

Abstracts – 7th European Congress of Mammalogy

Contents

| | | |
|----------|--|-----------|
| 1 | Abstracts for talk | 12 |
| T.1 | Hans Ahlgren: <i>WORKSHOP TALK: Prehistoric translocation or natural colonization? - the origin of mountain hares on Gotland</i> | 12 |
| T.2 | Tuomas Aivelo: <i>Rapid turnover in micro- and macrobiome of free-ranging primates, rufous mouse lemur (<i>Microcebus rufus</i>)</i> | 12 |
| T.3 | Paulo C. Alves: <i>WORKSHOP TALK: Reticulate evolution in Lagomorphs: conservation and management implications</i> . . | 13 |
| T.4 | Henrik Andrén: <i>Ecology and Landscapes - species interactions in heterogeneous landscapes</i> | 13 |
| T.5 | Malin Aronsson: <i>It's relative: Sex and resource heterogeneity influences the relationship between relatedness and home range overlap for a solitary predator</i> | 14 |
| T.6 | Irina Bakloushinskaya: <i>Is monobrachial homology the end or the start of chromosomal speciation? Ellobius' case</i> | 14 |
| T.7 | Ian Barnes: <i>Genomic Analyses of Museum Collections</i> | 15 |
| T.8 | Laszlo Bartosiewicz: <i>Cave lioness from the plain? Cranio-metric investigations on a Pleistocene lion skull from Hungary</i> | 15 |
| T.9 | Sabine Begall: <i>Magnetic alignment in mammals</i> | 16 |
| T.10 | Ulrika A Bergvall: <i>Small scale foraging decisions in moose in relation to plant defence and spatial distribution</i> | 16 |
| T.11 | Dominique Berteaux: <i>Species interactions of arctic fox on Bylot Island, Nunavut: hypothesis-testing at the meta-ecosystem scale</i> | 17 |
| T.12 | Dominique Berteaux: <i>WORKSHOP TALK - The arctic fox as model system to study trophic interactions</i> | 17 |
| T.13 | Boguslaw Bobek: <i>Changes in distribution ranges in wolf (<i>C. lupus</i>) in Poland during 1980-2014, and the impact of this species upon population of red deer (<i>C. elaphus</i>)</i> | 18 |
| T.14 | Zbigniew Borowski: <i>Direct effect of mechanical grass moving on small mammal population dynamics</i> | 18 |
| T.15 | Emma Boston: <i>Extra-Mediterranean glacial refugia illuminated through the study of bats</i> | 19 |
| T.16 | Selina Brace: <i>Evolutionary histories from mammals of the Caribbean: insights from ancient DNA</i> | 19 |

| | | |
|------|---|----|
| T.17 | Mike Bruford: <i>Conservation prioritisation using omic data: signal, noise and the power of domestication</i> | 20 |
| T.18 | Anthony Caravaggi: <i>Quantifying endemic uniqueness and ecological equivalency between native and invasive leporids</i> . . . | 20 |
| T.19 | Barbora Cerna Bolfikova: <i>Internal structure of Balkan refugium using white breasted hedgehog (<i>Erinaceus roumanicus</i>) as model species</i> | 21 |
| T.20 | Ana Cerveira: <i>Mate choice, hybridisation and hybrid fitness in two pine vole sister species, <i>Microtus duodecimcostatus</i> and <i>M. lusitanicus</i></i> | 21 |
| T.21 | Anaïs Charbonnel: <i>Influence of recent global change on the range contraction of an endangered semi-aquatic mammal, <i>Galemys Pyrenaicus</i>, in the French Pyrenees</i> | 22 |
| T.22 | Pascale Chevret: <i>Phylogeography, genetic structure and morphological evolution of the house mouse on the Orkney Archipelago</i> | 22 |
| T.23 | Tim Clutton-Brock: <i>The evolution of cooperation and cooperative breeding</i> | 23 |
| T.24 | David Cooper: <i>Predicted Pleistocene-Holocene range shifts of the tiger (<i>Panthera tigris</i>)</i> | 23 |
| T.25 | Joris Cromsigt: <i>Rewilding Europe's large grazer community: how functionally diverse are the diets of Europe's three largest mammalian herbivore species?</i> | 24 |
| T.26 | Melanie Dammhahn: <i>Energy-saving strategies and the pace-of-life syndrome in eastern chipmunks (<i>Tamias striatus</i>)</i> . . . | 24 |
| T.27 | Kjell Danell: <i>Mammalian Herbivory in Boreal Forests – Challenges and Methodology</i> | 25 |
| T.28 | Joost de Jong: <i>Genetic structure of European wild boar – 35k SNP analysis</i> | 25 |
| T.29 | Vlad Demartsev: <i>Can hyraxes sing the blues? Possible evidence for musical features in male rock hyrax (<i>Procavia capensis</i>) complex calls.</i> | 26 |
| T.30 | Karolina Doan: <i>Influence of environmental changes and human activities on late Quaternary red deer populations.</i> . . . | 26 |
| T.31 | Simon Dures: <i>Transfrontier lion conservation: applying genetics across time and space</i> | 27 |
| T.32 | Nina E. Eide: <i>Status and conservation goals for the critically endangered Arctic fox in Scandinavia. Is the mission completed?</i> | 27 |
| T.33 | Robert Ekblom: <i>Development of Genomic Resources for the Conservation of the Scandinavian Wolverine Population</i> . . . | 28 |
| T.34 | Bodil Elmhagen: <i>Carnivore interactions and climate change: Top-down and bottom-up cascades in time and space</i> | 28 |
| T.35 | Alan Fredy Eriksson: <i>Environment and host species composition effects on highly host-specific assemblages of ectoparasites of bats</i> | 29 |
| T.36 | Rasmus Erlandsson: <i>Home alone - Juvenile survival in relation to maternal experience and loneliness</i> | 29 |
| T.37 | Erik Ersmark: <i>The fall and rise of the Scandinavian brown bear</i> | 30 |

| | | |
|------|---|----|
| T.38 | Khammar Farida: <i>Reproductive and metabolic survival strategies in some Saharan rodents</i> | 30 |
| T.39 | Søren Faurby: <i>Historic and prehistoric human-driven extinctions have reshaped global mammal diversity patterns</i> | 31 |
| T.40 | António Ferreira: <i>Factors affecting southern water vole (<i>Arvicola sapidus</i>) detection and occupancy probabilities in Mediterranean farmland</i> | 31 |
| T.41 | Pablo Ferreras: <i>Do widespread generalist carnivores segregate their niches? A multidimensional study using red foxes and stone martens in Mediterranean Europe</i> | 32 |
| T.42 | Øystein Flagstad: <i>Genetic rescue in a severely inbred wolf population: A natural experiment</i> | 32 |
| T.43 | Øystein Flagstad: <i>Hybridization and domestic introgression in the wild: The extinction of a natural arctic fox population</i> | 33 |
| T.44 | Laurent Frantz: <i>Ancient dog genome provides insights into the evolutionary history of dogs.</i> | 33 |
| T.45 | Laurent Frantz: <i>Genomics reveal the importance of gene flow and strong artificial selection during pig domestication.</i> | 34 |
| T.46 | Pavel Gol'din: <i>Marine mammal fauna of the Middle and Late Miocene of the Central and Eastern Paratethys: chronology and biogeography</i> | 34 |
| T.47 | Anjali Goswami: <i>The macroevolutionary consequences of phenotypic integration: from development to deep time</i> | 35 |
| T.48 | Marianne Haage: <i>Evolutionary maintenance of personality via spatiotemporal fluctuations in the environment - A field experiment on European mink (<i>Mustela lutreola</i>)</i> | 35 |
| T.49 | Marko Haapakoski: <i>Antiparasitic medication increases vole survival in fragmented habitat</i> | 36 |
| T.50 | Klaus Hackländer: <i>WORKSHOP TALK: Impact of EU Common Agricultural Policy on hares</i> | 36 |
| T.51 | Thomas J.D. Halliday: <i>The Cretaceous-Palaeogene mass extinction and eutherian evolutionary dynamics</i> | 37 |
| T.52 | Guillaume Halliez: <i>Variation of predation pressure in a context of cyclic population outbreaks of grassland voles (<i>Arvicola scherman</i>).</i> | 37 |
| T.53 | Oliver Hawlitschek: <i>The project Barcoding Fauna Bavarica: Why DNA barcoding is also useful for mammals.</i> | 38 |
| T.54 | Matt Hayward: <i>No teddy bears picnic-a review of ungulate predation and prey selection by the brown bear in the Holarctic</i> | 38 |
| T.55 | Matti Heino: <i>Temporal genetic variation of the Saimaa ringed seal (<i>Phoca hispida saimensis</i>) in the 20th century</i> | 39 |
| T.56 | Heikki Henttonen: <i>Eco-epidemiological research on rodent-borne pathogens</i> | 39 |
| T.57 | Jeremy Herman: <i>Natural selection in a common small mammal: evidence from molecular data and implications for phylogeographic inference</i> | 40 |
| T.58 | Anne Hertel: <i>Effects of hunting on foraging behavior and efficiency: Do bears trade off good forage for security?</i> | 40 |
| T.59 | Russell Hill: <i>Human observers modulate perceived landscapes of fear</i> | 41 |

| | | |
|------|---|----|
| T.60 | Emilia Hofman-Kaminska: <i>Patterns of habitat use and diet of European bison and moose in Europe</i> | 41 |
| T.61 | Tim Hofmeester: <i>Traits, predators and deer as determinants of tick burdens of rodents: implications for Lyme borreliosis risk</i> | 42 |
| T.62 | Katja Holmala: <i>Avoiding predator or finding prey – habitat use and activity of Red fox in relation to Eurasian lynx in Southern Finland</i> | 42 |
| T.63 | Patrick Jansen: <i>eMammal, a system for processing images from large-scale camera-trap surveys</i> | 43 |
| T.64 | Thomas Secher Jensen: <i>Wolf recolonization of Denmark</i> . . . | 43 |
| T.65 | Chris Johnson: <i>Top predators and ecological cascades over a continent: dingoes, devils and diversity in Australia</i> | 44 |
| T.66 | Vendela K. Lagerholm: <i>Using ancient DNA to examine the postglacial consequences of range contractions in cold-adapted species</i> | 44 |
| T.67 | Eva Kallio: <i>Endemic pathogen infections and bank vole fitness</i> | 45 |
| T.68 | Veli-Matti Kangas: <i>Evidence of post-glacial secondary contact and subsequent anthropogenic influence upon the genetic composition of Fennoscandian moose (<i>Alces alces</i>)</i> | 45 |
| T.69 | Hussein Khalil: <i>Can shrews influence local hantavirus prevalence in bank voles?</i> | 46 |
| T.70 | Andrew Kitchener: <i>Geographical variation in the sand cat, <i>Felis margarita</i></i> | 46 |
| T.71 | Meeri Koivuniemi: <i>Photo-ID as a tool for studying and monitoring the critically endangered Saimaa ringed seal population</i> | 47 |
| T.72 | Marta Kolodziej-Sobocinska: <i>Does the blood-sucking nematode <i>Ashworthius sidemi</i> cause deterioration of blood parameters in endangered European bison (<i>Bison bonasus</i>)?</i> | 47 |
| T.73 | Alexander Kopatz: <i>Male mediated gene flow and the carnivore comeback: Y-chromosomal patterns during range expansion in a recovering brown bear population</i> | 48 |
| T.74 | Petr Kotlik: <i>Population replacement in British bank voles revealed by a large number of SNP markers</i> | 48 |
| T.75 | Rafal Kowalczyk: <i>Why has the European bison survived, while the other large beasts have gone</i> | 49 |
| T.76 | Anna Kukekova: <i>Genomic regions associated with selection for behavior in foxes (<i>Vulpes vulpes</i>)</i> | 49 |
| T.77 | Sara Lado: <i>Population history and taxonomy of North African hares (genus <i>Lepus</i>) inferred from genetic variation</i> | 50 |
| T.78 | Regina Lafuente: <i>Hunters' attitudes towards the reintroduction of the critically endangered Iberian lynx (<i>Lynx pardinus</i>)</i> | 50 |
| T.79 | Xavier Lambin: <i>Trophic interactions in asynchronously fluctuating populations: predation and the cost of dispersal</i> . . . | 51 |
| T.80 | Arild Landa: <i>Species at risk, Captive breeding and reintroduction: challenges, pit-falls and successes</i> | 51 |
| T.81 | Marietjie Landman: <i>Comparing the efficiency of DNA barcoding and microhistology methods to describe elephant diet: consequences for understanding elephant-plant dynamics</i> . . . | 52 |

| | | |
|-------|--|----|
| T.82 | Greger Larson: <i>The process and the pattern of dog domestication</i> | 52 |
| T.83 | Alice Latinne: <i>Past and future distributions of Southeast Asian murine rodents: the influence of climate changes</i> | 53 |
| T.84 | Jennifer Leonard: <i>Ecology in the Evolution of Wolves</i> | 53 |
| T.85 | Liza le Roux: <i>Behaviourally mediated trophic cascades in a megaherbivore dominated system</i> | 54 |
| T.86 | Riikka Levänen: <i>Abundance and distribution of hare hybrids in Finland</i> | 54 |
| T.87 | Anna Linderholm: <i>Unraveling the complexity of the Austronesian expansion and dispersal</i> | 55 |
| T.88 | Miriam Linnenbrink: <i>Territoriality and migration - implications on fitness in wild mice</i> | 55 |
| T.89 | Eline Lorenzen: <i>Population genomics reveal recent speciation and rapid evolutionary adaptation in polar bears</i> | 56 |
| T.90 | Juan Jose Luque-Larena: <i>Sperm competition in fluctuating populations of common voles in southern Europe: reversed relationship between relative testes size and density</i> | 56 |
| T.91 | Åke Lundkvist: <i>City rats - an emerging threat to the public health</i> | 57 |
| T.92 | Carly Lynsdale: <i>Individual Variation in Parasite Burden in a Population of Semi-Captive Asian Elephants (<i>Elephas maximus</i>)</i> | 57 |
| T.93 | David Macdonald: <i>Conserving big predators: case studies from the WildCRU</i> | 57 |
| T.94 | Allan McDevitt: <i>Signatures of selection in the genome and phenotype of the invading and expanding greater white-toothed shrew (<i>Crocidura russula</i>) in Ireland</i> | 58 |
| T.95 | Allan McDevitt: <i>Genomic variation and signatures of selection in European red foxes (<i>Vulpes vulpes</i>)</i> | 58 |
| T.96 | Clara Mendes Ferreira: <i>Fewer markers, similar accuracy? Cost-effective selection of genetic markers for parentage analysis based on noninvasive genetic sampling</i> | 59 |
| T.97 | Johan Michaux: <i>Genetic patterns of a successful recolonization of the Eurasian otter in France</i> | 59 |
| T.98 | Berit Annika Michler: <i>Unsuspecting immigrant or ecological threat - a long-term fieldwork study on the introduced raccoon in Germany</i> | 60 |
| T.99 | Christine Miller: <i>How to prove that you loose! Management of alpine chamois (<i>Rupicapra rupicapra</i>) to the brink of extinction in Germany</i> | 60 |
| T.100 | L. Scott Mills: <i>Seasonal Coat Color and Climate Change in Mammals: A Global Model System to Understand Adaptive Rescue</i> | 61 |
| T.101 | Pedro Monterroso: <i>Ecological Interactions and Species Coexistence in Iberian Mesocarnivore Communities</i> | 61 |
| T.102 | Ian Montgomery: <i>Invasive small mammals: trophic dynamism and modified food webs in Irish hedgerows</i> | 62 |
| T.103 | Raimondas Mozūraitis: <i>Estrous olfactory cues in domestic horse <i>Equus ferus caballus</i> L. (<i>Perissodactyla</i>, <i>Equidae</i>)</i> | 62 |

| | | |
|-------|--|----|
| T.104 | Morteza Naderi: <i>Combination of morphological, molecular and niche divergence to identify patterns of species delimitation: a case with the fat dormouse along the Hyrcanian forests</i> | 63 |
| T.105 | Magdalena Niedziałkowska: <i>Evolutionary history and genetic structure of moose population in Europe</i> | 63 |
| T.106 | Alina K Niskanen: <i>Prenatal selection in dog MHC loci</i> | 64 |
| T.107 | Anita Norman: <i>Landscape Relatedness: Insights into Contemporary Spatial Structure of a Top Predator</i> | 64 |
| T.108 | Karin Norén: <i>Tracking genetic footprints to reconstruct geographic patterns of expansion in Fennoscandian red foxes</i> | 65 |
| T.109 | Maria Orlova: <i>Genesis of the bat ectoparasite fauna of Siberia</i> | 65 |
| T.110 | Sakir Onder Ozkurt: <i>Determination of taxonomic status of <i>Mustela nivalis</i> subspecies in Turkey</i> | 66 |
| T.111 | Marianne Pasanen-Mortensen: <i>Can recolonizing apex predators reclaim their ecosystem function?</i> | 66 |
| T.112 | Ekaterina Pavlova: <i>Potential sources of pathogens for the Pallas cat in Daurian steppes, Russia</i> | 67 |
| T.113 | Claire R. Peart: <i>Influence of mating system on patterns of sex-linked genetic diversity across pinniped species</i> | 67 |
| T.114 | Jens Persson: <i>Patterns of reproduction result from age-related sensitivity to resources and reproductive costs in wolverines</i> | 68 |
| T.115 | Mia Persson: <i>Genetics of human-directed social behaviour in Beagles</i> | 68 |
| T.116 | Isabel Queirós Neves: <i>Species patterns and trends from sparse occurrence data. The case of Mozambique's mammals.</i> | 69 |
| T.117 | Neil Reid: <i>Herd-level bovine tuberculosis risk factors: assessing the role of low level badger population disturbance</i> | 69 |
| T.118 | Neil Reid: <i>Macroecology of the Order Lagomorpha; implications for the impact of global climate change</i> | 70 |
| T.119 | Sabrina Renaud: <i>Fast evolutionary response of house mice to anthropogenic disturbance on a Sub-Antarctic island</i> | 70 |
| T.120 | Erika Rosengren: <i>The colonisation history of Scandinavia presented through the subfossil finds along one of its major immigration routes; Scania, southern Sweden</i> | 71 |
| T.121 | Marcus Rowcliffe: <i>Analytical frontiers in analysing camera trap data</i> | 71 |
| T.122 | Ben Sacks: <i>Inbreeding, Outbreeding, and the Transformation of the Critically Endangered Sierra Nevada Red Fox: Genetic Rescue or Genomic Replacement?</i> | 72 |
| T.123 | Gustaf Samelius: <i>Snow leopard predation in a livestock-dominated landscape</i> | 72 |
| T.124 | Håkan Sand: <i>Predation ecology and top-down effects of wolves in a strongly anthropogenic influenced landscape – lessons from Scandinavia.</i> | 73 |
| T.125 | Peter Savolainen: <i>Origins of the domestic dog: Out of Southern East Asia</i> | 73 |
| T.126 | Stéphanie Schai-Braun: <i>Home range use by the European hare (<i>Lepus europaeus</i>) in an agricultural area with small fields analysed at a fine temporal scale</i> | 73 |

| | | |
|-------|---|----|
| T.127 | Irena Schneiderová: <i>The alarm call of the European ground squirrel (Spermophilus citellus): still quite unexplored field . . .</i> | 74 |
| T.128 | Irena Schneiderová: <i>Species determination of lesser galagos (Galago spp.) at zoos integrating molecular-genetic and bioacoustic data</i> | 74 |
| T.129 | Andreas Seiler: <i>Are animal-vehicle collisions a random event? – Analysis of the spatial distribution of accident reports . . .</i> | 75 |
| T.130 | Andreas Seiler: <i>Wildlife on tracks – an innovative project to mitigate ungulate-train collisions</i> | 75 |
| T.131 | Teodora Sin: <i>Wolf (Canis lupus, L. 1758) diet and prey selection in the South-Eastern Carpathian Mountains, Romania</i> | 76 |
| T.132 | Navinder Singh: <i>Linking migratory tactics with reproduction in a large mammal</i> | 76 |
| T.133 | Tarja Sironen: <i>Aleutian mink disease virus in free-ranging mustelids in Finland</i> | 77 |
| T.134 | Christina Skarpe: <i>Herbivores and landscapes</i> | 77 |
| T.135 | Mark Statham: <i>Range-wide multilocus phylogeography of the red fox reveals ancient continental divergence, minimal genomic exchange, and distinct demographic history</i> | 78 |
| T.136 | Joanna Stojak: <i>Contrasting and congruent patterns of genetic structuring in two Microtus vole species in Poland using museum specimens</i> | 78 |
| T.137 | Sally Street: <i>How introduction effort promotes invasion success in mammal species</i> | 79 |
| T.138 | Astrid Vik Stronen: <i>Genome-wide analyses suggest parallel selection for ubiquitous functions may eclipse local adaptation in European wolf (Canis lupus) populations</i> | 79 |
| T.139 | Aimee Tallian: <i>The role bison sex and group size in wolf-bison interactions</i> | 80 |
| T.140 | Joaquim Tapisso: <i>Dynamic of chromosomal evolution in two parapatric Rb races of house mouse in the island of Madeira</i> | 80 |
| T.141 | Ewa Tarnowska: <i>Maintenance of contact zone between two bank vole phylogenetic lineages in NE Poland</i> | 81 |
| T.142 | Anne-Mathilde Thierry: <i>Estimating dispersal in Arctic fox juveniles released from the Norwegian captive-breeding program</i> | 81 |
| T.143 | Carl-Gustaf Thulin: <i>WORKSHOP TALK: Analyses of hare and fox game bags in Sweden indicate population crash in southern mountain hares</i> | 82 |
| T.144 | Jean-Luc Tison: <i>Population structure and recent temporal changes in genetic variation in Eurasian otters from Sweden</i> | 82 |
| T.145 | Malgorzata Tokarska: <i>Genetic background of Posthitis in the European bison</i> | 83 |
| T.146 | David Tosh: <i>Monitoring small carnivore populations using citizen scientists</i> | 83 |
| T.147 | Alessia Uboni: <i>Widespread declines in ground lichens in northern Sweden: consequences for reindeer husbandry</i> | 84 |
| T.148 | Ester Rut Unnsteinsdottir: <i>Fecundity and population dynamics of the Icelandic arctic fox – a 50 year case study</i> | 84 |

