range of the endangered wild reindeer in eastern Finland. In this region moose densities were regulated by human harvest but wild reindeer was almost fully protected from hunting. Predation studies demonstrated moose being wolves' primary prey but reproductive rate in moose population was independent of the wolf population, and moose and wolf densities were not related. Reindeer population decreased rapidly after the return of wolves but has been stable during the second part of our study period while moose has been gradually decreasing. Reindeer population from year t to year t+1 was related to reproductive rate in year t, and the reproductive rate was related negatively to wolf population. I discuss about different management strategies for conservation the two endangered species, grey wolf and wild forest reindeer in Finland.

16. Rapid Discrimination of Wolves, Dogs and Their Recent Hybrids Using a Panel of Diagnostic SNPs

Jenni Harmoinen[1], *Alina von Thaden*[2,3], *Jouni Aspi*[1], *Laura Kvist*[1], *Berardino Cocchiararo*[2,4], *Anne Jarausch*[2,3], *Andrea Gazzola*[5], *Teodora Sin*[6,7], *Hannes Lohi*[8,9], *Astrid Vik Stronen*[10], *Romolo Caniglia*[11], *Federica Mattucci*[11], *Marco Galaverni*[12], *Raquel Godinho*[13], *Ettore Randi1*[14,15], *Violeta Muñoz-Fuentes*[2,16], *Carsten Nowak*[2,7]

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There have been reports of wolf-dog hybridization in many parts of Europe. However, the extent of the hybridization is still quite unknown. Microsatellite markers have been widely used in wolf research, but offer only limited resolution. Comparability of the datasets among researchers has been hampered due to the tedious calibration of the data. Whole-genome sequencing is becoming more and more common, but it is expensive and time-consuming for population monitoring purposes. We chose ancestry informative markers (AIMs) for wolves and dogs and tested the performance of the markers with a microfluidic chip.

This method is suitable for very short amplicons, making it particularly appropriate for non-invasively collected samples and for old sample materials. It is also cheap and fast to conduct. We selected a final panel of 96 markers based on the performance and readability of the results. We applied the panel to wolf, dog and hybrid samples of various sample materials. We showed that the final panel has low error rate and high accuracy to detect hybrids up to third-generation backcrosses to wolves. We demonstrated that the panel works for Eastern and Western European wolf populations, allowing scientists to obtain comparable data of wolf hybridization across Europe.

17. Population Genetics of the Wolverine in Finland: The Road to Recovery?

Gerhardus M.J. Lansink[1], *Rodrigo Esparza-Salas*[2], *Maija Joensuu*[1], *Anni Koskela*[3], *Dominika Bujnáková*[1], *Oddmund Kleven*[4], *Øystein Flagstad*[4], *Tuomo Ollila*[5], *Ilpo Kojola*[6], *Jouni Aspi*[1], *Laura Kvist*[1]

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18. Functional Features of Aquatic Plant Communities and Driving Factors over a 70-Year Period

Marja Lindholm[1]*, Janne Alahuhta*[1]*, Jani Heino*[2]*, Jan Hjort*[1]*, Heikki Toivonen*[1]

[1] Geography Research Unit, University of Oulu
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19. What About Rudolph? Identifying Castrated Reindeer Bones to Trace Reindeer Domestication in Fennoscandia

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Knowledge of the processes surrounding reindeer (*Rangifer tarandus*) domestication can give insight in the history of many past and contemporary circumpolar cultures. However, the time and origin of reindeer domestication remains hotly debated today. Determining the domestication status of reindeer in archaeological bone assemblages is problematic because wild and semi-domesticated reindeer are morphologically very similar. Many argue that castrated males were probably the key to reindeer domestication. Although the importance of castrates and their part in incipient reindeer domestication is widely recognized; no methods exist that can discern a reindeer gelding from a reindeer bull. We focus on the use of castrated reindeer and define the osteological manifestations of reindeer castration. This is a new approach to document human intervention in the population structure of this species. The premise of this method is that castration delays epiphyseal fusion and thus allows the elongation of the bones, and long bones in particular. For this study we measure reindeer bones of known age, sex, castration status, and subspecies extant in Fennoscandia before the 19th century to plot the osteometric differences between the categories. Here I present our preliminary findings from the front limb and hind limb bones. The outcomes of this research aids in evaluating a novel method of tracing (incipient) domestication also for other species.

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