| | | |
|----------|--|-----------|
| T.149 | Frank Van Langevelde: <i>How unusual is the terrestrial mammal community of Barro Colorado Island? A Neotropical cross-forest comparison using camera traps</i> | 85 |
| T.150 | Nagarjun Vijay: <i>Genome-culture coevolution promotes rapid divergence in the killer whale</i> | 85 |
| T.151 | Kristina Vogt: <i>Scent-marking in a stalking predator: Is there a trade-off between intra-specific communication and hunting behaviour in the Eurasian lynx <i>Lynx lynx</i>?</i> | 86 |
| T.152 | Märtha Wallgren: <i>Moose browsing patterns on young Scots pine with implications for forestry</i> | 86 |
| T.153 | Roselyn Ware: <i>The Role of Resource Partitioning in Supporting UK Bat Diversity</i> | 87 |
| T.154 | Sarah Woodfin: <i>The elusive Annamite striped rabbit <i>Nesolagus timminsi</i></i> | 87 |
| T.155 | Nobuyuki Yamaguchi: <i>Basking in the winter sun: thermoregulation in the Ethiopian hedgehog, <i>Paraechinus aethiopicus</i>, in Qatar</i> | 88 |
| T.156 | Nigel Yoccoz: <i>Modelling the impacts of climate change on mammals: how to open the ecosystem black box?</i> | 88 |
| T.157 | Marketa Zimova: <i>Camouflage mismatch in seasonal coat color due to decreased snow duration: Will snowshoe hares keep up with climate change?</i> | 89 |
| T.158 | Karol Zub: <i>Climate warming is affecting mortality of weasels due to camouflage mismatch</i> | 89 |
| T.159 | Sophie von Merten: <i>Does sociability relate to personality? A comparison between four species of shrews</i> | 90 |
| 2 | Abstracts for poster | 90 |
| P.1 | Marzena Albrycht: <i>Population dynamics of European hare <i>Lepus europaeus</i> in relation to intensity of agriculture and predation in Poland during 1976–2014 period</i> | 90 |
| P.2 | Amna Arshad Bajwa: <i>DNA metabarcoding for Diet and parasitic estimation of Markhor (<i>Capra falconeri</i>) in Chitral, Pakistan</i> | 91 |
| P.3 | Marjorie Biffi: <i>Some insights into the local habitat use of the semi-aquatic Pyrenean desman (<i>Galemys pyrenaicus</i>) in the French Pyrenees</i> | 91 |
| P.4 | Anthony Caravaggi: <i>The democratisation of conservation: public attitudes towards lethal control of invasive leporids and implications for species management</i> | 92 |
| P.5 | Rory Carroll: <i>Natural and anthropogenic drivers of bobcat (<i>Lynx rufus</i>) population structure in northeastern United States</i> | 92 |
| P.6 | Ana Cerveira: <i>Male quality assessment of two house mouse chromosomal races from Madeira Island</i> | 93 |
| P.7 | Derya Çetintürk: <i>Phylogenetic Relationships of Guentheri Group Species of the genus <i>Microtus</i> (Rodentia: Muridae) in Turkey based on mitochondrial COX1 Gene</i> | 93 |
| P.8 | Andrea Corradini: <i>Comparison of wolf (<i>Canis lupus</i>) and lynx (<i>Lynx lynx</i>) signs of presence in the Carpathian Mountains (Romania)</i> | 94 |

| | | |
|------|---|-----|
| P.9 | Gonçalo Curveira-Santos: <i>Drivers of badger occupancy in Northern Scotland</i> | 94 |
| P.10 | Miguel Delibes-Mateos: <i>The importance of prey subspecies: predator distribution and European rabbits in their native range</i> | 95 |
| P.11 | Jakub Drimaj: <i>Preliminary findings on the reproductive biology of wild pigs (<i>Sus scrofa</i> L.) in the Czech Republic</i> | 95 |
| P.12 | Francisco Díaz-Ruiz: <i>Assessing the influence of predator control on target and non-target carnivore populations using occupancy models</i> | 96 |
| P.13 | Simon Engelberger: <i>Behavioural response of Geoffroy's bats (<i>Myotis emarginatus</i>) to a predating tawny owl</i> | 96 |
| P.14 | Alan Fredy Eriksson: <i>Influence of bat <i>Artibeus Planirostris</i> abundance on the ectoparasites prevalence in a tropical wetland</i> | 97 |
| P.15 | Mariya Erofeeva: <i>Teratospermia affects reproductive success in domestic cat</i> | 97 |
| P.16 | Maria Fominykh: <i>Relationship between dental microwear patterns and diet in <i>Cl. glareolus</i> in a natural population and in two feeding experiments</i> | 98 |
| P.17 | Maria Fominykh: <i>Clethrionomys and Craseomys species in Quaternary faunas of the Urals</i> | 98 |
| P.18 | Emma Grocutt: <i>Fitness consequences of arctic fox cub personality</i> | 99 |
| P.19 | Klaus Hackländer: <i>Stress responses in snowshoe hares facing mismatch of coat colour and their environment</i> | 99 |
| P.20 | Jenni Harmoinen: <i>Unequal sampling can bias population genetic studies; an example from North American canids</i> | 100 |
| P.21 | Tomohiko Hori: <i>Dental microwear morphology of the Japanese dormice (<i>Glirulus japonicus</i>)</i> | 100 |
| P.22 | Ivan Horáček: <i>Pleistocene/Holocene transition in Central Europe: small mammals in a high-resolution fossil record</i> | 101 |
| P.23 | Saher Islam: <i>Population estimation and genetic inferences of Markhor (<i>Capra falconeri</i>) in Chitral, Pakistan using non-invasive sampling</i> | 101 |
| P.24 | Iris Kempter: <i>Seed predation and seed dispersal by small mammals in central European mixed forest ecosystems</i> | 102 |
| P.25 | Sang-In Kim: <i>Range-wide skull morphogeographic variation of red fox in the Northern Hemisphere</i> | 102 |
| P.26 | Andrew Kitchener: <i>The Atlas of European Mammals, 2nd Edition?</i> | 103 |
| P.27 | Markéta Knitlová: <i>The Holocene history of <i>Apodemus flavicollis</i> in Central Europe</i> | 103 |
| P.28 | Marta Kolodziej-Sobocinska: <i>Parasites of invasive American mink (<i>Neovison vison</i>) in Poland: does co-infection induce competition between parasites?</i> | 104 |
| P.29 | Sahila Kudalkar: <i>Habitat Correlates of the Forest Non-volant Small Mammal Community in Northeast India</i> | 104 |
| P.30 | Elin Lilja: <i>Seals and tourists: A worldwide investigation of codes of conduct for tourist behavior</i> | 105 |
| P.31 | Yilin Liu: <i>Sequencing of 1000 mtDNA genomes in a single Miseq run</i> | 105 |

| | | |
|------|---|-----|
| P.32 | Miroslava Loudová: <i>Population genomics of European hedgehogs</i> | 106 |
| P.33 | Johan Michaux: <i>Molecular phylogeny of all Apodemus species based on the complete mitochondrial genome and two nuclear genes</i> | 106 |
| P.34 | Pedro Monterroso: <i>New variant of the rabbit hemorrhagic disease virus in Portugal: Preliminary results of its evolution and impacts in rabbit populations</i> | 107 |
| P.35 | Adam Nadachowski: <i>Phylogeography of cave bear from Central and Eastern Europe in the light of ancient DNA studies</i> . | 107 |
| P.36 | Magdalena Niedziałkowska: <i>Habitat preferences of red deer (Cervus elaphus) in Late Pleistocene and Holocene in Europe, introduction to the on-going study</i> | 108 |
| P.37 | Stefan Prost: <i>Living in Extreme Environments: Genome Adaptation in Arctic, Desert and High-Altitude Foxes (genus: Vulpes)</i> | 108 |
| P.38 | Joao Queiros: <i>Tuberculosis, fitness and heterozygosity in the red deer</i> | 109 |
| P.39 | Benjamin Ramassamy: <i>A new long-snouted beaked whale from the Late Miocene of Denmark: evolution of sexual dimorphism in the Ziphiidae</i> | 109 |
| P.40 | Neil Reid: <i>Diversity, extinction, and threat status in Lagomorphs</i> | 110 |
| P.41 | Alba Rey de la Iglesia: <i>Mitogenomics of red deer (Cervus elaphus) in Iberia: insights into the post-LGM colonization of Europe</i> | 110 |
| P.42 | Juliana Ribeiro: <i>Isotopic niche of small mammals in a neotropical savanna</i> | 111 |
| P.43 | Gabriella Rizzardini: <i>Wolf detection using camera trapping: a pilot study in the southern part of the Eastern Carpathians, Romania.</i> | 111 |
| P.44 | Lars Rød-Eriksen: <i>Generalist species range expansion into alpine regions of Fennoscandia: the red fox</i> | 112 |
| P.45 | Fulya Saygılı: <i>Genetic Differentiation of Meriones tristrami (Mammalia:Rodentia) Subpopulations in Turkey; Inferring Allozyme Variations</i> | 112 |
| P.46 | Stéphanie Schai-Braun: <i>Spring and autumn habitat preferences of active European hare (Lepus europae-us) in a small-scale agricultural area with low hare density</i> | 113 |
| P.47 | Analena Severon: <i>Intrasexual home range overlap, kinship and dispersal in the European wildcat</i> | 113 |
| P.48 | Aaron B.A. Shafer: <i>The genomic legacy of human exploitation and extreme climatic oscillations in marine mammals</i> . | 114 |
| P.49 | André Silva: <i>Suitable climatic conditions for the jungle cat and leopard cat after the last-inter-glacial in the Indian subcontinent</i> | 114 |
| P.50 | Mark Statham: <i>Peninsulas and islands in a sea of red: phylogeography and population substructure of the European red fox.</i> | 115 |

| | | |
|------|---|-----|
| P.51 | Janne Sundell: <i>Field stations provide valuable infrastructure for environmental sciences and biology: introduction to UHEL research stations</i> | 115 |
| P.52 | Marta Szurlej: <i>Species composition, sexual structure and phenology of bats foundet by Tricity inhabitants</i> | 116 |
| P.53 | Joaquim Tapisso: <i>Phenotypic flexibility in the energetic strategy of the greater white-toothed shrew, Crocidura russula</i> . . . | 116 |
| P.54 | Philipp Tumasian: <i>An experience of development of artificial population of Piebald Shrew (Diplomesodon pulchellum Lichtenstein, 1823)</i> | 117 |
| P.55 | Kristine Ulvund: <i>Use of supplementary feeding stations by arctic foxes in Norway</i> | 117 |
| P.56 | Nina Vasilieva: <i>Prolonged handling time could affect the blood profile in the wild cat species</i> | 118 |
| P.57 | Johan Wallén: <i>Population history and northern recolonization in a generalist carnivore: the Scandinavian red fox</i> . . . | 118 |
| P.58 | Sergey Zykov: <i>Comparative analysis of dental enamel microstructure in the late quaternary and modern Microtus gregalis in the Urals</i> | 119 |

| | |
|-------------------------|------------|
| Index of authors | 120 |
|-------------------------|------------|

1 Abstracts for talk

T.1 Hans Ahlgren

WORKSHOP TALK: Prehistoric translocation or natural colonization? - the origin of mountain hares on Gotland

Hans Ahlgren <hans.ahlgren@arklab.su.se>^a

Archaeological Research Laboratory, Stockholm University, Sweden

Abstract for talk The majority of the present non-volant mammals on the island of Gotland have been introduced by people in modern times. One exception is the mountain hare (*Lepus timidus*) that was present on the island more than 9,000 years ago. This study investigates the origin and temporal change in genetic structure of the Gotland hares and the question of how mountain hares reached the island is asked. Two fragments of mtDNA, 130 + 164 BP from skeletal remains from ancient mountain hares from Gotland, the Swedish mainland and Lithuania were analysed and compared to 90 modern *lepus timidus* haplotypes from different locations in Eurasia and to the morphotype don-hare (*Lepus tanaiticus*). The ancient hares on Gotland fall into two different haplogroups separated by time which indicate that the mountain hare went extinct at one occasion with following events of re-colonization. Because of the isolated location of Gotland, it is probable that the hares were brought there by human mediated transports.

^aCo-authors: Karin Norén, Anders Angerbjörn and Kerstin Lidén

T.2 Tuomas Aivelo

Rapid turnover in micro- and macrobiome of free-ranging primates, rufous mouse lemur (*Microcebus rufus*)

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Institute of Biotechnology, University of Helsinki, Finland

Abstract for talk The strong ongoing research program to study microbiome has a distinct lack of studies connecting intestinal parasites to the dynamics of microbiome. Nevertheless, we expect the species co-inhabiting intestine to have community-shaping interactions. We mark-recaptured mouse lemurs in Ranomafana National Park, Madagascar, and tracked both microbiome and intestinal parasite community from feces. We identified communities by metabarcoding: standard 16S gene approach for microbiome and a new method to identify operational taxonomic units of nematodes using 18S gene. We also collected data for eimeriids and helminths and ectoparasitic lice and ticks. Intestinal communities are not stable as both micro- and macrobiome has rapid within-individuals turnover. In contrast, the host population-level community in both groups remained quite stable. The only observed correlation in community members was positive correlation between microbiome diversity and presence of eimeriids.

^aCo-authors: Alan Medlar, Ari Löytynoja, Juha Laakkonen, Jukka Jernvall

T.3 Paulo C. Alves

WORKSHOP TALK: Reticulate evolution in Lagomorphs: conservation and management implications

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(2) Wildlife Biology Program, University of Montana, USA, (1) Portugal, (2)
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Abstract for talk Lagomorphs are providing a remarkable window for evolutionary biology studies. Species of this mammal order are found across an enormous geographic range, occupying rather different ecological niches, spanning from arctic to arid habitats. This fact has facilitated a great diversity of evolutionary processes, namely reticulate and divergent diversification and adaptive radiations across extremely divergent environments. A major consequence of these evolutionary processes is the interspecific hybridization, which in fact is quite common among lagomorphs species, namely among hares (*Lepus*). In this talk, we will revise the major forces driving the natural and anthropogenic hybridization on lagomorphs, summarize the techniques to detect hybridization and discuss some of the consequences of this phenomenon in management and conservation.

^aCo-authors: Paulo C. Alves (1,2) and J. Melo-Ferreira (1)

T.4 Henrik Andrén

Ecology and Landscapes - species interactions in heterogeneous landscapes

Henrik Andrén <henrik.andren@slu.se>
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Abstract for talk What is ecology? What is a landscape? What is landscape ecology? How do different organisms respond to habitat changes in the landscape? How are species interactions influenced by habitat changes in the landscape? Species at higher trophic levels, e.g. predator compared with their prey, often have larger area requirements and the effect of habitat changes in the landscape may influence the predators and their prey differently. Predators and prey may also use the habitat in a landscape different, especially in multi-use human-dominated landscapes.

T.5 Malin Aronsson

It's relative: Sex and resource heterogeneity influences the relationship between relatedness and home range overlap for a solitary predator

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Department of Ecology, Swedish University of Agricultural Sciences, Sweden

Abstract for talk For territorial species, spacing patterns are the result of individual interactions and environmental factors to gain exclusive access to resources. Thus, kinship and resource heterogeneity may alter the cost/benefit ratio for territorial behaviour. We use 16 years of DNA and location data from adult Eurasian lynx (*Lynx lynx*) to assess the effect of relatedness on home range (HR) overlap (i.e. strength of territoriality) using zero-one-beta hurdle models in JAGS, comparing two distinct study areas (59° vs. 67° N) with different environmental productivity and prey availability (stationary vs. migratory). We found no effect for males whereas relatedness positively affected HR overlap for females. Mother-offspring overlapped more than equally related full-siblings, indicating importance of kin-recognition. However, the relatedness effect on territoriality was confined to the northern study area, where lynx density and reproductive rate is lower and HR size larger compared to the south.

^aCo-authors: M. Low, J. Persson, M. Åkesson, J-V. López-Bao, H. Andrén

T.6 Irina Bakloushinskaya

Is monobrachial homology the end or the start of chromosomal speciation? Ellobius' case

Irina Bakloushinskaya <irina.bakl@gmail.com>^a

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Abstract for talk In mammals Robertsonian fusions (Rb) are the most common chromosome mutations involved to speciation. They accelerate acquisition of reproductive isolation, especially if monobrachial homology of Rb occurs. When forms with such Rb undergo hybridization, the hybrids would be sterile or semi-fertile producing chain multiples at meiosis because of partial homology of chromosome arms. Nevertheless, there is another side. Our study of natural variability in *Ellobius tancrei* enables us to hypothesize that hybridization and meiotic drive may produce new chromosomal forms. For verifying the hypothesis, we carried out inbred crossings of two natural forms with monobrachially homologous Rb. After 7 years of breeding mole-voles, despite reduced fertility, we got 8 generations of hybrids. Instead of return to parental karyotypes, the hybrids obtained new chromosome sets, with different 2n and combinations of Rb. This trend may explain fast fixation of new chromosomal forms in nature.

^aCo-authors: V. Tambovtseva, Moscow State Univ. S. Romanenko, Inst Molecular and Cellular Biology, Novosibirsk S. Matveevsky, Vavilov Inst General Genetics Moscow

T.7 Ian Barnes

Genomic Analyses of Museum Collections

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Natural History Museum, London, UK

Abstract for talk Museums are often proposed as important storehouses of genomic information, and museum collections have the potential to contribute to problems where it would be difficult to obtain specimens, and where temporal or spatial series are required for analyses. Mammals are particularly important in this context, as most natural history museums have assembled disproportionately large mammal collections over the last two centuries, and because large numbers of mammalian populations and species have decreased in size and range over this time. However, despite the potential importance of museum specimens for genomic analyses, we still have a relatively poor understanding of the quality and potential of the DNA that can be recovered from museum material. In this talk, I will discuss the way that next generation sequencing can be used to characterize museum specimens, and provide some recent examples of how we are using this knowledge to resolve some important taxonomic problems.

T.8 Laszlo Bartosiewicz

Cave lioness from the plain? Craniometric investigations on a Pleistocene lion skull from Hungary

Laszlo Bartosiewicz <laszlo.bartosiewicz@ofl.su.se>
OFL Stockholm University, Sweden

Abstract for talk The complete calvarium of a lion was found in a Middle/Upper Pleistocene alluvial deposit at a depth of ca 4m near Ikreny-Szilagytanya within the Danube floodplain in North-West Hungary. The excellent preservation of the skull made ^{14}C dating (ca 36,380 BP) and traditional craniometric analysis possible. This specimen originates from an adult lioness, rather small in comparison with 37 extant lions from Central Africa used as a metric reference. It may be considered "feminine" as its neurocranium is largish relative to its size. This difference is less pronounced in dental dimensions. On the basis of this craniometric study alone it would be difficult to establish the exact taxonomic affiliation of this find. Ancient DNA studies would be needed to place this individual within the broader population of contemporaneous lions in Europe.

T.9 Sabine Begall

Magnetic alignment in mammals

Sabine Begall <sabine.begall@uni-due.de>^a

University of Duisburg-Essen, Germany

Abstract for talk Magnetic alignment constitutes the simplest directional response to the geomagnetic field. In contrast to magnetic compass orientation, magnetic alignment is not goal directed and represents a spontaneous, fixed directional response. It is usually expressed, if other factors (e.g. wind, sun, attractors) do not prevail. Magnetic alignment has been demonstrated among mammals in cattle, red and roe deer, red foxes, dogs and several rodent species. It can be expressed by animals during resting as well as on the move (e.g. while grazing, hunting, feeding, etc.). We present characteristic features and classical examples and summarize what is known about mechanisms underlying magnetic alignment. The phenomenon of magnetic alignment adds a new paradigm that can be exploited for investigation of magnetoreception in mammals.

^aCo-authors: E. Pascal Malkemper, Jaroslav Cervený, Vlastimil Hart, Petra Novakova, Pavel Nemeč, Hynek Burda

T.10 Ulrika A Bergvall

Small scale foraging decisions in moose in relation to plant defence and spatial distribution

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Stockholm University, Sweden

Abstract for talk This study examines moose foraging behavior on pines in cafeteria experiments. We measured browsing damage and dependent on treatment with additional defence in the form of birch bark extract applied to pines, in a randomized experimental design. The four different setups were: all treated, none treated, clumped (two patches of different quality) or scattered (mixed in each patch). Pines treated with birch bark were overall less browsed than untreated. We found an effect of treatment but not setup on browsing on apical shoots and bark. In addition, we found an interaction between setup and treatment for the proportion browsed branches so that branches from untreated pines were less eaten when were presented in a scattered setup than when presented in a clumped setup, indicating an effect of spatial distribution. In analyses of 278 filmed eating bouts we found an interaction between setup and treatment so that moose spent longer time on untreated pines in the clumped setup.

^aCo-authors: Charlotta Turner, Olof Leimar

T.11 Dominique Berteaux

Species interactions of arctic fox on Bylot Island, Nunavut: hypothesis-testing at the meta-ecosystem scale

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Université du Québec à Rimouski, Canada

Abstract for talk Predators and prey routinely cross ecosystem boundaries. This connects food webs, thereby structuring meta-ecosystems. Arctic foxes on Bylot Island (Nunavut) feed on lemmings and migrating geese in summer, and also seals in winter. Using stable isotopes and fox monitoring (10 years, 100 dens), we show how the large-scale migration of geese is a subsidy that strongly affects the functional and reproductive responses of foxes, with cascading effects on the tundra food web. Using satellite tracking (6 years, 66 foxes), we show that foxes compensate winter food shortage by commuting to the sea ice, thereby choosing residency with extra-territorial excursions over migration or nomadism. Contributions of both landscape and foraging ecology are thus needed to resolve the effects of subsidies on population dynamics of mammalian predators. And understanding the movement responses of predators to prey dynamics is needed to identify some critical aspects of the functioning of meta-ecosystems.

^aCo-authors: Sandra Lai, Marie-Andrée Giroux

T.12 Dominique Berteaux

WORKSHOP TALK - The arctic fox as model system to study trophic interactions

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Université du Québec à Rimouski, Canada

Abstract for talk The arctic fox inhabits a simplified food web where predators, competitors, and prey are few. In this context, identifying its preferred, alternative, and incidental prey is possible, as well as quantifying most trophic interactions structuring its tundra ecosystem. Arctic foxes can also use the sea ice as foraging habitat in winter. The above opens many opportunities for hypothesis testing at the community, ecosystem, and meta-ecosystem scales. I use 20 years of work from Bylot Island (Nunavut, Canada) to illustrate how foxes can be used as model system to study trophic interactions. In particular, I show how an ecosystem-based monitoring combined with state-of-the-art field (stable isotopes, satellite tracking, movement-triggered cameras, etc.) and modeling techniques have allowed recent progress in ecology, using foxes as study model. I also try to identify some of the attributes of *Vulpes* that make them interesting models to study trophic interactions.

T.13 Boguslaw Bobek

Changes in distribution ranges in wolf (*C. lupus*) in Poland during 1980-2014, and the impact of this species upon population of red deer (*C. elaphus*)

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Institute of Biology, Pedagogical University in Cracow, Poland

Abstract for talk Based on questionnaires obtained from all forest districts (FD), and national parks (NP) in Poland (n:448) the dynamics of ranges of wolf occurrence was estimated in 1980, 1990, 2010 and 2014. In 1980, wolves occurred in 44 FD and NP, on 9,750 km² of forest, whereas in 2014, the wolves were found in 238 FD and NP, in forest covering 53,700 km². In Polish Carpathians (661 km²) relative population densities of wolves and red deer were estimated by snow tracking on 180.2 km line transects. During tracking (10 plus 10 days) 130 wolves and 1069 red deer was registered. In 2000 and 2012 the densities of wolves did not change significantly and amounted to 0.123 - 0.009 (mean - SE) animals/ km x day-1 and 0.139 - 0.033 animals/km x day-1, respectively, whereas the density of red deer increased significantly from 0.569 - 0.035 animals/ km x day-1 to 1.155 - 0.095 animals/ km x day-1 (p: 0.000042, t: 7.3867). The importance of these results to forest and game management is discussed.

^aCo-authors: Jakub Furtek, Magdalena Dardzinska, Katarzyna Ziobrowska, Marta Wojciuch-Ploskonka

T.14 Zbigniew Borowski

Direct effect of mechanical grass moving on small mammal population dynamics

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Department of Forest Ecology, Forest Research Institute, Poland

Abstract for talk Large tracked mowers are often used in nature protection to combat with unwanted succession which is one of the main threat to biodiversity. We assessed the effects of this management on root vole population by comparing 3 pairs of mown and unmown plots in Biebrza National Park, NE Poland. We monitored survival rate and vole population structure before, 3 days, 8 and 28 weeks after the mowing respectively. Collected data indicate that such nature protection practice generates high vole mortality during the mowing. Additionally, voles depletion on mowed habitats was twice higher than on control areas. Moreover, mowing changed the age structure of vole population towards higher proportion of young individuals. Finally, the effect of such management was well visible even after seven months (on spring next year) causing much lower vole population density. This experiment shows that existing protection practice should be changed in the way to minimize the impact on small mammals.

^aCo-authors: Aleksandra Malinowska, Karol Zub, Anna Andruszkiewicz

T.15 Emma Boston

Extra-Mediterranean glacial refugia illuminated through the study of bats

Emma Boston <emma.boston@qub.ac.uk>^a
Quercus, Queen's University Belfast, United Kingdom

Abstract for talk The geographic ranges of European plants and animals underwent periods of contraction and re-colonisation during the climatic oscillations of the Pleistocene. The southern Mediterranean peninsulas have been considered the most likely refugia for temperate/warm adapted species. Recent studies however have revealed the existence of extra-Mediterranean refugia, including cryptic north west refugia during the Last Glacial Maxima (24 -14.6 kyr BP). Over the past six years our research group has studied the phylogeographic signal of several bat species widely distributed across western Europe. Bats, being our only volant mammals, offer good opportunity to study natural and potentially rapid recolonisation. Using mitochondrial DNA and palaeo-climatic modelling, this research changes how we view the re-colonisation of the British Isles post glacially, and highlights the unique history shared by many species on Europe's western fringe.

^aCo-authors: Paulo A. Prodöhl, Sebastien J. Puechmaile, Serena Dool, Daniel Buckley, Emma C. Teeling, W. Ian Montgomery

T.16 Selina Brace

Evolutionary histories from mammals of the Caribbean: insights from ancient DNA

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Natural History Museum London, UK

Abstract for talk Until very recently, the Caribbean hosted one of the world's most diverse insular land mammal faunas, with approximately 100 endemic species of rodents, insectivores, sloths and monkeys. However, Caribbean mammals have experienced the most severe post-glacial extinctions of any mammal fauna, and today only 15 putative species, mostly highly threatened capromyid rodents, survive in the region. In order to better understand the origins and evolution of this fascinating and formerly highly diverse fauna, we have been working on the recovery and analysis of ancient and degraded DNA from a range of Caribbean mammal remains. In this talk I will discuss our ongoing work to reconstruct the paleobiogeographic and evolutionary history of Caribbean mammalian fauna.

T.17 Mike Bruford

Conservation prioritisation using omic data: signal, noise and the power of domestication

Mike Bruford <brufordmw@cardiff.ac.uk>^a
Cardiff University, Wales, UK

Abstract for talk Omics studies are improving our ability to evaluate the role of demography and selection in shaping diversity in wild taxa. However, using omics data in management needs a framework that has yet to be fully developed, especially on the incorporation of different elements of omic diversity (eg neutral versus selected genomic regions, transcriptome variation, epigenomics) in population prioritization. In mammals, much of the core advances have come from domestic livestock and, increasingly, their wild relatives. Here we will review omic studies in mammals, contrasting what we have learned from livestock, their wild relatives and from undomesticated species - using examples from our laboratory and others. We will attempt to evaluate the likelihood that omic data will change biodiversity management, including identifying and prioritizing within-species conservation units.

^aCo-authors: Pablo Orozco-terWengel, Isa-Rita Russo, Zhijin Liu, Mario Barbato

T.18 Anthony Caravaggi

Quantifying endemic uniqueness and ecological equivalency between native and invasive leporids

Anthony Caravaggi <acaravaggi01@qub.ac.uk>^a
Queen's University Belfast, United Kingdom

Abstract for talk The Irish hare is endemic to Ireland, having been isolated from other mountain hares for ca. 30,000 years. It is behaviourally, ecologically and genetically distinct from other mountain hare sub-species populations in Europe. The European (brown) hare is a successful, globally invasive species and was introduced to Ireland in the late 1800s, representing a significant threat to the ecological integrity of the native species. We fitted Species Distribution Models (SDMs) for each species tested against one another and against other mountain hare populations in Europe. We hypothesise that: 1) Irish hares, having adapted to lowland grassland habitats in the absence of a competitor, are more ecologically equivalent to European hares than to other European populations of mountain hares, and 2) European hares are pre-adapted to the Irish landscape of pastoral agriculture interspersed by arable farming (i.e. European hare models will predict large areas of suitable habitat throughout Ireland).

^aCo-authors: Katie Leach, W. Ian Montgomery & Neil Reid

T.19 Barбора Cerna Bolfikova

Internal structure of Balkan refugium using white breasted hedgehog (*Erinaceus roumanicus*) as model species

Barbora Cerna Bolfikova <bolfikova@ftz.czu.cz>^a
Czech University of Life Sciences, Czech Republic

Abstract for talk Our study provides a description of the spatial distribution of genetic variability in the white breasted hedgehog (*E. roumanicus*), especially in the context of the Balkan and Central Europe. These areas are crucial for understanding the effects of Pleistocene climate oscillations on the genetics of species. Methods of landscape and population genetics have identified several isolated subpopulations within the surveyed area. An isolated population was found in Crete. This population was probably highly influenced by the mechanisms of island evolution. Significantly different from others was population from the Czech Republic, located in the secondary contact zone with *E. europeus*. This pattern may be result of interspecies interactions and possible introgression. Largest genetic distances among individuals, associated with the appearance of geographical barriers, were identified in the areas of Romania and south of the Balkan Peninsula. The project was supported by the GAUK 702214

^aCo-authors: Eliasova, K., Krystufek, B., Sandor, A., Loudova, M., Hulva

T.20 Ana Cerveira

Mate choice, hybridisation and hybrid fitness in two pine vole sister species, *Microtus duodecimcostatus* and *M. lusitanicus*

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Abstract for talk A crossbreeding experiment and mate preference tests were performed in the laboratory to determine the extent of reproductive isolation between the Mediterranean (*Microtus duodecimcostatus*) and the Lusitanian (*M. lusitanicus*) pine vole sister species. Crossbreeding revealed reduced fertility in hybrid females and sterility in hybrid males. Mate preference between opposite sex conspecifics vs heterospecifics and conspecifics vs hybrids was tested in a two-way choice test on the basis of chemical cues. Males of both pine vole species always preferred female conspecifics to heterospecifics or hybrids. Females of either species also showed a preference for conspecific males. Together these results show that both prezygotic (species specific mate recognition systems) and postzygotic (male hybrid sterility and female reduced fertility) barriers have evolved, and should limit hybridisation events between the two sister species under natural conditions to a great extent.

^aCo-authors: Ana. M. Cerveira (1), Joana A. Soares (1), Maria da Luz Mathias (1), Cristiane Bastos-Silveira (2)

T.21 Anaïs Charbonnel

Influence of recent global change on the range contraction of an endangered semi-aquatic mammal, *Galemys pyrenaicus*, in the French Pyrenees

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Laboratory Functional Ecology and Environment (Ecolab, UMR 5245
CNRS-UPS-INPT), France

Abstract for talk We compared an historical (1985–1992) and a current (2011–2013) sampling in the French Pyrenees to highlight habitat use and range shifts of the Pyrenean desman. Species Distribution Models were used to predict habitat suitability for the two periods while accounting for climate, hydrology (stream flow estimated through a hydrological model) and land-use changes. The range of the species has strongly contracted for the last two decades. Its distribution is mainly constrained by climate and hydrology. As climate change in the French Pyrenees is associated with warmer temperature and lower annual rainfall, which were highlighted to be unsuitable for the Pyrenean desman, it could be a severe threat. The observed range contraction was much higher than the one expected when accounting only for land-use, climate and hydrological changes that have occurred over the time period. Hence, other factors (e.g. biotic interactions) may have contributed to the recent reported decline of this species.

^aCo-authors: Pascal Laffaille, Marjorie Biffi, Frédéric Blanc, Mélanie Nemoz, Laëtitia Buisson

T.22 Pascale Chevret

Phylogeography, genetic structure and morphological evolution of the house mouse on the Orkney Archipelago

Pascale Chevret <pascale.chevret@univ-lyon1.fr>^a
Laboratoire de Biométrie et Biologie Evolutive, Lyon, France

Abstract for talk The house mouse has colonized numerous islands following human travelers. This has exposed it to a high variety of environments. The processes related to colonization can be traced using molecular markers and phenotypic variations. Preliminary works evidenced the repeated evolution of an elongated phenotype at the anterior part of the first upper molar in different islands. In 1992 and 2012, we collected more than 200 mice on eight Orkney islands. We performed a genetic analysis of these mice using mitochondrial D-loop sequences and 21 microsatellites. These datasets allowed us to determine the relationships of Orkney mice with Western European ones and the genetic structure within the archipelago. They were combined with a geometric morphometric approach of their teeth morphology. Both approaches evidenced a congruent structure, suggesting that tooth morphology evolved in a rather neutral way in isolated populations, and does not correspond to an adaptive divergence on islands.

^aCo-authors: Orkney field team, G. Ganem, S. Renaud

T.23 Tim Clutton-Brock

The evolution of cooperation and cooperative breeding

Tim Clutton-Brock <thcb@cam.ac.uk>

University of Cambridge, UK

Abstract for talk Focussing mainly on mammals, this lecture will explore the evolution of cooperation in general and of cooperative breeding in particular. Drawing on our research on Kalahari meerkats over the last twenty years, it will examine the costs and benefits of cooperation to helpers and dominant breeders and the strategies used by dominants to prevent subordinates from breeding. It will describe how singular cooperative breeding is associated with individual differences in female breeding success that exceed those observed in males in the most polygynous mammals and with intense competition between females for breeding opportunities. Finally, it will describe some of the unusual tactics used by females to gain and maintain breeding positions and their consequences for the evolution and ecology of cooperative breeders.

T.24 David Cooper

Predicted Pleistocene-Holocene range shifts of the tiger (*Panthera tigris*)

David Cooper <s1211133@sms.ed.ac.uk>^a

The University of Edinburgh/National Museums Scotland, United Kingdom

Abstract for talk The potential range shifts of tiger (*Panthera tigris*) populations over the Late Pleistocene and Holocene were modelled, in order to provide new insights into the evolutionary history of this endangered species. We used a maximum entropy, ecological niche approach to model potential distributions of tigers using bioclimatic conditions for the present day and Last Glacial Maximum (LGM), which were used to represent interglacial/glacial conditions of the Late Pleistocene. Results show that the maximum potential tiger range during modern climates would be continuous from India to Siberia. During the LGM, distributions are predicted to have contracted to India and Southeast Asia, and remained contiguous. Our data indicate the potential impacts of the Toba volcanic eruption (ca. 73ka) in separating Sunda Island and Asian mainland tiger populations. This study supports the idea of unimpeded gene flow between all populations (except Sunda tigers) throughout the Late Pleistocene and Holocene.

^aCo-authors: Andrew Dugmore, Bruce Gittings, Anne Scharf, Andreas Wilting, Andrew Kitchener

T.25 Joris Cromsigt

Rewilding Europe's large grazer community: how functionally diverse are the diets of Europe's three largest mammalian herbivore species?

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Dept. of Wildlife, Fish & Environmental studies, SLU, Sweden

Abstract for talk Rewilding is high on Europe's conservation and land-use agenda, defined as 'passive management of ecological succession with the goal of restoring natural ecosystem processes and reducing human control of landscapes'. A key example is the restoration of the process of grazing in (semi-) natural areas through introducing free-ranging cattle and horses as substitutes of extinct aurochs and tarpan. Europe is inhabited by a third large herbivore, European bison. The suggestion is that bison, as a large mixed feeder, fulfills a role that the pure grazers leave empty. However, we currently lack comparative analyses of the foraging ecology of these three grazers. This begs the question, how functionally diverse or redundant are their foraging behaviors and diets? I will discuss a unique pilot in the Netherlands, where we study the foraging ecology of free-ranging European bison, konik horse and Scottish highland cattle in a heterogeneous landscape of forest, grassland and shrubland.

T.26 Melanie Dammhahn

Energy-saving strategies and the pace-of-life syndrome in eastern chipmunks (*Tamias striatus*)

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Animal Ecology, University of Potsdam, Germany

Abstract for talk Based on a heuristic framework links between behavioural, physiological and life-history traits coevolved as response to long-term selection pressures forming the pace-of-life syndrome (POLS). Although POLS is supported at the between-species level, it remains open whether these links exist also among individuals within populations. Here, we tested for among- and between individual (co)variation between energy metabolism, behavioural phenotype and life-history in eastern chipmunks (*Tamias striatus*). We found large among-individual differences heterothermy expression in 55 individuals that were related to resting metabolic rate and had consequences for survival and reproductive success, indicating that among-individual differences in heterothermy-based energy-saving and metabolism are part of POLS. However, there was no clear support for covariation with behavioural traits. These findings are in line with other empirical studies and call for a refinement of the POLS concept.

^aCo-authors: Murray M. Humphries, Denis Réale

T.27 Kjell Danell

Mammalian Herbivory in Boreal Forests – Challenges and Methodology

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Abstract for talk I will focus on four main challenges in the studies on plant-mammalian interactions: (1) Food plant selection by the herbivore when feeding on a single food plant species, (2) food plant selection in plant stands with different composition and structure, (3) the role of induced defenses for future attack by herbivores, and (4) the impact of mammalian herbivores on ecosystem function and biodiversity. Firstly, I will deal with the herbivore selection pattern among genotypes, phenotypes and sexes of plants, and secondly on feeding behavior in plant stands composed of a mix of palatable and less palatable food plant species. Thereafter, I will explore if browsing on plants makes them more or less palatable later on. Finally, I will exemplify some ecosystem effects due to large ungulates. I will share my experiences on experimental design of field studies with different large herbivores in boreal forests. My focus will be more on approaches, design and techniques than on published results.

T.28 Joost de Jong

Genetic structure of European wild boar – 35k SNP analysis

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Resource Ecology Group, Wageningen UR, The Netherlands

Abstract for talk Wild boar populations of Europe have been subject to a variety of human influences. Notwithstanding its recent comeback all across the continent, populations were severely depleted during the modern era. As a means of restocking, in some regions animals were introduced from other countries. Furthermore, since the early time of domestication up till today, introgression with pigs has been polluting the genetic variation of the wild stock. In this study, we sought to obtain a better understanding of the impact of these anthropogenic influences on the genetic structure of wild boar, which is thought to be mainly shaped by separate colonization events from western and eastern refugia after the last glacial maximum. To this means, we genotyped 35K SNPs of hundreds of wild boar of tens of populations across Europe so as to accurately estimate the continental-wide genetic structure. In my talk, I will present our findings and discuss those within an natural and historical perspective.

T.29 Vlad Demartsev

Can hyraxes sing the blues? Possible evidence for musical features in male rock hyrax (*Procavia capensis*) complex calls.

Vlad Demartsev <demartsev@gmail.com>^a
Tel-Aviv University, Israel

Abstract for talk Most vocal signal structure research focuses on signals discriminate units. Such approach allows easy analysis of repertoire sizes and specific component production but reveals only first order features, not accounting for signal dynamics. Continuous features as phrase formation and unfolding of rhythms might bind discriminate elements into one percept. This received some attention in bird songs, but not in mammalian signaling. We tested male rock hyrax songs for temporal changes in structural and acoustical parameters. Our results show extension of singing bouts and increase in fundamental and peak frequencies towards a song ending. The increase is not gradual but culminating in the last 15% of a song. Known as cadence in music, this phenomenon conveys a sense of finality to listeners. In animal communication, it can serve to mark signal boundaries and to draw receiver attention. Currently we test if hyrax songs "musical" features are informative and if they affect listener behavior.

^aCo-authors: Amyiaal Ilany, Adi Barocas, Einat Bar-Ziv, Lee Koren, Eli Geffen

T.30 Karolina Doan

Influence of environmental changes and human activities on late Quaternary red deer populations.

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Abstract for talk Red deer is one of the most widespread and important game species in the world. Its current distribution have been strongly influenced by environmental changes and migration history during the Late Pleistocene. Geographic distribution of distinct mtDNA lineages is believed to have occurred due to isolation in refugia and recolonization events in interglacials. However, translocations that have been practiced by humans for millennia could have blurred natural genetic structure. In our study we analysed European and Asian samples from late Quaternary to investigate complex population history of red deer. Ancient DNA analysis and 14C dating revealed that the distribution of mtDNA lineages in the Pleistocene differs significantly from that observed today. We identified Pleistocene contact zones of European and Asian lineages in Crimea and the Urals, reconstruct possible migration routes of this species in the late Quaternary and correlate them with climatic events and human activities.

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T.31 Simon Dures

Transfrontier lion conservation: applying genetics across time and space

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Zoological Society of London, Institute of Zoology, United Kingdom

Abstract for talk As global landscapes and habitats become increasingly fragmented under pressure from anthropogenic development, it is essential that we gain a better understanding of species functional responses to such change, and the degree of connectivity between populations. I use genetics to assess the functional connectivity of lions in the Kavango-Zambezi Transfrontier Conservation Area (KAZA), a vulnerable, wide-ranging mammal which moves across multiple geopolitical boundaries. I determine the important isolating mechanisms across the landscape, both environmental and anthropogenic, with a view to guiding future management of this mammal. I further demonstrate how genetics can reveal unexpected cryptic patterns of gene flow that more traditional methods may miss. Finally, by incorporating DNA from 19th century museum collections we develop an assessment of changes in population structure and its relevance to conservation status.

^aCo-authors: Chris Carbone, Vincent Savolainen, Dada Gottelli

T.32 Nina E. Eide

Status and conservation goals for the critically endangered Arctic fox in Scandinavia. Is the mission completed?

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Norwegian Institute for Nature Research (NINA), Norway

Abstract for talk The arctic fox is listed as critically endangered, despite 80 years of protection in Scandinavia. Following intensive action programs over the last 15 years, the population has increased from less than 50 to more than 200 individuals. Sub-populations are reestablished and the connectivity is about to be restored. Actions comprised of red fox culling, supplemental feeding and release of captive breed foxes. Long lasting conservation programs need goals, to be targeted and effective, to keep priority for funding within environmental agencies, as well as legitimacy in the society. Although the Scandinavian arctic fox population has increased, actions are needed to reach a viable population. We calculated the carrying capacity of different subpopulations based on landscape productivity. Distance from carrying capacity and importance for connectivity, target the need for actions at the level of sub-populations, trying to estimate the date until mission completed.

^aCo-authors: Anders Angerbjörn, Arild Landa, Bodil Elmhagen, Karin Noren, Øystein Flagstad, Heikki Henttonen, Tuomo Ollila

T.33 Robert Ekblom

Development of Genomic Resources for the Conservation of the Scandinavian Wolverine Population

Robert Ekblom <robert.ekblom@ebc.uu.se>^a
Uppsala University, Sverige

Abstract for talk Natural selection may rapidly lead to local adaptation in genetically structured populations of threatened species. With the advent of high throughput sequencing and genotyping it has now become possible to identify adaptive genetic variation at a genome wide scale. I will present data from a conservation genomics project of the wolverine (*Gulo gulo*). Scandinavian wolverine populations are subjected to habitat fragmentation and high mortality from poaching due to conflicts with livestock herders. Genetic monitoring is already an important part of the national conservation programmes for this species in Sweden and Norway, but the resolution and applications of genetic data have been hampered by a lack of genomic tools. By whole genome sequencing, population re-sequencing and SNP genotyping, we now take this system to a new level. We describe how these novel genomic resources are utilised in monitoring and to investigate genomic signatures of population subdivision of this species.

^aCo-authors: Linnéa Smeds, Birte Brechlin, Malin Johansson, Jessica Magnusson, Hans Ellegren

T.34 Bodil Elmhagen

Carnivore interactions and climate change: Top-down and bottom-up cascades in time and space

Bodil Elmhagen <bodil.elmhagen@zoologi.su.se>
Stockholm University, Sweden

Abstract for talk Top-down cascades triggered by changes in large carnivore status and bottom-up cascades triggered by climate change can both restructure ecological communities, but how do these cascades interact? Theory predicts that top-down cascades should be more pervasive in productive (southern) ecosystems, but climate warming should activate bottom-up cascades. In unproductive (northern) ecosystems, bottom-up cascades should favour resource-demanding species and strengthen carnivore top-down cascades. I will explore cascade theory in light of observed transformations of the Fennoscandian mammal community since the 19th century: Top-down cascades following large carnivore extinction and recolonisation, and bottom-up cascades causing northern advance in southern mammals, retreat in northern mammals, changes in community dynamics and - potentially - top-down cascades.

T.35 Alan Fredy Eriksson

Environment and host species composition effects on highly host-specific assemblages of ectoparasites of bats

Alan Fredy Eriksson <aferiksson@hotmail.com>^a
Laboratório de Ecologia, CCBS, UFMS, Brazil

Abstract for talk It is expected that assemblages of host-specific parasites would be correlated to the host species composition. However, on a large scale, available data supports that environmental traits are the most important factors shaping these assemblages. In small scale we predicted that assemblages of local specialist ectoparasite would depend on host species composition more than on the local environment. We addressed this by capturing bats and collecting the ectoparasites in nine sites in the Brazilian savannah, distant 0.6 to 17.3 km from each other. We measured vegetation cover and soil exposition as environmental variables. The assemblage of ectoparasites was correlated to host-species composition (p 0.01, Mantel), but not to the environment. Therefore, on a small scale, ectoparasites do not tend to switch among species of hosts, and environmental characteristics have not shown effect. Results indicate that patterns of ectoparasite assemblages can differ drastically at different scales.

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T.36 Rasmus Erlandsson

Home alone - Juvenile survival in relation to maternal experience and loneliness

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Abstract for talk Reproductive experience is linked to juvenile survival in a wide range of mammals, e.g. due to different foraging capacity and predation rates. We studied how reproductive experience and prey availability affected arctic fox (*Vulpes lagopus*) juvenile summer survival rates, using data from 7 years (including a complete small rodent cycle), comprising data from 69 litters and 449 cubs. Small rodent abundance positively affected survival, but cubs of first time breeding females were sensitive to low prey abundance. We limited the direct effect of low prey abundance with supplementary feeding. Instead we suggest that intra guild predation is the main cause of mortality. We also found a association between survival and cub attendance, suggesting that parental behaviour affects predation risk. We propose that a prey switch in top predators related to small rodent abundance cause fluctuations in intra guild predation pressure, and that inexperienced females leave their cubs more home alone.

^aCo-authors: Tomas Meijer, Stockholms universitet, Sofie Wagenius, Stockholms universitet, Anders Angerbjörn, Stockholms universitet

T.37 Erik Ersmark

The fall and rise of the Scandinavian brown bear

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Zoology Department, Stockholm University and the Swedish Museum of Natural History, Sweden

Abstract for talk The ca. 100-year-old bottleneck in the Scandinavian brown bear was investigated, using mitochondrial and microsatellite DNA markers on samples from before and after the event. Simulation and multivariate analysis suggested the same genetic structure for the historical and modern samples, which are clustered into three subpopulations in southern, central and northern Scandinavia. However, the southern subpopulation appears to have gone through a marked change in allele frequencies. When comparing the mtDNA diversity in the whole population, we found a major decline in haplotype numbers across the bottleneck. However, the loss of autosomal genetic diversity was less pronounced, although a significant decline in allelic richness was observed in the southern subpopulation. These results indicate a recent loss in genetic diversity, and also that the current genetic structure may have been caused by historical ecological processes rather than recent anthropogenic persecution.

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T.38 Khammar Farida

Reproductive and metabolic survival strategies in some Saharan rodents

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USTHB, Algeria

Abstract for talk The ecophysiological processes of reproductive and metabolic pattern in desert rodents are imposed by the harsh environment constraints. Our study focused on the reproductive-metabolism seasonal interactions in some Saharan Gerbils. In the diurnal *Psammomys obesus*, testicular endocrine activity was highest in autumn and winter then decreased throughout spring. However the reproductive seasonal cycles of nocturnal *Meriones libycus* and *Gerbillus tarabuli* have an active period during spring and lowest activity in summer until early winter. In these three species gonadal hormones deprivation induce increases in adrenal cortex volume with hypertrophy of reticularis zona. Moreover, glucocorticoid and plasma ACTH levels were also altered. Furthermore, for all species adrenals expressed androgen receptors indicating direct effect of gonadal hormones in adrenal activity. The knowledge of adaptive strategies in Saharan rodents may help to conserve these species in their biotope.

^aCo-authors: Zaina Amirat, Abdelouafi Benmouloud, Naouel Aknoun-Sail, Yamina Zatra, Arezki Kheddache, Jean-Marie Exbrayat, Osborne Almeida and Farida Khammar

T.39 Søren Faurby

Historic and prehistoric human-driven extinctions have reshaped global mammal diversity patterns

Søren Faurby <faurby@mncn.csic.es>^a
MNCN, Spain

Abstract for talk To assess the extent to which humans have reshaped Earth's biodiversity, we estimated natural taxonomic, functional, and phylogenetic diversity patterns for all historically extant mammals (5747 species) and compared them to current patterns. We find drastic changes between current and natural diversities virtually everywhere outside sub-Saharan Africa. The changes were most drastic for terrestrial megafauna but also important when looking across all mammals. We show that the current diversity patterns have been drastically modified by current and historical anthropogenic influences. These changes in diversity patterns are large enough to influence conclusions in studies on the ecological and evolutionary drivers of diversity gradients. Our results show that the fundamental diversity patterns in nature have been reshaped by human-driven species and range losses, highlighting that humans have become a major force in the Earth system.

^aCo-authors: Jens-Christian Svenning

T.40 António Ferreira

Factors affecting southern water vole (*Arvicola sapidus*) detection and occupancy probabilities in Mediterranean farmland

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CIBIO Évora, Portugal

Abstract for talk Imperfect detection (ID) may greatly affect predictions on species occupancy probabilities (OP), though it is still largely disregarded in many occupancy studies. We modelled for the first time OP of southern water vole (SWV) patchy populations, while accounting for ID. Based on repeated presence sign searches conducted in autumn and winter, we used a spatially explicit occupancy modelling approach to test the effects of vegetation characteristics, sampling effort, observer experience, and rainfall on SWV detection probability. We then tested whether OP relates to patch size, isolation, and habitat quality, after correcting for ID. Detection probabilities were high (over 0.70) and little affected by covariates. After controlling for ID, OPs were about 0.3 in both seasons and were positively related to patch size and water presence, and negatively to patch isolation. Results suggest that failure to control for ID may be negligible in SWV but should be considered for robust OP estimates.

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T.41 Pablo Ferreras

Do widespread generalist carnivores segregate their niches? A multidimensional study using red foxes and stone martens in Mediterranean Europe

Pablo Ferreras <pablo.ferreras@uclm.es>^a

IREC (Spanish Game Research Institute), CSIC (Spanish Research Council), Spain

Abstract for talk Interspecific relationships between generalist species involve several ecological dimensions. The red fox (*Vulpes vulpes*) and the stone marten (*Martes foina*) are two generalist predators coexisting in large areas of Europe. We studied three-dimensional niche partitioning between them in two Iberian Mediterranean areas using three data sources: camera-trapping (spatial, temporal), radio-tagged individuals (spatial) and analysis of scats (trophic). Occupancy models indicate that the presence of each species was independent of the other. At the individual level, most stone martens were located with 25% probability within red fox home ranges. Their temporal overlap was overall large (min. 64%), but lowest in the scrubland, where most resources were found. Diets of both species highly overlapped (Pianka's $O:0.6-0.9$), and were based in each season on the most abundant foods. Results indicate that the coexistence between both species is mediated by a shared use of the most abundant resources.

^aCo-authors: Francisco Díaz-Ruiz, Paulo Célio Alves and Pedro Monterroso

T.42 Øystein Flagstad

Genetic rescue in a severely inbred wolf population: A natural experiment

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NINA, Norway

Abstract for talk In small and highly inbred populations, the introduction of only a few immigrants may increase the vital rate significantly. Here, we demonstrate significantly higher pairing and breeding success for offspring to immigrants compared to offspring from native, inbred pairs after a recent incident of natural immigration to the severely inbred Scandinavian wolf population. We argue that inbreeding depression is the underlying mechanism for the profound difference in breeding success. Highly inbred wolves may have lower survival during natal dispersal as well as competitive disadvantage to find a partner. Moreover, the likelihood of breeding among paired individuals appears to be negatively affected by inbreeding. Indeed, our data demonstrate the profound impact single immigrants can have in small, inbred populations, and is one of very few documented cases of genetic rescue in a population of large carnivores.

^aCo-authors: Mikael Åkesson, Olof Liberg, Håkan Sand, Petter Wabakken, Staffan Bensch

T.43 Øystein Flagstad

Hybridization and domestic introgression in the wild: The extinction of a natural arctic fox population

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Abstract for talk Scandinavian arctic foxes were previously abundant, but declined dramatically in the early 1900s. Despite legal protection since 1930, the population has failed to recover and is today classified as critically endangered. Habitat fragmentation, unstable food resources, red fox expansion, and allee effects are major challenges. However, hybridization and genetic introgression from domestic foxes may pose an additional and severe threat to this small population. Here, we describe a hybridization event in the Southern part of the population, followed by genetic swamping until wild foxes had disappeared from the area a few years later. A single line of domestic foxes that were kept at a tourist hut situated nearby were the source of the domestic introgression. Our data demonstrate massive escape or release from this site, which in turn contributed to the extinction of the original wild population.

^aCo-authors: Nina Eide, Arild Landa, Karin Noren

T.44 Laurent Frantz

Ancient dog genome provides insights into the evolutionary history of dogs.

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University of Oxford, United Kingdom

Abstract for talk Dogs provide an extreme case of phenotypic alteration by humans through artificial selection. Such strong selection has left evident footprints in the genome of modern dogs. However, we know very little about the origin of this process. To address this question we sequenced and analysed the genome of a 4,000 years old dog from Newgrange (Ireland). We generated a high quality ancient genome, providing the oldest whole genome of a domestic canid to date. We analysed our ancient sample together with over 100 publicly available canid genomes. This large data set allowed us to tackle multiple questions such as: i) assessing the existence of an ancestry continuum in European dogs since the Neolithic ii) comparing the strength of inbreeding and artificial selection in ancient and modern dog genomes. Together our results provide a unique insight into the ancestry and the breeding history of dogs over the last 4,000 years.

^aCo-authors: Victoria Mullin, Greger Larson and Dan Bradley

T.45 Laurent Frantz

Genomics reveal the importance of gene flow and strong artificial selection during pig domestication.

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University of Oxford, United Kingdom

Abstract for talk The process of animal domestication led to striking phenotypic changes. Traditional models of domestication involve strong bottlenecks and reproductive isolation between wild and domestic forms. However, novel views suggest the existence of gene flow during the process of animal domestication but such lack of reproductive isolation has yet to be tested. Moreover, the possibility of gene flow between wild and domestic raises question about the mechanisms that maintains morphological differentiation. Here I will present novel results based over 100 genome sequences from wild and domestic pigs. I will first demonstrate how models involving gene flow between wild and domestic pigs fits this data set significantly better than traditional models with reproductive isolation. Secondly, I will show how artificial selection has counteracted the homogenising effect of gene flow; thus allowing for differentiation between wild and domestic pigs at important traits, such as body length.

T.46 Pavel Gol'din

Marine mammal fauna of the Middle and Late Miocene of the Central and Eastern Paratethys: chronology and biogeography

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Department of Natural History and Palaeontology, The Museum of Southern Jutland, Denmark

Abstract for talk The regional fauna of marine mammals included baleen whales, toothed whales, phocid seals and unidentified sirenians. At least two chronological fauna complexes can be identified: the earlier one (Badenian-Sarmatian or Chokrakian-Bessarabian), with the marine environments, and the later one (Pannonian or Chersonian), with the increasing brackish environments. All family-level groups were cosmopolitan; however, most of genera were unique for the region. The greatest diversity of genera, including most of the cosmopolitan or Atlantic taxa, was recorded from the earlier marine complex, but lately the local taxa intensively evolved (Cetotheriinae and Phocinae). No links with the faunas of the Gram Formation (Denmark) and Mediterranean localities were observed, whereas there were some affinities with the south North Sea. Two trends in morphological evolution across the taxa can be traced: dwarfism and pachyostosis of the skeleton.

T.47 Anjali Goswami

The macroevolutionary consequences of phenotypic integration: from development to deep time

Anjali Goswami <a.goswami@ucl.ac.uk>
University College London, United Kingdom

Abstract for talk Phenotypic integration is a pervasive characteristic of organisms. Analyses of living and fossil mammals have demonstrated that patterns of integration are conserved across large clades, but significant variation exists. Heterochronic shifts related to mammalian reproductive strategies are reflected in postcranial skeletal integration and in coordination of bone ossification, opening the possibility of identifying reproductive strategies in stem mammals. Integration and modularity have also been hypothesized to shape morphological evolution, and analyses confirm that trait integration can influence both the trajectory and magnitude of evolutionary change, but not necessarily its rate. Simulations also demonstrate that phenotypic integration can produce both more and less disparate organisms than expected by repartitioning variance in preferred directions. This effect can also be expected to favour convergent evolution and may also mediate organismal response to climate change.

T.48 Marianne Haage

Evolutionary maintenance of personality via spatiotemporal fluctuations in the environment - A field experiment on European mink (*Mustela lutreola*)

Marianne Haage <marianne.haage@zoologi.su.se>^a
Stockholm University, Sweden

Abstract for talk Little is known on how variation in personality is maintained over evolutionary time. Fluctuating selection pressure due to spatiotemporal environmental variation has been suggested as a mechanism but it is unknown if it is a major mechanism or if different mechanisms act on different personality trait domains. Here we used a European mink reintroduction programme to test if personality is maintained by fluctuating selection acting via survival, and if there are differences between boldness, sociability and exploration. Animals were personality tested and released in two different years and islands. Survival was monitored by radio-tracking. Sociability had no impact on survival and boldness was positive. Exploration, however, was negative or positive depending on year/island. This shows a complex relationship between personality and survival and suggests that fluctuating selection maintains exploration whilst boldness and sociability might be maintained by other mechanisms.

^aCo-authors: Tiit Maran, Ulrika Alm Bergvall, Bodil Elmhagen, Anders Angerbjörn

T.49 Marko Haapakoski

Antiparasitic medication increases vole survival in fragmented habitat

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University of Jyväskylä / Konnevesi Research Station, Finland

Abstract for talk Habitat fragmentation is known to cause population declines but the mechanisms leading to the decline are not fully understood. Also parasites may affect negatively on host fitness. We tested how antiparasitic medication (Stronghold) affects bank vole (*Myodes glareolus*) behavior and fitness in fragmented enclosures consisting of either non-fragmented (one patch) or fragmented (four patches) habitats of the same total area. Especially non-medicated control males in fragmented habitat moved more in the risky matrix compared to medicated males. Male survival was significantly poorer in fragmented habitat, especially among the control males as well as among the most active males who moved more during radio tracking. Medication seemed to reduce the number of females that a male was siring pups with, but we found no other fitness effects of medication. Our results suggest that parasites may play important role in the fitness of animals especially in the fragmented habitat.

^aCo-authors: Juuli Alm, Janne Sundell, Hannu Ylönen

T.50 Klaus Hackländer

WORKSHOP TALK: Impact of EU Common Agricultural Policy on hares

Klaus Hackländer <klaus.hacklaender@boku.ac.at>
University of Natural Resources and Life Sciences, Vienna (BOKU), Austria

Abstract for talk Hares followed man after agricultural land use lead to open landscapes suitable for this lagomorph species. In line with land use changes habitat suitability for small game varied over the last centuries. Currently, the fate of European hares is predominantly affected by the Common Agricultural Policy (CAP) of the European Union and the global market of agricultural products. We studied the effects of land use, field size, crop types on hares dwelling in arable land for 15 years. With the help of telemetry, hunting bag analysis, food selection indices and reproductive parameters I will show the challenges for hares in our current agriculture and I will present future directions to reconcile sustainable land use and the conservation of small game species.

T.51 Thomas J.D. Halliday

The Cretaceous-Palaeogene mass extinction and eutherian evolutionary dynamics

Thomas J.D. Halliday <thomas.halliday.11@ucl.ac.uk>
University College London, United Kingdom

Abstract for talk The first uncontested crown placental mammal fossils appeared in the early Palaeogene. Many studies find no change in evolutionary rate or disparity for eutherian mammals across the Cretaceous-Palaeogene (K-Pg) boundary, but do not explicitly consider early Palaeogene taxa, largely due to a lack of a resolved phylogeny. I conducted the largest cladistic analysis of Cretaceous and Paleocene mammals to date, dating the resultant trees using stochastic methods, and finding a Cretaceous origin but Cenozoic diversification of Placentalia. Ancestral character states were reconstructed on the dated trees, and morphological disparity and rates of evolution through time were calculated. Rates of evolution and range-based disparity increased at the K-Pg boundary, while variance-based disparity reduced in the Maastrichtian, increasing only in the late Paleocene. This suggests that a rapid diversification followed by increased ecological disparity characterised early placental evolution.

T.52 Guillaume Halliez

Variation of predation pressure in a context of cyclic population outbreaks of grassland voles (*Arvicola scherman*).

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Fédération Départementale des chasseurs du Doubs, Université de
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Abstract for talk We address the question of how predators may respond to alternative prey presence in a context of multiannual variations of vole population. We recorded predation on 400 lures (especially designed sausages) for 4 nights using camera traps in the Jura Mountains. 50% of the observed predators were mammals (mostly red fox) and 50% birds (mostly corvids). 50% of the lures were found by predators after 4 nights. Time to lure discovery was 1.2 times larger for mammals than birds. Lure survival was positively correlated to vole abundance but in an extremely noisy context, as was predator abundance. Lures were found quicker during vole population increase. Increase in lure survival and in lure consumer abundance during the peak of vole density indicate a prey switching and suggest a dependent relationship between predator (red fox, corvids) abundance and vole abundance.

^aCo-authors: François Renault, Pauline Defrasne, Clémence Becel, Gilles Farny, Patrick Longchamp, Geoffroy Couval, Denis Truchetet, Patrick Giraudoux

T.53 Oliver Hawlitschek

The project **Barcoding Fauna Bavarica: Why DNA barcoding is also useful for mammals.**

Oliver Hawlitschek <oliver.hawlitschek@gmx.de>^a

Staatliche naturwissenschaftliche Sammlungen Bayerns, Zoologische Staatssammlung München, Münchhausenstr. 21, 81247 Munich, Germany

Abstract for talk DNA barcoding uses the COI gene as a standard for species identification, but depends on a reliable reference database. The project 'Barcoding Fauna Bavarica' (BFB) is one of the most successful barcoding campaigns worldwide. More than 14,000 of the ca. 34,000 Bavarian animal species have been barcoded since 2009, including ca. 70% of mammal species. All data is uploaded to the Barcode of Life Database (BOLD), in which sequences are assigned a Barcode Index Number (BIN) and clustered to operational taxonomical units highlighting potential cases of synonymy or cryptic diversity. A 100% match between BINs and existing taxonomy could not be achieved in any of the animal groups previously studied in the BFB project. Mammals so far are the first group studied with a 100% match. This confirms the status of some previously debated species, facilitates identification from hair, tissues, faeces, or dry museum material, and underlines the potential of DNA barcoding for studying mammal faunas.

^aCo-authors: Jérôme Morinière, Axel Hausmann, Gerhard Haszprunar

T.54 Matt Hayward

No teddy bears picnic-a review of ungulate predation and prey selection by the brown bear in the Holarctic

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Abstract for talk We reviewed the literature of brown/grizzly bear diet from throughout the Holarctic (incl.data from Russia that have been excluded from reviews until now). Ungulate meat made up about 17.0% of brown bear diet, although those in North America kill significantly more ungulates than those in Eurasia. We contend that the arrival of humans in North America and the subsequent megafaunal extinctions have opened up an increasingly carnivorous niche for the brown bear. Ungulates peak in the diet of brown bears in spring, immediately after hibernation, when ungulate young are born and the bears are able to traverse snow more easily than their prey. A second peak in ungulate predation occurred in autumn in North America. Brown bears at higher latitudes include more ungulates in their diet. Brown bears preferentially prey on moose throughout its range, with red deer/elk and wild boar also important secondary prey. Bear density is related to that of moose.

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T.55 Matti Heino

Temporal genetic variation of the Saimaa ringed seal (*Phoca hispida saimensis*) in the 20th century

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Abstract for talk The Saimaa ringed seal (*Phoca hispida saimensis*) is a highly endangered subspecies of ringed seal which inhabits the Lake Saimaa in Finland. In this study we examined how the genetic variation of the Saimaa ringed seal has changed during the 20th century, when mainly human-caused decline in the population size has been observed. We sequenced part of the mitochondrial control region of 50 museum specimens which originate from the late 19th century till the 1970s, and included genetic data from 215 close to modern day individuals in the analyses. The results show that part of the genetic variation of the Saimaa ringed seal has most likely been lost during the 20th century. Additionally, the population size of the Saimaa ringed seal seems to have declined already during the 19th century, but during the 20th century the decline has become more pronounced. Our study highlights the usefulness of DNA extracted from museum material in deciphering the demographic histories of populations.

^aCo-authors: Jenni Harmoinen, Minna Ruokonen, Jukka U. Palo, Mia Valtonen, Tommi Nyman, Mervi Kunnasranta, Malgorzata Pilot, Jouni Aspi

T.56 Heikki Henttonen

Eco-epidemiological research on rodent-borne pathogens

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Abstract for talk Eco-epidemiological research on rodent-borne (robo) zoonotic pathogens is expanding. I will review some general trends in robo research, will pay attention to the importance of understanding the demography and seasonal heterogeneity of rodent populations and in population structure. Then I will use as a model system the long-term comparative research on Puumala hantavirus in Europe. Hantaviral epidemiological patterns depend on the dynamics of reservoir species, and in Europe there are biome-dependent differences in the causes of rodent fluctuations, masting vs specialist predation. In the large collaborative EU projects EDEN and EDENext our aim was to understand the human epidemiology of hantaviral disease between boreal and temperate Europe, in different climatic conditions. In addition to host population dynamics, we have studied e.g. the roles of landscape ecology, landscape genetics, immunogenetics, virus shedding, virus survival, viral kinetics in host and impact on host.

T.57 Jeremy Herman

Natural selection in a common small mammal: evidence from molecular data and implications for phylogeographic inference

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National Museums Scotland, UK

Abstract for talk The Eurasian field vole (*Microtus agrestis*) has been the subject of numerous phylogeographic and other molecular evolutionary studies. Both existing mitochondrial and new Y-chromosome sequence data reveal an extremely skewed distribution of genetic variation within the British Isles. Single Y-chromosome intron (SMCY7) and mitochondrial (cytochrome b) haplotypes predominate in southern Britain, contrary to the much higher diversity that we have found in northern Britain and in the rest of the species' range, respectively. This pattern may derive from a selective sweep affecting the genome of field voles in southern Britain. Evidence for such an event is examined using a multi-locus approach incorporating the maternally-inherited mitochondrial sequences, the paternally-inherited Y-chromosome intron and a series of microsatellite markers representing the autosomal nuclear genome. The wider implications of selective sweeps for phylogeographic inference are considered.

^aCo-authors: Joanna Stojak, Maarit Jaarola, Jan M Wójcik, Jeremy B Searle

T.58 Anne Hertel

Effects of hunting on foraging behavior and efficiency: Do bears trade off good forage for security?

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Abstract for talk In Sweden, brown bears rely on bilberries to increase body mass for hibernation. However, human disturbance, like hunting, affects habitat use and activity patterns, and may decrease foraging efficiency. We identified feeding locations from movement trajectories of seven GPS collared bears in the two weeks before and after onset of the hunting season. In comparison to random locations bears selected for locations with significantly higher bilberry abundances. We further found strong evidence that circadian foraging patterns were affected by onset of hunting. Foraging peaked during the main activity periods in the morning and afternoon, in the first two weeks. Once the hunting season started, activity patterns were less pronounced and bears foraged less efficiently. This study shows that bears selectively choose high abundance bilberry foraging locations. But also that hunting affects foraging behavior and efficiency in a nutritionally critical period of the year.

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T.59 Russell Hill

Human observers modulate perceived landscapes of fear

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Durham University, UK

Abstract for talk Nonlethal effects of predation risk have substantial impacts on almost every aspect of prey behaviour. We examined the landscape of fear of samango monkeys (*Cercopithecus mitis erythrarchus*) in the Soutpansberg Mountains, South Africa. In a spatial analysis, risk from eagles was more important than ecological factors such as food availability in determining ranging behaviour, but we found no effect of the landscape of fear from leopards despite previous studies highlighting its importance to other sympatric primates. We thus tested whether the 'human shield effect' could account for this using giving up densities. Human observers lowered the perceived risk of terrestrial predators and so affected foraging decisions near ground level. However, these effects did not extend to another site where monkeys were exposed to risk from both humans and domestic dogs. These results have significant implications for future studies of predation risk based on habituation and observational methods.

^aCo-authors: Katarzyna Nowak, Ben T. Coleman

T.60 Emilia Hofman-Kaminska

Patterns of habitat use and diet of European bison and moose in Europe

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Abstract for talk European bison and moose are the largest extant herbivores in Europe, which survived climatic and environmental changes after last glaciation. However, contemporary distribution range, abundance and conservation status of these two species are different. We investigated pattern of habitat use and diet of the two herbivores by means of stable isotopes ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) concentration analysis in bone collagen. Modern populations of bison showed high variation of habitat use and diet in comparison to moose. This probably reflects the variety of habitats into which the bison were reintroduced during the restoration of the species and more natural habitat selection in moose populations. The only factor explaining $\delta^{13}\text{C}$ variation was forest cover in both species. Habitat use by modern bison populations differed from this by Early Holocene bison, while was mostly similar when comparing modern and Early Holocene moose. The study financed by the NCN 2013/11/B/NZ8/00914 grant.

^aCo-authors: Herve Bocherens, Rafal Kowalczyk

T.61 Tim Hofmeester

Traits, predators and deer as determinants of tick burdens of rodents: implications for Lyme borreliosis risk

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Wageningen University, the Netherlands

Abstract for talk The distribution of vectors over different hosts is a key determinant of vector-borne pathogen prevalence. To understand which factors influence the distribution of vectors over hosts, we compared *Ixodes ricinus* burdens of bank voles (*Myodes glareolus*) and wood mice (*Apodemus sylvaticus*) between 20 forest fragments across the Netherlands. As explanatory variables we measured species, sex and weight of the rodents; the abundance of deer as a proxy for tick density and; the abundances of rodents and predators as determinants of rodent spatial behaviour. We found that tick burden was best explained by a model including all factors. The abundance of predators and deer had the highest standardized regression coefficients. This suggests that behavioural responses of rodents to predation risk and the abundance of ticks in the environment were the main determinants of rodent tick burden. Tick burden was positively correlated with the density of questing nymphs infected with *Borrelia afzelii*.

^aCo-authors: Patrick Jansen & Sip van Wieren

T.62 Katja Holmala

Avoiding predator or finding prey – habitat use and activity of Red fox in relation to Eurasian lynx in Southern Finland

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Abstract for talk The habitat use and circadian activity of red foxes (*Vulpes vulpes*) and Eurasian lynx (*Lynx lynx*) were studied in southern Finland between 2009 and 2014. The aim was to find out how red fox habitat use is affected by both landscape (available habitat types) and the presence of a larger predator. Also the asymmetry of the circadian activity of these two species was studied. Foxes showed individual variation in their habitat selection/use but selected fields in landscape level and sparse tree cover habitats in home range level. There were significant differences in the composition of day and night time habitats used by foxes. During night time foxes seemed to use more such areas that lynxes used less, for example fields and areas near human infrastructure and were less often in forest. Analysis of the circadian activity further demonstrated the predator avoidance by showing that fox activity continued longer in late mornings and early evenings when lynxes were less active

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T.63 Patrick Jansen

eMammal, a system for processing images from large-scale camera-trap surveys

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Smithsonian Tropical Research Institute & Wageningen University, Panama & The Netherlands

Abstract for talk Camera traps are non-invasive survey tools for terrestrial mammals that produce observations with a photo voucher and with a community context. While they can be used at large scales relatively cheaply and easily, surveys with camera traps also produce massive amounts of images that can overwhelm researchers. Moreover, the images and data are often not stored safely, and are thus ephemeral and at risk. We present the cyberinfrastructure of eMammal, a workflow to efficiently process and permanently archive camera-trap photos, and a platform for collaboration among researchers and citizen scientists. eMammal includes custom software, computer vision, cloud-based workflows, expert data review, and a variety tools. The process moves photos and data into a permanent repository where they can be curated. eMammal aggregates data from projects across the world to be used for research and conservation. eMammal can be used to create a permanent record of the rapidly changing mammal communities

^aCo-authors: Robert Costello, Tavis Forrester, William J. McShea, Roland Kays

T.64 Thomas Secher Jensen

Wolf recolonization of Denmark

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Natural History Museum, Aarhus, Denmark

Abstract for talk In November 2012, after 200 years of absence a male wolf was found dead in northern Denmark. Since then visual observations, discoveries of dead domestic animals and game species, finds of faeces, tracks and camera trappings, have added to the knowledge of wolf in Denmark. DNA analysis and camera traps reveal that wolves have been roaming in most parts of the peninsula of Jutland, although most samples come from Central Jutland, in areas with widespread forests and heathland. Several wolf attacks on sheep and lambs have taken place. Until now, 23 individual wolves have been identified through DNA analysis. Two of these can be traced back to a German wolf pack, and two others are closely related to a Polish pack, both at least 800 km away. Most individuals are only found once, however, one individual has been detected in 9 locations over the past 2 years. Individual wolves are both males and females, although females were documented much later than males; there is no proof of cubs.

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T.65 Chris Johnson

Top predators and ecological cascades over a continent: dingoes, devils and diversity in Australia

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University of Tasmania, Australia

Abstract for talk This paper reviews the significance of top predators in maintaining biodiversity at continental scales, as exemplified by Australia. On mainland Australia, the dingo is a keystone species that regulates population size of generalist large herbivores and suppresses mesopredator abundance and behaviour. It is also regarded as a threat to livestock, and so is widely persecuted. Reduction of dingo populations causes cascading effects that result in extirpation of smaller mammals and shifts in vegetation structure and composition. On the large island of Tasmania, the devil is in rapid decline because of a contagious cancer. Early evidence suggests that this may have led to changes including release of native herbivores and feral cats. Effective protection of biodiversity and ecological function will depend on maintenance and restoration of these predators.

^aCo-authors: Michael Letnic (Uni New South Wales), Menna Jones (Uni Tasmania)

T.66 Vendela K. Lagerholm

Using ancient DNA to examine the postglacial consequences of range contractions in cold-adapted species

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Swedish Museum of Natural History, Sweden

Abstract for talk During the last glaciation, most of mid-latitude Europe was inhabited by several species that today are only found in Arctic or Alpine regions. As temperatures started to increase at the start of the Holocene, cold-adapted animals disappeared from these southern lowland regions. However, it has been unclear whether these populations became extinct, or whether they survived by moving northwards or into high-altitude regions in concert with the changing climate. This presentation will outline the results from several recent studies where ancient mitochondrial DNA from cold-adapted species has been recovered from Late Pleistocene bones and teeth in an attempt to examine to what extent southern populations contributed to the gene pool of contemporary Arctic taxa.

T.67 Eva Kallio

Endemic pathogen infections and bank vole fitness

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Abstract for talk It is now widely acknowledged that endemic pathogens, which do not cause clinical illness in their hosts, may still affect fitness by reducing the survival and/or reproductive rates of infected individuals. Consequently, endemic pathogens may alter their host populations, which may be translated into the transmission dynamics of the pathogen itself. Understanding these effects has fundamental epidemiological relevance when the pathogen is zoonotic, as the disease dynamics in the host population determine the risks posed to humans. We have studied the effect of endemic pathogens, including rodent- and tick-borne infections, on the bank vole fitness and show that infections may have both negative and positive influence on the host fitness, depending on the host age and study season. We will discuss the potential host population level and pathogen transmission dynamics consequences of the fitness effects.

T.68 Veli-Matti Kangas

Evidence of post-glacial secondary contact and subsequent anthropogenic influence upon the genetic composition of Fennoscandian moose (*Alces alces*)

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Abstract for talk In this study, we investigated whether genetic evidences for the post-glacial re-colonisation and more recent anthropogenic processes are detectable in a present-day population of moose (*Alces alces*). Altogether 574 Finnish and Russian Karelian moose were genotyped at 16 microsatellite loci, in addition to 224 individuals sequenced at mtDNA control-region. Bayesian clustering, multivariate and spatial autocorrelation methods were applied together with F-statistics to study the genetic structures. The demographic history of the species was explored with coalescence analysis and skyline plots. Our results indicate post-glacial secondary contact of distinct moose mtDNA lineages diverged during the Pleistocene, whereas three genetic clusters differentiated after the re-colonisation of Fennoscandia were detected with the microsatellites. In addition, we observed genetic bottlenecks, which coincide with recorded historical population declines in the 18th century.

T.69 Hussein Khalil

Can shrews influence local hantavirus prevalence in bank voles?

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Abstract for talk The bank vole (*Myodes glareolus*) is the host for Puumala hantavirus (PUUV), a zoonotic virus that causes hemorrhagic fever in humans. Here, we aim to understand the role of the abundance of sympatric non-competent host small mammals in general, and shrews in particular, for the spatio-temporal dynamics of PUUV prevalence in bank voles. The analysis was based on long-term trapping and serology data (1979–1986; 2003–2013) in 58 trapping plots within a 100 × 100 km study area in northern Sweden. PUUV prevalence was negatively related to shrew abundance, suggesting presence of the dilution effect, i.e. reduction in disease risk by high proportion of non-competent hosts occurring in diverse animal communities. To shed further light on the role of shrews on PUUV prevalence, we discuss our results in relation to the niche overlap between bank voles and shrews at the scale of the trapping plots.

^aCo-authors: Frauke Ecke, Birger Hörnfeldt

T.70 Andrew Kitchener

Geographical variation in the sand cat, *Felis margarita*

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Abstract for talk The sand cat has a wide distribution in the sandy and stony deserts of North Africa, the Arabian Peninsula and SW Asia. Four subspecies are currently recognised in North Africa (*margarita*), the Arabian Peninsula (*harrisoni*), Pakistan (*scheffeli*) and Turkmenistan (*thinobia*), based apparently on isolated populations. However, this distribution pattern may represent sampling bias in a species that has a very low population density throughout its range. We present the first comprehensive study of geographical variation in the sand cat throughout its range using both molecular and morphological data. Variation in pelage coloration and pattern, skull morphometrics and mtDNA are examined with respect to putative subspecies to determine actual geographical variation, connectivity between populations and colonisation of the current range following climatic and environmental change since the late Pleistocene.

^aCo-authors: Alexei Abramov, Geraldine Veron, Lisa Banfield, Myyas Al Qarqaz, Hessa Al Qahtani, Mark Craig, Arshad Toosy, Helen Senn

T.71 Meeri Koivuniemi

Photo-ID as a tool for studying and monitoring the critically endangered Saimaa ringed seal population

Meeri Koivuniemi <meeri.koivuniemi@uef.fi>^a

University of Eastern Finland, Finland

Abstract for talk Non-invasive photo-identification of distinctive characteristics of individuals provides effective way to get information on animal populations. Especially in the case of endangered and rare species, remote based photo-ID studies enhance estimates on e.g. survival rates, population size and distribution. Here we describe use of the photo-ID method for studying and monitoring the critically endangered Saimaa ringed seal, *Phoca hispida saimensis* (population size ca. 300 individuals). The camera trapping was done using game cameras at the haulout sites during annual moulting in 2010–2014. Identification of individuals is based on life-long unique ring-shaped fur patterns. The total of 165 seals was identified in central Lake Saimaa and 72 of them were observed in multiple years. Our results indicate limited movement patterns and high degree of site fidelity. Photo-ID may provide more accurate population estimates and insights to social behavior of the Saimaa ringed seal.

^aCo-authors: Miina Auttila, Marja Niemi, Riikka Levänen and Mervi Kunnasranta

T.72 Marta Kolodziej-Sobocinska

Does the blood-sucking nematode *Ashworthius sidemi* cause deterioration of blood parameters in endangered European bison (*Bison bonasus*)?

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Abstract for talk European bison, after extinction in the wild in 1919, were reintroduced in over 30 free-ranging populations in Europe. Major threats to this species include disease and parasites. Recently, the highly pathogenic blood-sucking nematode *Ashworthius sidemi*, has been found within the bison abomasa. We investigated the impact of this invasion on selected blood parameters in 90 bison from NE Poland (Bialowieza and Knyszyn Forests). We observed a significant decrease in HGB, HCT, and Fe relative to *A. sidemi* infection intensity. Furthermore, the RBC, PLT count and Fe concentration were lower, and the percentage of RET was increased in highly infected free-living bison in comparison to captive ones. Study indicates the urgent need to change the traditional conservation management of herds, that includes supplementary feeding causing a large concentration of bison in winter that leads to increase in parasitic load, which ultimately impacts on their condition. (Grant NCN 2012/07/B/NZ8/00066).

^aCo-authors: Aleksander W. Demiaszkiewicz, Anna M. Pyziel, Barbara Marczuk, Rafal Kowalczyk

T.73 Alexander Kopatz

Male mediated gene flow and the carnivore comeback: Y-chromosomal patterns during range expansion in a recovering brown bear population

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Abstract for talk Dispersal in brown bears is male-biased, therefore male bears are assumed to be the driving force for range expansion and gene flow among regions during population recovery. Male-inherited Y chromosome markers have shown to be a useful tool for genetic analyses of paternal lineages in wildlife species. We use Y-chromosomal microsatellite (Y-STRs) and Y-chromosomal single nucleotide polymorphism markers (Y-SNPs) to study the influence of male mediated gene flow among populations of brown bears (*Ursus arctos*) in northern Europe and to what extent it was responsible for the rapid recovery and range expansion in the Finnish brown bear. The bear populations in northern Europe, i.e. Norway, Sweden, Finland and Russia, declined dramatically in numbers and geographic distribution during the last centuries, but have been expanding again until recently. We therefore regard the brown bear as a suitable model species to study the genetic patterns during demographic recovery and range expansion.

^aCo-authors: Julia Schregel, Hans Geir Eiken, Jouni Aspi, Ilpo Kojola, Snorre B. Hagen

T.74 Petr Kotlik

Population replacement in British bank voles revealed by a large number of SNP markers

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Abstract for talk Bank voles (*Clethrionomys glareolus*) in Britain belong to two mtDNA phylogroups, one of which has a peripheral distribution relative to the second one. The explanation is a two-phase post-glacial colonization with replacement, but it was not known whether it involved a selective sweep of mtDNA or a full population replacement. Our analysis of a large number of SNP loci derived from the bank vole transcriptome revealed a clear north-south gradient in admixture from the second colonizing population, with only the northernmost locality (Aberdeen) retaining the genome without admixture, while at the two southernmost localities (Cornwall and Devon) the genes of the first colonists were completely replaced with genes of the second colonists. This rejects the possibility that the phylogeographic pattern was the result of an mtDNA selective sweep and shows how large SNP datasets can be used to reveal true population replacements and distinguish them from selective sweeps at one of a few loci.

^aCo-authors: Silvia Markova, Mateusz Konczal, Karolina Filipi, Michaela Straznicka, Jeremy B Searle

T.75 Rafal Kowalczyk

Why has the European bison survived, while the other large beasts have gone

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Abstract for talk Increasing replacement of open steppe by forest after the last postglacial period and expansion of human in Europe over the last millennia had a dramatic effect on the distribution and densities of large herbivores. Most of them disappeared, while European bison, the largest terrestrial mammal in Europe, has survived. Bison recolonised Europe after the last glacial maximum but was never as abundant and widely distributed as aurochs. These two species can be viewed as refugee species confined to suboptimal or marginal habitats, with consequences of decreased fitness and density, and increasing risk of extinction. Bison survived until the 20th century, while aurochs became extinct in the 17th century. Stable isotope and teeth microwear analysis shows the great plasticity of bison in habitat selection and foraging habits that allowed them to adapt to changing environment and survive, while the other large beasts got extinct. The study financed by NCN 2013/11/B/NZ8/00914 grant.

^aCo-authors: Emilia Hofman-Kaminska, Tomasz Samojlik, Daniel Makowiecki, Gildas Merceron, Herve Bocherens

T.76 Anna Kukekova

Genomic regions associated with selection for behavior in foxes (Vulpes vulpes)

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University of Illinois at Urbana-Champaign, USA

Abstract for talk Two strains of foxes demonstrating markedly different behaviors to humans have been developed in an effort know as Farm-fox experiment. Foxes from the tame strain are eager to establish human contact, while foxes from the aggressive strain avoid contact and demonstrate aggressive response to humans. To identify genomic targets of selection for behavior, the genomes of ten foxes from each of three populations (tame, aggressive, and conventional) were sequenced using Illumina. The fox reads were aligned against the scaffolds of the newly available draft of the fox genome. The homozygosity analysis using a sliding window approach identified 96 windows in tame, 60 in aggressive, and 14 in conventional population. Comparison of the regions of increased homozygosity with the genomic regions identified by genetic mapping allowed to refine previously identified behavioral loci and pinpoint positional candidate genes implicated in behavioral differences between the fox strains.

^aCo-authors: Johnson JL, Kharlamova AV, Gulevich RG, Vladimirova AV, Herbeck YE, Shepeleva DV, Rando HM, Hekman JP, Shaohong F, Xiang X, Liu S, Zhang G, Trut LN

T.77 Sara Lado

Population history and taxonomy of North African hares (genus *Lepus*) inferred from genetic variation

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Abstract for talk The taxonomy of genus *Lepus* is still controversial in many aspects, and species described from Africa are no exception. All hares from North Africa are classified as *Lepus capensis* (cape hare), but previous studies based on morphological or mitochondrial DNA data suggested that different diverging entities may in fact exist in the region. In order to better understand the population history and the taxonomy of hares from this region, multilocus genotype (18 microsatellites) and sequence data (5 nuclear and 1 mtDNA loci) were collected and used to assess population structure, demographic history and genetic divergence. This work will provide valuable information to understand the evolutionary history, the biogeographic patterns and the phylogenetic relationships of North African hares.

^aCo-authors: Paulo C. Alves, J. C. Brito, José Melo-Ferreira

T.78 Regina Lafuente

Hunters' attitudes towards the reintroduction of the critically endangered Iberian lynx (*Lynx pardinus*)

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Abstract for talk The Iberian lynx (*Lynx pardinus*) is the most endangered large carnivore in Europe with less than 400 individuals occurring in the Iberian Peninsula. Lynx mostly prey on European rabbits (*Oryctolagus cuniculus*). Declines in rabbit populations and illegal killing by hunters are thought to be limiting lynx populations. A reintroduction program was launched in 2006, releasing captive-bred lynx and enhancing rabbit populations in suitable target areas. The social context is critical to the success of reintroduction programmes. Before the first releases, we therefore interviewed 600 hunters in 3 target areas to explore their attitudes towards the reintroductions. Support varied from 89% to 76% between areas with hunters identifying perceived costs and benefits of a reintroduction. Findings suggested a favourable social context for a reintroduction programme with some variation between areas. A repeat survey is necessary to explore how attitudes have changed in response to reintroductions

^aCo-authors: Delibes-Mateos, M. (presenting author), Garrido, F., Redpath, S., Villafuerte, R. & Moyano, E.

T.79 Xavier Lambin

Trophic interactions in asynchronously fluctuating populations: predation and the cost of dispersal

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University of Aberdeen, UK

Abstract for talk Classically, predation and other trophic interactions are seen as agents synchronising the fluctuations of spatially disparate populations. While spatial synchrony is the norm, many rodent populations do not fluctuate in unison, with spatial dynamics resembling either organised traveling waves, disorganised spatial chaos or extinction-recolonisation metapopulation patterns. Drawing on empirical studies of rodent populations with diverse spatial dynamics, I will illustrate how asynchrony in prey populations affects predator-prey interactions. While predators may loosely bind the dynamics of prey populations within their foraging range, larger scale dispersal may also free such predators from food limitation, if they are able to exploit multiple asynchronous populations of a given prey species as if they were alternative preys. I will suggest that the outcome of such interactions is contingent upon the cost of predator dispersal that may be imposed by other, larger predators.

T.80 Arild Landa

Species at risk, Captive breeding and reintroduction: challenges, pit-falls and successes

Arild Landa <arild.landa@nina.no>
Norwegian institute for nature research (NINA), Norway

Abstract for talk Captive breeding and reintroduction programs are increasingly implemented as a conservation action for species at risk. Successful reintroduction of threatened species often include ecosystem restoration approaches that involve the manipulation of other keystone species and/or habitat modifications. Common criteria to achieve success include long-term commitment and multidisciplinary scientific approaches. Poor planning, lack of research, and/or poor long-term monitoring limit the possibilities to evaluate and adjust implemented actions, and to document the successes and failures. Research on the target species responses to environmental changes and stressors (Cons. Phys.) will likely provide advances in optimizing reintroduction programs. Being circumpolar abundant, the arctic fox is critical endangered in Fennoscandia. The captive breeding program to save it has so far been a success, but- what are the prospects when global warming seems to be the ultimate driver for its retreat?

T.81 Marietjie Landman

Comparing the efficiency of DNA barcoding and microhistology methods to describe elephant diet: consequences for understanding elephant-plant dynamics

Marietjie Landman <marietjie.landman@nmmu.ac.za>^a
Nelson Mandela Metropolitan University, South Africa

Abstract for talk Understanding the role of herbivores requires insight into their diet. However, understanding the diet is limited by the difficulty of accurately/efficiently determining the foods eaten. While traditional microhistology methods are labour intensive and lack taxonomic resolution, novel DNA barcoding tools promise increased resolution and accuracy. We contrast the diet of African elephants using DNA barcoding and microhistology, showing that taxa identified in the diet are comparable between approaches, but that DNA barcoding provides more taxonomically detailed results. Importantly, plants most vulnerable to elephant feeding (e.g. endemics, rare taxa) were more frequently identified with the DNA approach; these are underrepresented in the microhistology diet. The high resolution of DNA barcoding is particularly useful for assessing elephant feeding impacts on rare plants, a role previously underestimated. These outcomes are important in all systems with subtle herbivore effects.

^aCo-authors: Graham I Kerley, Eric Coissac, Pierre Taberlet

T.82 Greger Larson

The process and the pattern of dog domestication

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University of Oxford, United Kingdom

Abstract for talk Despite being the first domesticated animal, and the only animal domesticated prior to the advent of agriculture, we know very little about the specific about either how the relationship between humans and wolves led to domestication, or how many times this process took place. I will firstly discuss theoretical aspects associated with animal domestication before presenting a hypothesis about how the process may have taken place using the concept of ecotypes and examples taken from other animal species. I will then describe our latest results of a large collaborative project to generate next generation genetic data alongside geometric morphometric data from several thousands dogs and wolves to understand the fundamentals of dog domestication.

T.83 Alice Latinne

Past and future distributions of Southeast Asian murine rodents: the influence of climate changes

Alice Latinne <alice.latinne@ulg.ac.be>^a
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Abstract for talk Our study, involving species distribution modelling techniques, aimed at assessing the influence of past and future climatic fluctuations on Southeast Asian small mammal distributions using two forest-dwelling (*Leopoldamys herberti* and *Leopoldamys sabanus*) and one karst endemic (*Leopoldamys neilli*) rodent species as models. Our model predictions contradict the well-established hypothesis that Southeast Asian forest-dwelling species were confined to small refugia during the LGM. Moreover, these results suggest that the distribution of several East and Southeast Asian taxa were in their refugial state during Pleistocene interglacial periods rather than during glacial periods. This could be because of vegetation changes that may have occurred at that time as a result of the increased seasonality observed during the LIG. The two future climate change scenarios used in this study predicted that large climatically suitable areas would still be available in the future for the three species.

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T.84 Jennifer Leonard

Ecology in the Evolution of Wolves

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Abstract for talk Gray wolves (*Canis lupus*) are a widespread, Holarctic species. They are distributed across a wide variety of habitats, including deserts, dry plains, boreal forests and the high arctic. They are generalist carnivores, feeding on a wide variety of species throughout their range. Wolves also have an incredible potential to disperse, with multiple records of over 1000 km. Despite this, surprising examples of differentiation between contiguous wolf populations have been described. How can population differentiation arise and be maintained in a continuously distributed, generalist species? How does this structure impact evolution and conservation?

T.85 Liza le Roux

Behaviourally mediated trophic cascades in a megaherbivore dominated system

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Abstract for talk Mammalian predators may play an important role in ecosystem function. However, most current evidence for predator induced trophic cascades in terrestrial systems comes from simple systems with one carnivore and one prey species. Many systems host diverse predator and prey species, yet evidence for trophic cascades from such systems is remarkably rare. Particularly interesting are systems dominated by megaherbivores; very large herbivores that escape predation. How does the presence of megaherbivores modify trophic cascades? We studied this by manipulating top-down and bottom-up forces in a full-factorial experiment in a diverse herbivore community in an African savanna ecosystem. We created areas that vary in visibility and thus the potential risk by ambush predators and artificially enhanced resource quality by adding nutrient fertilizers. We assessed how variation in anti-predatory response of herbivores affected lower trophic levels by monitoring vegetation and soil and plant nutrients.

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T.86 Riikka Levänen

Abundance and distribution of hare hybrids in Finland

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Abstract for talk Shorter winters have a negative effect on the mountain hare (*Lepus timidus*) population, which has declined 40% over the last two decades in Finland. Simultaneously, the brown hare (*L. europaeus*) population has increased. Thus, interaction and cross-breeding between these two species may have increased. In hares, hybridization seems to be unidirectional: mountain hare females mate with brown hare males. Hybridization can be tracked over the generations by analyzing the cross-species introgression of maternally inherited mitochondrial DNA (mtDNA). This study aims to examine the abundance and distribution of hare hybrids for the first time in Finland. According to preliminary results, from over 500 samples obtained from hunters, around 15% of brown hares carry mountain hare mtDNA. No mountain hares with brown hare mtDNA were found. In future the overall genetic variation will be studied using next generation genotyping by sequencing approach and correlated with ecological interaction.

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T.87 Anna Linderholm

Unraveling the complexity of the Austronesian expansion and dispersal

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Abstract for talk The peopling of Oceania over the last three millennia marked the culmination of a global colonization process that began when humans left Africa. Several models, which attempt to explain the origins and dispersal of Austronesian farmers through ISEA into Oceania have been proposed, all of which rely upon traditional lines of evidence (material culture, linguistics and modern human genetics). Several models that describe the origins of the Lapita cultural complex (the immediate ancestors of the Polynesians and many other Oceanic cultures) focus on a single and complete cultural and biological package moving from Taiwan to the Pacific. These contrast with others that claim the origins of Lapita to be found across broader regions of mainland Asia and even ISEA. Here we are looking to test the Out of Taiwan model as an explanation for the Austronesian origins and dispersal by using ancient DNA from pigs as proxy.

T.88 Miriam Linnenbrink

Territoriality and migration - implications on fitness in wild mice

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Abstract for talk Territoriality is defined as "behavioristic trait manifested by a display of property ownership - a defense of certain positions or things.."(Burt et al. 1943). We address the question of territoriality in the context of population divergence and fitness by using two recently diverged wild mouse populations. Our experimental approaches include a cage experiment letting two individuals encounter each other. Second, we provided a semi-natural environment inhabited by individuals of both populations. Mouse movement was recorded several months by RFID antennae technique and thus territory use could be determined. Successful matings are defined by microsatellite genotyping. Preliminary results show a different competitive potential of both populations with clear existence of territoriality, even though more prominent in males. Individuals with higher competitive potential migrate and use inhabited space in a self-evident way, whereas submissive individuals are restricted in their space use.

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T.89 Eline Lorenzen

Population genomics reveal recent speciation and rapid evolutionary adaptation in polar bears

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Abstract for talk Polar bears are uniquely adapted to life in the High Arctic and have undergone drastic physiological changes in response to Arctic climates and a hyper-lipid diet of primarily marine mammal prey. We analyzed 89 complete genomes of polar bear and brown bear using population genomic modeling and show that the species diverged only 479–343 thousand years BP. We find that genes on the polar bear lineage have been under stronger positive selection than in brown bears; nine of the top 16 genes under strong positive selection are associated with cardiomyopathy and vascular disease, implying important reorganization of the cardiovascular system. One of the genes showing the strongest evidence of selection, APOB, encodes the primary lipoprotein component of low-density lipoprotein (LDL); functional mutations in APOB may explain how polar bears are able to cope with life-long elevated LDL levels that are associated with high risk of heart disease in humans.

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T.90 Juan Jose Luque-Larena

Sperm competition in fluctuating populations of common voles in southern Europe: reversed relationship between relative testes size and density

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Abstract for talk Investment in sperm numbers is a key predictor of success in sperm competition and there is usually a positive relationship between sperm competition level and male reproductive effort on ejaculates, which is often measured using relative testes size (RTS). Demographic processes can drastically alter levels of sperm competition and we should expect males to respond to increasing competition risk (RTS increase with density). Here we investigate whether RTS of common voles respond to fluctuations in population density. We evaluated variation of RTS depending on current and recent densities of conspecifics, also taking into account the condition of individual males (fat levels and parasite loads). Contrary to our prediction and in line with recent findings reporting ambiguous results among other vole species, we found a reversed relationship between RTS and density. Our data show that demographic factors can strongly affect RTS and we discuss possible mechanisms to explain these findings.

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T.91 Åke Lundkvist

City rats - an emerging threat to the public health

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Abstract for talk Brown rats have become more visible in Swedish cities during recent years. The resistance to rodenticides has increased and the number of rodent exterminations in Sweden has almost doubled since 2006. Based on our finding of Seoul hantavirus (causing hemorrhagic fever with renal syndrome in humans) in Swedish pet rats, we initiated a nation-wide project, investigating wild rats for the presence of zoonotic agents. The project has been expanded to other European countries and will also include a study on the genetic structure of the global rat population and the surveillance of rat-borne diseases in man. Leptospirosis is an emerging zoonosis of global concern; however, its contemporary occurrence in Sweden is poorly known. Four out of 30 brown rats, captured within urban districts in Sweden, were found to be positive for antibodies to *Leptospira interrogans* serovar *Icterohaemorrhagiae*, which causes Weil's disease in man; a severe infection with jaundice, renal failure and haemorrhage.

T.92 Carly Lynsdale

Individual Variation in Parasite Burden in a Population of Semi-Captive Asian Elephants (*Elephas maximus*)

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Abstract for talk Parasites can threaten endangered mammalian populations by reducing host health, survival and fitness. However, the extent to which such impacts are felt is not uniform, with hosts varying in their ability to resist, tolerate and succumb to parasitic infection. We investigated individual variation in gastro-intestinal helminth burden in semi-captive Asian elephants (*Elephas maximus*) in Myanmar. Firstly, using a longitudinal database (2000 individuals) we determined patterns of age-specific mortality caused directly and indirectly by parasitism. Secondly, we investigated current variation in parasite burden relative to host age, sex and body condition in 120 elephants. Our results highlight the importance of variation in host resistance and susceptibility, and provide data on parasite associated mortality risk across a lifetime. Through determining individuals at risk of infection, we provide important insights for the conservation, welfare and management practices of Asian elephants.

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T.93 David Macdonald

Conserving big predators: case studies from the WildCRU

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T.94 Allan McDevitt

Signatures of selection in the genome and phenotype of the invading and expanding greater white-toothed shrew (*Crocidura russula*) in Ireland

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Abstract for talk The greater white-toothed shrew was discovered in Ireland in 2007. It has been expanding its range rapidly at a rate of 5.5 km/year. Such populations are ideal for studying the effects of range expansions on the evolution of both genotype and phenotype. Shrews were sampled along four independent transects from the epicentre out to the invasion edge. 978 SNPs were identified in 200 individuals using RAD-seq. A decline in genetic diversity was observed towards the range edge. Using two outlier detection methods, SNPs were identified as being under selection in regions associated with immunological, physiological and cellular processes. We also investigated if phenotypic traits associated with dispersal ability (body size, weight and foot length) are evolving towards the range edge. We found that individuals increased in weight towards the range edge. Such changes are indicative that range expansions can generate strong selective pressures, even during the early stages of expansion.

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T.95 Allan McDevitt

Genomic variation and signatures of selection in European red foxes (*Vulpes vulpes*)

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Mammal Research Institute, Poland

Abstract for talk WORKSHOP. The advent of next-generation sequencing techniques has the potential to revolutionize our understanding of phylogeographic and adaptive processes in mammals at the continental scale. A total of 373 red foxes were genotyped in 24 populations using genotype-by-sequencing (GBS) to identify patterns of variation and signatures of selection in the genomes of red foxes across Europe. Almost 22,000 SNPs were retained after various quality control and filtering steps. Levels of genomic diversity were similar among populations but were generally lower in the most northerly populations in Scandinavia and the island populations. Fst-outlier analysis identified a large number of SNPs showing evidence of selection across a wide variety of genomic regions. Ongoing work will incorporate additional samples from Britain, the Mediterranean peninsulas and Russia in order to further elucidate phylogeographic and adaptive processes in this charismatic carnivore across Europe.

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T.96 Clara Mendes Ferreira

Fewer markers, similar accuracy? Cost-effective selection of genetic markers for parentage analysis based on noninvasive genetic sampling

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Abstract for talk Genetic parentage analysis (GPA) is widely used to assess key population traits such as dispersal rates and mating systems. Successful GPA depends mostly on the number of markers used, which is often limited for noninvasive genetics due to the low DNA yield. Here we used empirically-based simulations focused on the threatened Cabrera vole to assess how the number of markers affects GPA accuracy. We amplified 20 microsatellites in 31 tissue samples, and then used 11 of these to genotype 326 faecal samples from a 78-ha area. We obtained 146 genotypes corresponding to 88 individuals, and estimated allelic frequencies to simulate a virtual population with known kinships. GPA accuracy was assessed considering different numbers of markers and population sizes using COLONY. We found that the subset of 11 loci is sufficient for our analysis, and discuss the trade-offs of using fewer markers when analysing empirical data from noninvasive samples.

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T.97 Johan Michaux

Genetic patterns of a successful recolonization of the Eurasian otter in France

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Abstract for talk At the dawn of the 20th century, the Eurasian otter (*Lutra lutra*) was widely distributed in France but by the early 1970s, just before its legal protection, it was extirpated in most regions. However, for more than 20 years, the otter has been reconquering several parts of its original area. We studied the genetic differentiation and diversity of several otter populations from Western France and Northern Spain, based on 14 microsatellite loci. Clustering methods suggest five distinct groups, well correlated with the suspected refugia where otter probably survived during the 20th century. Two clusters are particularly differentiated and correspond to the Pyrenees and Brittany populations, respectively. The three other clusters are centered in the Limousin, Massif Central and Atlantic Coast. The results also suggest mixing between the lineages. Finally, a demographic approach reveals the putative link between ancient human pressures and population fragmentation.

T.98 Berit Annika Michler

Unsuspecting immigrant or ecological threat - a long-term fieldwork study on the introduced raccoon in Germany

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Abstract for talk Alien species like the North American raccoon can play a significant role in the ecological balance of their newly encountered biotope. Against the background of a vast increase of raccoon numbers in Germany within the last years, a controversial discussion arose regarding the influence of the new inhabitant on indigenous species and the potential transmission of diseases and parasites. Extensive knowledge about the effects of raccoon settlement, primarily in natural landscapes, is lacking entirely so far. Aiming to elucidate the wildlife biology of this introduced species, a large perennial project has been initiated in the northeastern area of distribution (Müritzer National Park; www.projekt-waschbaer.de). Within 16 different sub studies and having 69 raccoons under telemetric control profound data on the population biology could be ascertained for the first time. The talk will introduce the project along with the key topics of the study and focus on the nutritional aspects of research

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T.99 Christine Miller

How to prove that you loose! Management of alpine chamois (*Rupicapra rupicapra*) to the brink of extinction in Germany

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Abstract for talk Chamois are protected under Annex V of the EU-FFH directive. Yet, in the alpine region of Bavaria (Germany) the indigenous chamois population is heavily hunted. Over the last 30 years hunting pressure has steadily increased. Especially in the wintering habitat of the species explicit culling programs are in action since about 10 years. The hunting quota in the area is not based on any population related data, e.g. monitoring. Also, the age of the shot animals are not recorded, which does not allow to reconstruct a population trend. While there is circumstantial evidence that the populations are severely depleted, the official hunting bag does not show a decline. In lack of direct monitoring we use indirect evidence via GIS based modelling and documentation of preferred winter habitat and areas with severe hunting pressure and culling programs, to show that the chamois population is not managed sustainably and the Bavarian hunting regulations are in breach of the EU FFH directive.

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T.100 L. Scott Mills

Seasonal Coat Color and Climate Change in Mammals: A Global Model System to Understand Adaptive Rescue

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Abstract for talk At least 13 high profile and strongly-interacting mammal species worldwide undergo seasonal coat color molts from brown to white to match the absence or presence of snow in temperate regions. Reduced snow cover duration due to climate change can lead to compromised camouflage in these species, producing a direct and visually compelling global model system to understand adaptive response of wild vertebrates to climate change. Building on our work to date with snowshoe hare camouflage mismatch, we are now combining multiple conceptual approaches across multiple countries and mammal species to quantify adaptation in the past and prospects for adaptation in the future for this functional trait. Based on an integrative framework of snow duration modeling, experimental mechanistic responses (e.g. physiological, genetic, behavioral), and measures of fitness costs in the wild, we are connecting climate-change induced camouflage mismatch to population dynamic responses.

T.101 Pedro Monterroso

Ecological Interactions and Species Coexistence in Iberian Mesocarnivore Communities

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Abstract for talk The structure of mesocarnivore communities is complex, and results from a multidimensional web of relations, upheld through top-down and bottom-up effects, intraguild interactions and habitat quality. Using a combination of noninvasive techniques (camera trapping and molecular scatology), we assess the strategies involved in mesocarnivore coexistence in SW European communities. Our results suggest that the interactions between co-occurring mesocarnivores are dynamic, and their strength and direction may vary seasonally and geographically. Spatial displacements are not frequent. However, in areas of co-occurrence, some behavioral responses may take place. Potentially stressful interactions appear to be preferably handled by displacements along the temporal and trophic niche dimensions. Segregation along the temporal niche dimension constitutes a recurrent strategy in facilitating carnivore coexistence, and is more pronounced in more complex communities.

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T.102 Ian Montgomery

Invasive small mammals: trophic dynamism and modified food webs in Irish hedgerows

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Abstract for talk Wood mouse and pygmy shrew are being replaced by invasive alien species (IAS), bank vole and greater white toothed shrew in Ireland. IAS are a threat to biodiversity and specifically to ecosystem services provided by hedgerows. We examine: (1) whether species replacement involves trophic equivalence using Stable Isotope Analyses (SIA); (2) indirect effects of IAS by comparing species biomass and species with similar trophic signatures where there are no invaders, 1 invader, and 2 invaders. SIA confirm conventional descriptions of shrews as insectivores, wood mice as omnivores and bank voles as primarily herbivores with omnivorous tendencies. IAS are a direct replacement of like with like insectivores, but not a direct replacement of like with like rodent species. Small mammal biomass increases where IAS occur. There is also a trend towards insectivory and herbivory where IAS occur. We also examine top-down effects of IAS on their invertebrate prey communities.

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T.103 Raimondas Mozūraitis

Estrous olfactory cues in domestic horse *Equus ferus caballus* L. (Perissodactyla, Equidae)

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Abstract for talk Like many other mammalian species, horses use olfactory communication to coordinate their reproductive and social activities. Comparison of chromatographic profiles of volatile substances collected from urine samples of 14 mares revealed that concentrations of m- and p-cresols were significantly greater during estrus versus diestrus periods peaking 1 day before ovulation. Data from a two choice behavioral test demonstrated that stallions spent significantly more time sniffing p-cresol as compared to o-, and m-cresols. The stallions' extent of erection differed significantly in response to each sample type including pure water, diestrus urine of a mare and a sample comprised of the diestrus urine of a mare containing synthetic p-cresol at the half of amount found in the estrous urine samples. Consequently, p-cresol should be considered as the sex pheromone component of horses and could be used in a noninvasive test to determine a precise insemination time.

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T.104 Morteza Naderi

Combination of morphological, molecular and niche divergence to identify patterns of species delineation: a case with the fat dormouse along the Hyrcanian forests

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Abstract for talk Fat dormouse, a species from monotypic genus is the only member of Gliridae family that can be seen in Iran. Recently, a phylogenetic study based on mitochondrial Cytb confirmed Hyrcanian forests role as a refugium during Quaternary climatic oscillations. Further investigation, detailed sampling and combination of different data sets allowed us to identify two clearly and new divergent haplogroups of the Fat Dormouse along the Hyrcanian refugium of Northern Iran. Comparison of lower mandibles and skull characteristics of the specimens as well as sequencing one mitochondrial gene and three nuclear genes for new specimens revealed that the population restricted to the eastern most part of its global distribution in Iran, had been trapped in Kalaleh microrefugium and experienced distinct evolutionary history. The statistical analyses such as PCA, MANCOVA and DA applied to the morphological and ecological data confirmed the separation of the Kalaleh population as new subspecies.

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T.105 Magdalena Niedziałkowska

Evolutionary history and genetic structure of moose population in Europe

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Abstract for talk We sampled moose from throughout its European range to determine its demographic history and recolonization patterns of Europe, using both mtDNA and microsatellites. Belarussian and Russian populations were characterized by the highest genetic diversity and Scandinavian populations by the lowest. All analyses showed that the species is divided into two main genetic clusters: Scandinavian and Continental, with the Baltic Sea representing a barrier to gene flow; moreover, further substructure was observed. Genetic structure determined by microsatellites and mtDNA were concordant. The split of genetic lineages calculated using approximate Bayesian computation occurred 29 000 - 28 000 yrs BP and a range-wide bottleneck occurred 1800 - 1200 yrs BP, depending on the kind of marker used in the analyses. The most recent decline of the moose population occurred in the 18th - early 20th century. Past and contemporary processes have had an impact on present genetic diversity of European moose.

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T.106 Alina K Niskanen

Prenatal selection in dog MHC loci

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Abstract for talk The major histocompatibility complex (MHC) genes have a crucial role in immune defence and are thus under intense natural selection. However, the potential selection points in domestic dogs are fewer than in wild animals, due to veterinary care and breeding selection conducted by humans. We studied the prenatal selection in MHC class II loci (DLA-DRB1, -DQB1 and -DQA1) of 110 dog families. We examined the segregation of genotypes and inheritance of maternal and paternal type alleles at the peptide-binding site, MHC locus, three-locus haplotype and supertype levels. We also made the first canine supertype classification based on in silico analysis of peptide-binding amino-acid polymorphism. We did not find deviation from expected genotype frequencies in most loci and levels, but one peptide-binding site in DLA-DRB1 had an excess of heterozygotes among the offspring. Also, we found that offspring tended to inherit from the father more often the same DLA-DRB1 allele than their mother had.

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T.107 Anita Norman

Landscape Relatedness: Insights into Contemporary Spatial Structure of a Top Predator

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Abstract for talk Population sub-structuring is typically identified through genetic differentiation between spatial areas. However, a lack of genomic resolution, uninformative markers, skewed sampling, or a lack of sampling resolution can lead to inferences that are not representative of the actual underlying sub-structure. In this study, we use a set of 96 SNPs designed for the purpose of inferring relatedness in the Scandinavian brown bear (*Ursus arctos*). Consequently, the SNPs lack the characteristics to properly show population sub-structuring since they are fairly evenly distributed throughout the geographic range. To maximize the utility of the SNPs, we take a different approach to studying spatial structuring. Our approach uses pairwise relatedness with 412 individuals to predict overall relatedness across a landscape larger than 46,000 km². The results of this interpolation reveal novel insights into kin-structuring of brown bear. We show that some areas contain individuals that are significant!

^aCo-authors: Astrid Vik Stronen, Jonas Kindberg, Aritz Ruiz-González, Geir-Arne Fuglstad, Göran Spong

T.108 Karin Norén

Tracking genetic footprints to reconstruct geographic patterns of expansion in Fennoscandian red foxes

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Abstract for talk Boreal population expansions are among the most substantial consequences of climate change, transforming the processes in northern ecosystems. Still, little is known about the factors underlying expansion dynamics. Red foxes (*Vulpes vulpes*) are forecasted to become a keystone species due to population expansions that began in the 19th century. To identify the roles of geographic and demographic factors and the source of Fennoscandian red fox expansion, we genotyped 21 microsatellite loci in modern and historical individuals. We identified weak population subdivision with source-sink dynamics, whereby northern populations received immigrants from multiple sources. There were no clear signatures of unidirectional south-to-north expansion. Instead, migration inferences, demographic models, and temporal analyses suggested that dispersal from multiple sources combined with demographic growth, influence genetic structuring in this expanding species.

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T.109 Maria Orlova

Genesis of the bat ectoparasite fauna of Siberia

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Abstract for talk Siberia occupies a huge territory with a wide variety of climatic conditions and geographic landscapes (forests, steppes and mountains); about 15 bat species (Chiroptera: Vespertilionidae) were described for Siberian boreal and mountain lands. We found 31 bat ectoparasite species (gamasid mites (Spinturnicidae, Macronyssidae), ixodid ticks (Ixodidae) and insects: Diptera (Nycteribiidae), Siphonaptera (Ischnopsyllidae), Heteroptera (Cimicidae)), belonging to four faunistic complexes. Siberian - Far East and transpalearctic (holarctic) species dominate (22 species - two thirds); few European-Ural and subboreal parasite species reached the study area with the general hosts. The barrier to the bat distribution through the territory of Western Siberia and further east is the small number of winter shelters (including anthropogenic).

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T.110 Sakir Onder Ozkurt

Determination of taxonomic status of *Mustela nivalis* subspecies in Turkey

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Assoc. Prof. Dr. (in bio), Dr. (in antrp), Turkey

Abstract for talk A total of 29 *Mustela nivalis* specimens sampled in Turkey were evaluated to determine the current subspecies status and their distribution. In this study, we used the same diagnostic characters that Abramow (2000) compiled together in his taxonomic evaluations. Fur changes and colouring, results of DNA sequence analysis of mitochondrial Cyt-B region, geometric morphometric analysis, karyotype, baculum morphology, craniometric and classic morphometric measurements were evaluated altogether and compared with the literature. According to the results obtained, it is determined that there are two geographical forms in Turkey. It is concluded that in Thrace (European part of Turkey) region *Mustela nivalis vulgaris* Erxleben, 1777 and in Anatolian geography *Mustela nivalis caucasica* (Barrett-Hamilton, 1900) subspecies were present. **Keywords:** *Mustela nivalis*, subspecies, taxonomy, distribution, Turkey.

^aCo-authors: İrfan Kandemir, Reyhan Çolak, Ercüment Çolak

T.111 Marianne Pasanen-Mortensen

Can recolonizing apex predators reclaim their ecosystem function?

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Abstract for talk In many parts of the world, apex predators have declined or become extinct over the past centuries. Their importance in structuring ecosystems is often first discovered when these generally large predators are lost and community compositions change, e.g. when mesopredator (inferior predators) abundance increases. Restoration of apex predators is a current issue, not only to conserve predators themselves, but also to restore ecosystems. But can recolonizing apex predators retain their ecosystem function? We have modeled the effects of eradication and recovery of the Eurasian lynx (*Lynx lynx*, apex predator) on red fox (*Vulpes vulpes*, mesopredator), in relation to changes in land use and climate over two centuries. Based on the results we argue that recovery of large predators can be important to restore ecosystem, but that we cannot always expect apex predators to have very same influence as before their extinction, if also environmental changes has taken place in the ecosystem.

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T.112 Ekaterina Pavlova

Potential sources of pathogens for the Pallas cat in Daurian steppes, Russia

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Abstract for talk Pallas cats are considered to be threatened with high mortality of kittens from diseases in captivity. The aim of our study is to detect sources of pathogens for Pallas cats in their native habitats. The study was conducted in Dauriskii Reserve, Russia and based on serological analysis of serum blood samples from Pallas cats (24 ind), their preys (303 ind) and domestic cats (61 ind). We found that domestic cats and preys are potential sources of 6 from 7 tested pathogens (*Toxoplasma gondii* (Tg), herpes virus, feline leukemia virus (FeLV), feline panleukopenia virus (FPV), feline calicivirus (FCV), feline immunodeficiency virus (FIV), Influenza A virus (A)). In Pallas cats the prevalence of four detected pathogens was low (Tg-9%, FeLV and FIV-5%, A-21%). It might be caused by high mortality of Pallas cats from FCV and FPV, features of arid climate, low frequency of contacts between Pallas cats and domestic cats and their excretes, solitary life style and large territories of habitat. This study was supported by RFBR (No 14-04-01119; 15-34-20526).

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T.113 Claire R. Peart

Influence of mating system on patterns of sex-linked genetic diversity across pinniped species

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Abstract for talk The mating system of an organism is predicted to affect the relative diversity of sex chromosomes compared to the autosomes. For example, polygynous species are expected to have excess polymorphism on the X chromosome as there are more breeding females than males whereas in monogamous species the ratio of X-chromosomal diversity to autosomal diversity is predicted to be 0.75. In this study we investigate the genetic signatures of mating systems in pinnipeds using a comparative approach sampling 15 species from across the pinniped phylogeny with breeding systems ranging from monogamy to extreme polygyny. Studies investigating the relative diversity of sex chromosomes are sensitive to marker choice and results are influenced by demographic processes. In order to address these concerns we use double digest restriction site associated DNA sequencing (ddRAD) to generate loci from across the genome and discuss our results in light of the differing demographic histories of pinniped species.

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T.114 Jens Persson

Patterns of reproduction result from age-related sensitivity to resources and reproductive costs in wolverines

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Abstract for talk Reproductive output is mostly driven by individual quality, resource availability and an organism's life history, arising from a trade-off between current and future reproductive success. In a long-term study (18 yrs.) of 53 wolverine females, we assessed how different factors interact in explaining variation in reproductive output. We show how age-related variation in reproduction, was explained by interactions between costs of reproduction, resource availability and age, which, in turn was driven by four processes: 1) Maturation is independent of resource availability, 2) the probability of breeding two years in a row declines with age, 3) age-specific reproductive output is influenced by resource availability months preceding parturition, modulating the probability of breeding 2 years in a row, 4) the influence of resources on costs of reproduction is also age-dependent, as females at prime age are more responsive to resource availability than those at other ages.

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T.115 Mia Persson

Genetics of human-directed social behaviour in Beagles

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Abstract for talk During at least 15.000 years of dog-human co-evolution, dogs have acquired certain social skills enabling them to communicate with us. E.g. in contrast to wolves, when faced with an unsolvable task, dogs turn to nearby humans for help. The aim of this research is to investigate within breed variation in human-directed social behaviours and to shed some light on the genetics behind dog's social skills. To do this, 500 laboratory beagles, bred and kept under standardised conditions, were tested in an unsolvable problem-task. This revealed variation in help seeking behaviours where females were seeking more physical contact than males and eye contact seeking were increased with age. Narrow sense heritability (h^2) was estimated to 0.23 for a principal component related to human interactions, indicating a significant genetic basis to these behaviours. Now, a genome-wide association study is ongoing to reveal possible candidate genes associated with human-directed social skills in dogs.

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T.116 Isabel Queirós Neves

Species patterns and trends from sparse occurrence data. The case of Mozambique's mammals.

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Abstract for talk Biodiversity in Mozambique was poorly sampled over the years. Armed conflicts in the 90's led to mammal extirpations, mainly in larger species. Consequences for other mammal groups are not known. It is important to establish a baseline for the country and analyze biodiversity change. Integrating the occurrence data stored in natural history museums and in the literature is vital for this task. We identified ecological modeling procedures that can deal with the limitations of sparse occurrence data. Mammal occurrences from Mozambique were obtained by compiling information from natural history collections, scientific literature and surveys. Dynamic site-occupancy modeling was selected to estimate artiodactyla and chiroptera occupancy trends before and after the war. Distribution of less known rodents was computed using niche models. Trends and patterns found can guide further research in the country. The approaches here presented can be extremely useful in similar cases of sparse data.

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T.117 Neil Reid

Herd-level bovine tuberculosis risk factors: assessing the role of low level badger population disturbance

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Abstract for talk Bovine tuberculosis (bTB) is endemic in British and Irish cattle and has eluded eradication despite considerable expenditure, amid debate over the relative roles of badgers and cattle in disease transmission. We investigated interactions between host populations in the first large scale risk factor analysis for new herd breakdowns to combine data on both species. Cattle risk factors (movements, international imports, bTB history, neighbours with bTB) were more strongly associated with herd risk than badger social group density or persecution (sett disturbance). Highest risks were in areas of high badger social group density and high rates of persecution, potentially representing both responsive persecution of badgers in high cattle risk areas and effects of persecution on cattle bTB risk through badger social group disruption. Badger persecution did not reduce cattle bTB risk and may contribute towards sustaining bTB hotspots.

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T.118 Neil Reid

Macroecology of the Order Lagomorpha; implications for the impact of global climate change

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Abstract for talk Expertly-validated SDMs and phylogenetically-controlled regression suggest that responses to climate change are related to species traits in the Lagomorpha. Climate change may impact more than two-thirds of lagomorphs by 2080, with leporids (rabbits, hares and jackrabbits) likely to undertake poleward shifts with little change in range extent, whilst pikas are likely to show shifts to higher altitudes associated with range declines. Model predictions based on abiotic variables may be misleading. Interspecific interactions are widely reported in the Order with closely related, large-bodied, similarly-sized species in agricultural landscapes or at high elevations likely to have competitive interactions. Hierarchical spatial models suggest that for some species biotic (mutualistic and competitive) interactions are important and we propose developing network analyses to quantify the strength of such biotic interactions to assess ecological network stability under future conditions.

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T.119 Sabrina Renaud

Fast evolutionary response of house mice to anthropogenic disturbance on a Sub-Antarctic island

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Abstract for talk Invasions and anthropogenic disturbances challenge species with rapid environmental changes. The house mouse on the Sub-Antarctic Guillou Island (Kerguelen Archipelago) had to face such challenges twice: first when invading the island two centuries ago; and nowadays when coping with an in-depth remodelling of its habitat due to a cohort of anthropogenic changes. Morphometric and biomechanical results show that the initial invasion triggered the evolution of a jaw shape adapted to the local food resources. Contemporary changes are also associated to changes in jaw morphology, but are not directly functionally relevant. A complex response integrating feeding behaviour, investment in feeding structure, and bone mineralization, may provide the mice with a better tool to exploit wider resources utilization in a changing habitat. These Sub-Antarctic mice exemplify that success of invasive species rely on the capacity of facing rapidly varying environments through integrated responses.

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T.120 Erika Rosengren

The colonisation history of Scandinavia presented through the subfossil finds along one of its major immigration routes; Scania, southern Sweden

Erika Rosengren <erika.rosengren@luhm.lu.se>
Lund University Historical Museum, Sweden

Abstract for talk Most of the Swedish subfossil finds of terrestrial mammals have been recovered from Scania. The contributing factors may be that Late Weichselian sediment basins have been exposed through extensive peat cutting, and that the public awareness of the significance of the bones and antlers found led to them being acquired to research collections. They have come to form the basis for the reconstruction of the postglacial re-colonisation history of the terrestrial fauna. Scania, through the recurrent establishment of a land bridge connecting it to the European mainland, represented one of the major immigration routes into Scandinavia. Already in the Late Glacial the inhabitants of the disintegrating mammoth steppe colonised the newly deglaciated land. It was, however, mainly between c. 12,400 and 9500 cal. years BP, in part due to the existence of a more long lasting land bridge and the continuing amelioration of the climate, that the postglacial fauna in Sweden was formed.

T.121 Marcus Rowcliffe

Analytical frontiers in analysing camera trap data

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ZSL Institute of Zoology, United Kingdom

Abstract for talk Camera traps have become a core tool for mammalogists, providing a cost-effective means of detecting a wide range of species which are otherwise difficult to observe systematically in the wild. Camera trap records are accumulating rapidly and globally, providing a huge opportunity for deeper understanding of mammal ecology, but the analytical methods for making best use of these records are lagging. In this talk, I will introduce a set of linked methods for extracting information on animal activity, movement and abundance from camera trap data for species which are not individually recognisable, for which few alternative methods currently exist.

^aCo-authors: Parick Jansen, Chris Carbone, Roland Kays, Bart Kranstauber

T.122 Ben Sacks

Inbreeding, Outbreeding, and the Transformation of the Critically Endangered Sierra Nevada Red Fox: Genetic Rescue or Genomic Replacement?

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University of California, Davis, USA

Abstract for talk The Sierra Nevada red fox (*Vulpes vulpes necator*) is the rarest of three subspecies of montane red fox, an evolutionarily distinct lineage restricted to the subalpine environments of the western USA. The historically largest population was thought to be extirpated until discovery in 2010 of a remnant population. We used noninvasive genetic methods to confirm the purely indigenous origins of this population and to monitor its membership over the next 5 years. We observed low genetic diversity, abundance, and recruitment, consistent with inbreeding depression. In year 3, two nonnative males arrived by unknown means, paired with two native females, and produced litters, with several offspring surviving and, in at least one case, reproducing. We detected no offspring born to the fully native pairs. Whether the unplanned outbreeding to nonnative males was best viewed as genetic rescue or a step toward genetic extirpation is considered.

^aCo-authors: Cate Quinn

T.123 Gustaf Samelius

Snow leopard predation in a livestock-dominated landscape

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(1) Snow Leopard Trust, (2) Swedish University of Agricultural Sciences (SLU), (3) Nordens Ark, (4) Panthera, (5) Snow Leopard Conservation Foundation, (6) Nature Conservation Foundation, Sweden

Abstract for talk Livestock predation is a major challenge for conservation of large carnivores in many parts of the world. In the mountains of central Asia, livestock predation by snow leopards results in financial hardship for herders and is the cause of retaliatory killing of snow leopards. In this study, we examined predation patterns of snow leopards by identifying prey remains in areas where GPS-collared cats had stayed for extended periods (i.e. areas of aggregated GPS positions). Snow leopards killed, on average, one ungulate every 8 days with wild prey (73%) being more common than livestock (27%) despite livestock abundance being at least one order of magnitude higher. Kill rates were considerably higher than previous scat-based estimates and kill rates of females were higher than that of males although adult males killed larger prey and 2–6 times more livestock compared to females and young males.

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T.124 Håkan Sand

Predation ecology and top-down effects of wolves in a strongly anthropogenic influenced landscape – lessons from Scandinavia.

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T.125 Peter Savolainen

Origins of the domestic dog: Out of Southern East Asia

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Abstract for talk Based on a unique global sample from 4,000 dogs, all kinds of genetic data (mtDNA, Y-chromosome DNA and whole genome sequences) present similar pictures: Southern East Asia harbors the full range of the universal dog gene pool while other populations have only a subset, and diversity follows a gradient across Eurasia. For example, in similarity to the human mtDNA tree indicating the "Out of Africa" scenario, only Southern East Asia has all the 10 deepest-branching dog mtDNA haplogroups, and the number of haplogroups follow a gradient down to only 5 in e.g. Europe and the Middle East. Likewise, PCA based on nuclear SNPs shows dogs in Southern East Asia closest to wolf and a gradient correlated to the geographical distance from Southern East Asia. In similarity to humans, domestic dogs have interbred with "archaic populations", i.e. wolves, in numerous locations, e.g., Scandinavia, the Middle East, Japan and Siberia, contributing around 5% of the genetic diversity in today's dogs.

T.126 Stéphanie Schai-Braun

Home range use by the European hare (*Lepus europaeus*) in an agricultural area with small fields analysed at a fine temporal scale

Stéphanie Schai-Braun <stephanie.schai-braun@boku.ac.at>^a

University of Natural Resources and Life Sciences, Vienna, Institute of Wildlife Biology and Game Management, Austria

Abstract for talk European hare (*Lepus europaeus*) home ranging behaviour has been studied only in agricultural areas with medium to large fields. We tracked nine European hares by means of GPS and VHF collars in an agricultural area with small fields in Austria. In particular, we analysed the hares' space use at a fine temporal scale. Furthermore, we compared data calculated from GPS and VHF telemetry. Home ranges were smaller in this agricultural area with small fields than has ever been measured. Our findings suggest that with GPS it is possible to distinguish between the movement path and the relative location of distinctly used areas within an animal's home range, whereas with VHF these two parameters may be difficult to separate. In conclusion, our results show that in areas where resources are easily accessible, such as in agricultural areas with small fields, the European hare is able to reduce its home range size to almost half of the minimum size that has been recorded so far in other habitats.

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T.127 Irena Schneiderová

The alarm call of the European ground squirrel (*Spermophilus citellus*): still quite unexplored field

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Abstract for talk Although there has been quite intensive research on alarm calls of Holarctic ground squirrels, less attention has been paid to Palearctic species, including the European ground squirrel (*Spermophilus citellus*). Studies that I have conducted together with my colleagues showed that alarm call of this species, and also two closely related species, usually consists of two structurally different elements. The first element has constant frequency whether the second element is more frequency-modulated. We have found that alarm calls containing only the first element are often produced but the functional significance of such structural variability is still unknown. The talk will summarize our present knowledge about acoustic structure of alarm calls emitted by the European ground squirrel and will emphasize that it is still quite unexplored field.

T.128 Irena Schneiderová

Species determination of lesser galagos (*Galago* spp.) at zoos integrating molecular-genetic and bioacoustic data

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Abstract for talk Lesser galagos (*Galago* spp.) show a lack of morphological diversity which complicate their correct determination. Therefore, the location of capture of founding animals has been the prevailing cue used by zoos for their determination. We used molecular-genetic and bioacoustic approaches to determine the lesser galagos with unclear taxonomic status kept at European zoos. All major lines kept at these zoos were sampled for DNA and their advertisement calls were recorded. Both approaches were applied successfully. Together with data extracted from studbooks, our results confirmed that *G. moholi* is kept at five, and *G. senegalensis* at 18 European zoos. Surprisingly, molecular-genetic data showed that there are two clearly separated genetic lineages of *G. senegalensis*. The first lineage is represented by animals originating from Ghana and Togo and the second lineage by animals originating from Guinea. Bioacoustic data indicated that the observed variability is at an intra-species level.

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T.129 Andreas Seiler

Are animal-vehicle collisions a random event? – Analysis of the spatial distribution of accident reports

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Abstract for talk Ungulate-vehicle collisions (UVC) in Sweden are an increasing traffic safety issue. Conventional prevention methods seem not cost-effective and both Transport and Wildlife administrations call for better mitigation strategies. We present first analysis of UVC location data provided by hunters during 2010 to 2014 and applied a modified kernel density estimation technique to identify significant clusters. Of the 116000 UVC we could study, up to 45% were distributed in a significantly aggregated pattern. UVC clusters corresponded for less than 3% of the road network, but there were important differences between species and regions. We conclude that only a small portion of the road network needs to be mitigated by physical mitigation measures such as fences or fauna passages to affect a substantial part of UVC. Still, a major part of UVC occurs randomly and thus needs a different mitigation approach that focuses on global factors such as wildlife population densities and driver behaviour.

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T.130 Andreas Seiler

Wildlife on tracks – an innovative project to mitigate ungulate-train collisions

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Abstract for talk Train drivers in Sweden report thousands of collisions with ungulates (UTC) per year. New statistics on repair costs indicate high corporative expenses for train operators and consequent delays in rail traffic produce additional socio-economic costs. We present a new project started in 2015 that aims at developing innovative and adapted alerting systems to reduce the risk for UTC. Our approach seeks to teach animals to respond adequately and timely to approaching trains, while allowing free movements across railroads when no trains are near. In preparation, we analyzed the spatial and temporal distribution of UVC on railways reported during 2001 to 2012 and identified hotspots where experimental test sites can be installed cost-efficiently. We also employed video documentation from approaching trains to study the reaction of animals to trains and to optical and acoustical warning signals. We will present first results from these studies and discuss implications for mitigation.

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T.131 Teodora Sin

Wolf (*Canis lupus*, L. 1758) diet and prey selection in the South-Eastern Carpathian Mountains, Romania

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Abstract for talk The Romanian wolf population, one of the largest in Europe, occupies a total home-range of 90000 sqkm and is spread across a variety of landscapes - from highly anthropized hills and plateaus to remote, densely forested mountains. However, up to now there are no reliable studies to document the feeding habits of the species. From November 2013 to October 2014, 252 scat samples were collected by following pre-established transects (total length of 590 km). The study area (500 sqkm) is a multi-prey species ecosystem in the southern sector of the Eastern Romanian Carpathians. Wolf diet was expressed as: i) frequency of occurrence of food items, ii) relative volume of food items, iii) percentage of biomass consumed. Feeding habits were assessed in relation to prey species availability. Our study represents a first step to analyzing wolf's foraging behavior in the Romanian Carpathians and is useful to address the complex issues of wolf and wild ungulate populations management.

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T.132 Navinder Singh

Linking migratory tactics with reproduction in a large mammal

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Abstract for talk A crucial decision during an animal's life cycle is when to migrate in relation to giving birth, which may have lasting consequences on their population demography and fitness. How does this decision synchronize at an individual level and how does life history influence this decision? In this study, we tested the effect of timing of birth and individual life history on distance, timing, stop overs and duration of migration of 190 moose (*Alces alces*) females that have been tracked for multiple years. We then contrasted these characteristics across females with different reproductive status and related them to the start of the growing season. Females were observed to give birth before, during or after migration. These multiple migratory tactics in relation to giving birth have not been reported earlier in any other species. We discuss the implications for such strategies in terms of foraging theory and green wave hypothesis.

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T.133 Tarja Sironen

Aleutian mink disease virus in free-ranging mustelids in Finland

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University of Helsinki, Finland

Abstract for talk Aleutian mink disease virus (AMDV) can cause an immune complex disease in American mink. AMDV has been detected in several other mustelid species with potential negative impact on their health and population. A molecular and cross-sectional epidemiologic study was conducted to gain data on the prevalence, distribution, transmission, and diversity of AMDV strains in Finnish free-ranging mustelids and risk factors associated with infection. The presence of anti-AMDV antibodies and/or AMDV DNA was tested from 308 samples representing 8 mustelid species and 17 regions. . Positive samples were detected in 54% of feral American mink, 27% of badgers, 7% of polecats. This study showed that AMDV is prevalent in certain species of Finnish free-ranging mustelids and widely distributed across the country. Furthermore, the free-ranging mustelids carry both strains similar to those found in farmed mink, but also distinct strains that may represent novel amdoparvoviruses.

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T.134 Christina Skarpe

Herbivores and landscapes

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Abstract for talk Large herbivores exploiting landscape heterogeneity may thereby create their own landscape. The Chobe savannas consist of nutrient-poor sand. Only patches at the river are nutrient-rich alluvium. The largest of these were described by Selous 1874 as to the greater part open, though here and there with patches of bush. Between 1874 and 1900 elephants in the area were exterminated by ivory hunters. From 1896 rinderpest killed most pair-toed animals. So, by 1900 the area was virtually without large herbivores - and trees grew to a tall and dense woodland on the alluvium. By 1960 elephants and ungulates were back, preferring to feed on the alluvium. Elephants spectacularly killed the old trees and impala secretly ate the regeneration. The alluvium has preferred vegetation and will always be heavily utilized by passing elephants and stationary antelopes. The area is today to the greater part open though here and there with patches of bush.

T.135 Mark Statham

Range-wide multilocus phylogeography of the red fox reveals ancient continental divergence, minimal genomic exchange, and distinct demographic history

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Abstract for talk We conducted the most geographically and genomically comprehensive study to date of the red fox (*Vulpes vulpes*). Analyses of mitochondrial sequence in over 1000 individuals suggested an ancient Middle Eastern origin for all extant red foxes and a 400 kya origin of the primary North American clade. Demographic analyses indicated an expansion in Eurasia during the last glaciation (50 kya), coinciding with the secondary transfer of a single matriline to North America. Analyses of 11 autosomal loci from a subset of foxes supported the colonization timeframe suggested by mtDNA (and the fossil record), but, in contrast, reflected no detectable secondary transfer, resulting in the most fundamental genomic division of red foxes at the Bering Strait. Endemic continental Y-chromosome clades concurred with this subdivision. Our findings support a model of peripatric speciation and are consistent with the previous classification of the North American red fox as a distinct species, *V. fulva*.

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T.136 Joanna Stojak

Contrasting and congruent patterns of genetic structuring in two *Microtus vole* species in Poland using museum specimens

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Abstract for talk The common vole *Microtus arvalis* and the field vole *Microtus agrestis* are morphologically similar species, but have contrasting evolutionary histories and ecological requirements. In this study, we analysed genetic variation in these two vole species across a phylogeographic suture zone in Poland using microsatellite DNA markers obtained from museum specimens from the 1960s and 1970s. We genotyped 190 individuals of the common vole at 11 loci and 190 individuals of the field vole at 13 loci. Overall F_{st} was higher in the common vole than in the field vole. Bayesian clustering analysis demonstrated that there were two genetic groups for each species. Despite the different phylogeographic histories of the two species in the region using mitochondrial DNA, they display similar patterns of contemporary genetic structure using microsatellites. It is therefore evident that both ancient and contemporary events are leaving different signals in related vole species.

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T.137 Sally Street

How introduction effort promotes invasion success in mammal species

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Abstract for talk The best predictor of invasion success is 'introduction effort' - the total number of introduced individuals. Recent theoretical models however make contrasting predictions; either invasion success increases with few releases of large populations to oppose demographic stochasticity (Cassey et al. 2014), or many releases of small populations to overcome environmental heterogeneity (Duncan et al. 2014). We test these predictions on mammalian invasions, using phylogenetically informed analyses. We find that species introduced to more locations are more likely to establish and spread. Controlling for number of locations, the probability of establishment and spread does not increase with greater total individuals released or mean individuals per location. Therefore, our results suggest that overcoming environmental heterogeneity is the main barrier to the establishment and spread of introduced mammalian species, rather than extinction risks associated with small population size.

^aCo-authors: Will Allen, Chris Venditti, Isabella Capellini

T.138 Astrid Vik Stronen

Genome-wide analyses suggest parallel selection for ubiquitous functions may eclipse local adaptation in European wolf (*Canis lupus*) populations

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Abstract for talk Local adaptation may occur across short distances in the presence of strong environmental gradients and European wolves exhibit distinct north-south structure. We investigated 67K SNP loci in 59 unrelated wolves from four populations (North-central, Carpathian Mountains, Dinaric-Balkan, Ukrainian Steppe). Our study combined outlier identification with genome-wide association of individual profiles and 12 environmental variables. We identified 353 SNPs and examined their position and surroundings (1Mb) in the dog genome for genes potentially under selection. We observed functional genes for e.g. temperature regulation that suggests influence of local adaptation. We detected strong outliers not associated with any variable, which may indicate selection associated with unmeasured factors. Most results entailed universally important traits, including sensory and cognitive functions, with associated SNPs typically showing marked differences in allele frequencies among population clusters.

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T.139 Aimee Tallian

The role bison sex and group size in wolf-bison interactions

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Abstract for talk Due to the large scale destruction of wolf-bison systems in North America during the 19th century, we know little about how these two species interact in the wild. We looked at the influence of bison group size on wolf hunting success and bison behavioral response in Yellowstone National Park, and found significant differences in these effects between bison sex-specific groups. We found a cumulative nonlinear effect of mixed group size on wolf hunting success, while bull group size had no overall effect. Mixed groups of bison were more likely to be attacked than bull groups, and bison behavioral response was an important overall predictor of wolf hunting success. The probability of a confrontational response decreased with bull group size and increased with mixed group size. Understanding behavioral relationships between wolves and bison, which ultimately affect population, community and evolutionary dynamics, is an important conservation and management issue.

^aCo-authors: Dr. Daniel MacNulty

T.140 Joaquim Tapisso

Dynamic of chromosomal evolution in two parapatric Rb races of house mouse in the island of Madeira

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CESAM-Lisboa, Departamento de Biologia Animal, Faculdade de Ciências da Universidade de Lisboa, Portugal

Abstract for talk The house mouse has a standard karyotype composed by 40 acrocentric chromosomes. However, some populations exhibit metacentric chromosomes resulting from Robertsonian (Rb) fusions. The fixation of fusions results in the occurrence of Rb races that often come in contact. Here we report a temporal comparative analysis (1999–2002 vs. 2012–2014) involving two Rb races that come in contact in Madeira island. They are characterized by 8 fusions of which they share 7, thus differing by the presence of Rb (6.7), Estreito da Calheta race and Rb (7.15), Achadas da Cruz race. The karyotype analysis during the first period indicated a population dynamic congruent with a source-sink model, with E. da Calheta acting as source and A. da Cruz acting as sink. One of the most important evidence supporting such assumption is the prevalence of the fusion 6.7 in the contact zone. The results concerning the most recent period reinforce the hypothesis of a source-sink dynamic.

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T.141 Ewa Tarnowska

Maintenance of contact zone between two bank vole phylogenetic lineages in NE Poland

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Abstract for talk Two phylogenetic lineages of bank vole (Eastern and Carpathian) which survived in different glacial refugia, have come to secondary contact in NE Poland. The aim of our project is to study the evolutionary and ecological mechanisms, which maintain the contact zone. We analysed a fragment of cyt b gene to map this contact zone. To verify susceptibility for Lyme disease as a factor, which can determine spatial distribution of two lineages we analysed partial sequence of TLR2 gene. We checked if the distribution of the two lineages correlated with different environmental conditions in habitats where they occurred. The contact zone between lineages was from 45 to 273 km wide. Genetic diversity was twice as high in the Carpathian lineage. The distribution of two bank vole clades was strongly correlated with environmental factors, which can be related to conditions in refugia where they survived. TLR2 gene analysis, showed presence of two haplogroups, which differ in Lyme disease prevalence.

^aCo-authors: Bogumiła Jędrzejewska, Joanna Gerc, Zofia Korbut and Magdalena Niedziakowska

T.142 Anne-Mathilde Thierry

Estimating dispersal in Arctic fox juveniles released from the Norwegian captive-breeding program

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Abstract for talk Dispersal is a key determinant of population dynamics and fundamental to the persistence of wild populations. Patterns of dispersal are influenced by various environmental parameters, including geographical barriers, and by inter- and intra-specific interactions. In territorial species living in fragmented habitats and relying on fluctuating resources like the Arctic fox (*Vulpes lagopus*), the dispersal and settlement of immigrants may be the key to population persistence. I will present on-going work on dispersal in Arctic fox juveniles released from a captive-breeding and reintroduction program in Norway. This program is part of the national action plan to protect Arctic fox populations in Norway, where the species is threatened. Monitoring of wild- and captive-born foxes over a large geographical range, from birth or release to establishment and reproduction, reveals capacity for long-range movements of Arctic foxes among fragmented mountain areas.

^aCo-authors: Veronika Areskoug, Nina E. Eide, Øystein Flagstad, Kristine Ulvund, Anders Angerbjörn, Karin Norén, Arild Landa

T.143 Carl-Gustaf Thulin

WORKSHOP TALK: Analyses of hare and fox game bags in Sweden indicate population crash in southern mountain hares

Carl-Gustaf Thulin <carl-gustaf.thulin@slu.se >
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Abstract for talk Scientific and undocumented observations indicate a decreasing population trend among mountain hares (*Lepus timidus*) across Fennoscandia (Finland, Sweden,

T.144 Jean-Luc Tison

Population structure and recent temporal changes in genetic variation in Eurasian otters from Sweden

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Swedish Museum of Natural History, Sweden

Abstract for talk The Eurasian otter (*Lutra lutra*) population in Sweden went through a drastic decline in population size between the 1950s and 1980s. However, after the bans of PCBs and DDT in the 1970s, the population began to recover in the 1990s. This study compares microsatellite data across twelve loci from historical and contemporary otter samples to investigate whether there has been a change in population structure and genetic diversity across time in various locations throughout Sweden. The results suggest that otters in the south were more severely affected by the bottleneck, demonstrated by a decline in genetic diversity and a shift in genetic composition. In contrast, the genetic composition in otters from northern Sweden remained mostly unchanged, indicating that the decline was not uniform across the country. Moreover, our analyses of historical samples provide an overview of the level of genetic variation and population structure that existed prior to the bottleneck. In press *Conserv.Gen*

^aCo-authors: Victor Blennow, Eleftheria Palkopoulou, Petra Gustafsson, Anna Roos, Love Dalén

T.145 Malgorzata Tokarska

Genetic background of Posthitis in the European bison

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Abstract for talk Posthitis is a necrotic inflammation of prepus which starts with swelling of the genitals with purulent exudate, later appear necrotic changes that lead to auto-amputation of penis and subsequently to death due to overall infection. This severe disease of unknown background affects approx. 6% of the European bison males every year. The results of GWAS analysis based on high density BSP microarray confirmed the existence of genetic prevalence in bison posthitis. The areas showing association with posthitis include genes responsible, in human, for atopic dermatitis, formation of endometrial cancer, cancer metastasis process and pathogenesis of various types of dermatoses, the development of skin cancer and testicular cancer.

^aCo-authors: Kamil Oleński, Stanisław Kamiński, Dorota Maria Hering, Paulina Puckowska, Anna Ruś, Cino Pertoldi

T.146 David Tosh

Monitoring small carnivore populations using citizen scientists

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Abstract for talk Monitoring the distribution of a species is fundamental to its effective conservation and management. However, conventional monitoring methods can require specialist training and techniques (i.e. scat surveys), and can be expensive and time consuming. We therefore present a simple method that overcomes these limitations and has been effectively utilized by "citizen scientists" to rapidly assess the distribution of pine marten (*Martes martes*). More than 60% of the 250 sites visited were surveyed by the 70 citizen scientists who participated over 3 months. Pine marten were recorded in 20% of sites visited and in over 30% of 10 km squares surveyed. Our results reveal how the combination of a simple methodology with enthusiastic citizen scientists can be effective in monitoring species distributions. We advocate the use of citizen scientists in monitoring species distributions in the future.

T.147 Alessia Uboni

**Widespread declines in ground lichens in northern Sweden:
consequences for reindeer husbandry**

Alessia Uboni <auboni@mtu.edu>
Umeå University, Sweden

Abstract for talk In Sweden, all reindeer are semi-domesticated but range freely for most of the year and are thus dependent on the availability of natural forage. Winter forage is the limiting factor in most herding districts. In the last century, northern Sweden has experienced profound changes in land use, such as an increase in infrastructures, forest harvesting and mining activities. Consequently, we would expect to observe a loss in areas suitable as reindeer pastures and a decline in reindeer numbers. We analyzed the availability of reindeer winter forage, i.e. ground lichens, in the last 60 years at the national, county and reindeer herding district level. We found consistent declines in ground lichens, with northern areas experiencing the strongest declines. Paradoxically, reindeer numbers do not seem to have been influenced by those declines. I will present the results of those analyses and discuss how reindeer husbandry might have coped with habitat loss.

T.148 Ester Rut Unnsteinsdottir

**Fecundity and population dynamics of the Icelandic arctic fox – a 50
year case study**

Ester Rut Unnsteinsdottir <ester@ni.is>
The Icelandic Institute of Natural History, Iceland

Abstract for talk The Icelandic arctic fox population declined from a potential maximum in early 1950s to a minimum of 1000 individuals in late 1970s. Since then it grew constantly for 30 years and had reached almost 10000 individuals in September 2008. Detailed hunting statistics is available since 1958 and age estimation has been conducted on a significant sample of the annual kill since 1979, in order to estimate population size by cohort analysis. Fertility has been measured since 1986 by counting placental scars in killed fox vixens. The arctic fox is a monogamous, territorial species and breeding only occurs once a year. Thus available territories and mates, as well as body condition during the winter should be amongst potential explanatory factors. In other countries, fertility and breeding success have been shown to concur with peaks of rodent abundance. In Iceland, where no cycling rodents exist, other forces are believed to drive the population dynamics of the arctic fox than in areas where fluctuating rodents are the main prey.

T.149 Frank Van Langevelde

How unusual is the terrestrial mammal community of Barro Colorado Island? A Neotropical cross-forest comparison using camera traps

Frank Van Langevelde <frank.vanlangevelde@wur.nl>^a
Wageningen University, The Netherlands

Abstract for talk Barro Colorado Island (BCI), Panama, is one of the world's most influential field sites in tropical forest ecology. However, the intactness and representativeness of its fauna have been questioned, but only based on assessments that themselves were criticized for methodological bias. We used standardized camera-trapping data representing a total sampling effort of 133 years to compare the terrestrial mammal communities of BCI and 12 relatively remote and intact Neotropical forest sites. We found that each area has a different representation of mammal guilds. BCI stood out by having relatively low species richness and evenness, and a high representation of the granivores and frugivores. However, in terms of guilds, BCI was not more different from other sites than were other individual sites. We conclude that terrestrial mammal communities are highly variable among intact Neotropical sites, and that given this variation the terrestrial mammal community of BCI is not particularly unusual.

^aCo-authors: D. Ros Oller, J. Giacalone-Willis, Chantal Vogels, C. Lázaro San Andres, H. Esser, Y. Liefting, R. Kays, N. Meyer, P.A. Jansen

T.150 Nagarjun Vijay

Genome-culture coevolution promotes rapid divergence in the killer whale

Nagarjun Vijay <nagarjun.vijay@ebc.uu.se>^a
Evolutionary Biology Center, Uppsala university, Sweden

Abstract for talk The interaction between ecology, culture and genomic evolution remains poorly understood. To explore this, we analyzed population genomic data for differentiation among divergent ecotypes of killer whale, and found that stable behavioral and ecological variation are better predictors of genetic structuring than geography. Our findings are consistent with expansion of small founder groups into novel niches by an initial plastic behavioral response, perpetuated by social learning imposing an altered natural selection regime. The study thus constitutes an important step toward understanding the complex interaction between demographic history, culture, ecological adaptation and evolution at the genomic level.

^aCo-authors: A. D. Foote,¹³ authors, M. T. P. Gilbert, J. B.W. Wolf

T.151 Kristina Vogt

Scent-marking in a stalking predator: Is there a trade-off between intra-specific communication and hunting behaviour in the Eurasian lynx *Lynx lynx*?

Kristina Vogt <k.vogt@kora.ch>^a
University of Basel/ KORA, Switzerland

Abstract for talk The costs of signalling are often expressed in terms of increased predation risk to the signaller; however, whether signalling predators bear costs due to eavesdropping by prey has not been studied extensively. In this study, we investigated whether there is a trade-off between scent-marking and the risk of alerting prey in a stalking predator, the Eurasian lynx. We followed tracks of wild lynx in the snow and recorded scent-marks and hunting events. Lynx preferred conspicuous objects for marking. On tracks with evidence of hunting behaviour, lynx engaged less in scent-marking but increased marking rate when walking along linear structures. During the mating season, they increased marking rates when they were not hunting. Time and distance to the last kill were not associated with marking rate. We found evidence that lynx face a trade-off between enhancing detection of scent-marks by conspecifics and avoiding eavesdropping by prey, but marking rate is influenced by several factors.

^aCo-authors: Elizabeth Hofer, Andreas Ryser, Mathias Kölliker, Urs Breitenmoser

T.152 Märtha Wallgren

Moose browsing patterns on young Scots pine with implications for forestry

Märtha Wallgren <martha.wallgren@skogforsk.se>
Forestry Research Institute of Sweden, Sweden

Abstract for talk The Swedish moose (*Alces alces*) population is among the densest in the world and important from social aspects, primarily hunting, as well as for ecological services. The most important winter forage for moose is Scots pine (*Pinus sylvestris*), which is also one of the two most important tree species for Swedish forestry. Moose browsing on young Scots pine may affect the trees in terms of retarded growth, increased risk of mortality and altered stem structure. A current research challenge is to understand underlying determinants of moose browsing patterns, as well as to find means for reducing the negative effects for forestry. Our results reveal complex relationships between browsing intensity and explanatory variables, but also that appropriate management methods can diminish browsing damages to young pines. Such methods should be evaluated in relation to other factors, such as level of browsing pressure and various forest parameters, as well as be applied on relevant spatial scales.

T.153 Roselyn Ware

The Role of Resource Partitioning in Supporting UK Bat Diversity

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Abstract for talk An understanding of the dietary niches occupied by bats is a valuable tool for informing conservation strategies. There are numerous methods used for studying bat diets; each with benefits and drawbacks. Past research has compared small numbers of species at a time, making inter-species comparisons difficult. Our large repository of bat guano samples, collected from around the UK, has allowed us to study the bat species under one methodological 'umbrella'. We took two approaches. The first is metagenomic, providing information about the prey species, about the bat itself, and associated bacterium. Analyses of this data show that there are several dietary forms seen between the species. The second is a barcoding approach, using arthropod-specific primers, allowing the development of a high-resolution picture of the prey species. This talk compares the efficacy of the methods, assesses the role of resource partitioning in bat species co-existence, and reports on our findings.

^aCo-authors: Robin Allaby

T.154 Sarah Woodfin

The elusive Annamite striped rabbit *Nesolagus timminsi*

Sarah Woodfin <s.woodfin@uea.ac.uk>^a
University of East Anglia, United Kingdom

Abstract for talk In 1990s, biologist Rob Timmins (WCS) discovered the remains of a striped rabbit in a local market in Laos. In collaboration with Diana Bell's research group at the University of East Anglia, genetic analysis revealed that this was a new species in the genus *Nesolagus* which contains the Sumatran striped rabbit *N. netscheri* and that the two appeared to have diverged several million years ago (Nature 1999). Since then both rabbits have been captured on camera traps but nothing is known about the ecology or conservation status of either species. In March 2015 Sarah Woodfin conducted surveys of the habitat in the Central Annamite mountains in Vietnam at location where *N. timminsi* had been photographed. This paper presents the results of this research and discusses the implications for the conservation of this new species to science. Sarah was also fortunate enough to be the first scientist to capture and collect morphometrics on a rabbit which was then released back into the forest.

^aCo-authors: Anders Angerbjörn and Diana Bell

T.155 Nobuyuki Yamaguchi

Basking in the winter sun: thermoregulation in the Ethiopian hedgehog, *Paraechinus aethiopicus*, in Qatar

Nobuyuki Yamaguchi <yamaguchi@qu.edu.qa>^a

Department of Biological and Environmental Sciences, Qatar University, Qatar

Abstract for talk Biologists focus on thermoregulation of desert mammals in terms of how they minimise heat gain during hotter months, and put less effort on how they maximise heat gain during cooler months. Heat gain may contribute to energy savings of desert mammals during cooler period when the ambient temperature in desert is substantially lower than their body temperatures. We investigated the thermoregulation in free-ranging Ethiopian hedgehogs, *Paraechinus aethiopicus*, during winter using radio-telemetry in Qatar. Temperatures detected by the tag attached to hedgehogs were significantly higher than ambient temperatures throughout the day, and the difference was more extreme during the mid-day. We also observed several hedgehogs basking with their radio-tags exposed to direct sunlight. It is possible that basking is beneficial for the hedgehog's winter thermoregulation in the desert where plenty of solar radiation is available. This is the first report of basking in the subfamily Erinaceinae.

^aCo-authors: Mohammad A. Abu Baker, Nigel Reeve, Ivan Mohedano, April A. T. Conkey, David W. Macdonald

T.156 Nigel Yoccoz

Modelling the impacts of climate change on mammals: how to open the ecosystem black box?

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UiT The Arctic University of Norway, Norway

Abstract for talk The question today is not if climate change will have an impact. Ecosystems and their mammalian populations will change, sometimes in surprising ways. Models should play an important role in analyzing, understanding and predicting these impacts. However, while models of single-species population dynamics are powerful analytical and prediction tools, models of ecosystem dynamics are still elementary in terms of robustness. We might know qualitatively mechanisms driving ecosystem dynamics, but the data available do not allow for an in-depth analysis at relevant temporal and spatial scales. One example is predator-prey interactions in the context of small mammal cycles, a driver of ecosystem dynamics in northern regions. We still do not have reliable data on weather, prey and predator populations that can separate among models making different predictions. Given the large uncertainty, integrating more closely monitoring and modelling should help us opening the ecosystem black box.

T.157 Marketa Zimova

Camouflage mismatch in seasonal coat color due to decreased snow duration: Will snowshoe hares keep up with climate change?

Marketa Zimova <marketzimova@gmail.com>^a
North Carolina State University, United States

Abstract for talk Reduction in snow duration represents a direct potential stressor for species undergoing seasonal color molts. We investigated whether snowshoe hares may adapt to mismatch between their coat color and background through phenotypic plasticity and evolution. We observed nearly 200 wild hares over 3 widely disparate snow years and 2 study sites in Montana, USA, and found minimal plasticity in response to camouflage mismatch in molt phenology and anti-predatory behaviors. Thus, adaptive responses to mismatch will require evolutionary changes. We found high individual variation in coat color and consequently in mismatch, and detected high fitness costs of mismatch, with hares suffering up to 7% lower weekly survival rates when mismatched. In the absence of evolution we expect drastic hare population declines of up to 24% by late century. Our results indicate that persistence of this prey mammal species and their ecosystem under climate change will require fostering evolutionary rescue.

^aCo-authors: L. S. Mills, M. Mitchell, P. Lukacs, and J. J. Novak

T.158 Karol Zub

Climate warming is affecting mortality of weasels due to camouflage mismatch

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Mammal Research Institute, Białowieża, Poland

Abstract for talk In Poland exist two subspecies of weasel *Mustela nivalis*, which differ in winter pelage, white in *M. n. nivalis* and brown in *M. n. vulgaris*. Weasels are vulnerable to attacks from other predators, thus cryptic coat color may affect their mortality. Thus we hypothesize that natural selection should favor one of phenotypes, according to prevailing weather conditions during winter. Analyze of trapping data from the Białowieża Forest, where both subspecies occur sympatrically, revealed that proportion of *M. n. vulgaris* increased along with decreasing number of days with snow cover and increasing mean ambient temperature. To demonstrate that white or brown winter pelage gives advantage, by affecting predation rates, we performed a field experiment using weasel models (white and brown) exposed against different background color. Preliminary results demonstrated that white models of weasels were attacked significantly more often by predators when exposed on the dark background.

^aCo-authors: Anna Andruszkiewicz

T.159 Sophie von Merten

Does sociability relate to personality? A comparison between four species of shrews

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Department for Systematic Zoology, Adam Mickewicz University, Poznań,
Poland

Abstract for talk The sociability of animal species influences different aspects of their behaviour and life history. We hypothesise that a species' sociability also relates to its personality and behavioural plasticity, with more sociable species showing a wider range of personality types and higher levels of plasticity. We tested our hypothesis using 4 species of shrews differing in their sociability: while *Neomys fodiens*, *Sorex araneus*, *S. minutus* are solitary, *N. anomalus* shows a higher tolerance to conspecifics. To assess differences in personality and plasticity, we analysed the influence of tested individual and encountered species on behavioural parameters during intra- and interspecies dyadic encounters using linear mixed models. Confirming our hypothesis, we found that the more sociable *N. anomalus* shows more different personality types and higher levels of plasticity. Likely, higher numbers of social interactions can help to establish and maintain different personality types and vice versa.

^aCo-authors: Rafał Zwolak, Leszek Rychlik

2 Abstracts for poster

P.1 Marzena Albrycht

Population dynamics of European hare *Lepus europaeus* in relation to intensity of agriculture and predation in Poland during 1976–2014 period

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Institute of Biology, Pedagogical University in Cracow, Poland

Abstract for poster The harvesting of European hare decreased from 700,000 in 1970 to 13,000 in 2014. The drop in 1997–2014 has been caused by the decrease in the diversity of cultivated crops as the share of cereals and oil plants increased ($r: 0.98$, $p: 0.00$) and biodiversity decrease (Simpson coefficient $r: -0.90$, $p: 0.00$). During introduction of monocultures baulks were eliminated which provide hares with food and shelter in winter. The use of herbicides increased ($r: 0.98$, $p: 0.00$) decreasing the species diversity. The mortality of hares was increased with the mechanization of agriculture which is reflected by the increase in the number of tractors from 619 to 1466 thousand (1980–2010). The predation increased because of vaccination against rabies for mesopredators and protection of birds of prey and synantropic predators. Improving hiding/thermal cover and winter food resources, together with reduction the number of foxes, raccoon dogs and stray dogs should rebuilt hare population in Poland.

P.2 Amna Arshad Bajwa

DNA metabarcoding for Diet and parasitic estimation of Markhor (*Capra falconeri*) in Chitral, Pakistan

Amna Arshad Bajwa <amnaarshadbajwa@gmail.com>^a
University of Veterinary & Animal Sciences Lahore, Pakistan

Abstract for poster Markhor (*Capra falconeri*) population in Pakistan is facing a number of threats and IUCN has enlisted this wild goat as endangered according to observational studies. Markhor has been found to be the definite hosts of parasitic nematodes and can be an additional cause of decreasing the population. The domestic goat is a potential competitor with the markhor due to habitat overlap. This study will demonstrate that non-invasive fecal DNA sampling is feasible for wild goat population diet analysis and estimation of gastrointestinal parasitic load. Diet habit of markhor will be estimated by exploiting vascular plants specific metabarcode markers followed by Next Generation Sequencing technologies. Similar strategy will be used for the estimation of parasitic disease load, especially nematodes, using nematodes specific primers. The sequencing results will be analyzed by exploiting bioinformatics tools for the diet and nematodes identification of markhor species.

^aCo-authors: Saher Islam and Wasim Shehzad

P.3 Marjorie Biffi

Some insights into the local habitat use of the semi-aquatic Pyrenean desman (*Galemys pyrenaicus*) in the French Pyrenees

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Abstract for poster A comparative approach was used to investigate potential differences in local habitat of the endangered and endemic Pyrenean desman between the three main hydrological regions of the French Pyrenees. An Ecological Niche Factor Analysis was applied to a recent dataset describing its spatial distribution to provide the first quantitative estimate of local habitat use by this mammal. Key habitat variables were mainly related to riverbed (i.e. high heterogeneity of shelters and river substrates) and riverbank (i.e. high proportion of rocks) characteristics. A difference in habitat use between the three regions was highlighted, suggesting a spatial structure in desman populations regarding local factors. These results stress the importance of an effective and sustainable river management for the habitat quality of this endangered species. They also highlight the importance of accounting for the contrast between habitat preferences that can exist for geographically distinct populations.

^aCo-authors: Anaïs Charbonnel, Laëtitia Buisson, Frédéric Blanc, Mélanie Nemoz, Pascal Laffaille

P.4 Anthony Caravaggi

The democratisation of conservation: public attitudes towards lethal control of invasive leporids and implications for species management

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Queen's University Belfast, United Kingdom

Abstract for poster Invasive, non-native species are a global threat to biodiversity, most notably native ecological competitors. Invaders are subject to national and international legislation which aims to mitigate their impact. However, species control in the United Kingdom is a controversial issue in which the general public are increasingly influential. The European brown hare was introduced to Ireland over 100 years ago. The only extant population exists in mid-Ulster, where the invasive range is expanding, to the detriment of the endemic Irish hare. Northern Ireland is largely comprised of small agricultural fields; landowners are likely to be influential in deciding which management measures may be adopted. 1,680 questionnaires were delivered across Northern Ireland to investigate the level of awareness of the invasive species issue and ascertain whether governmental intervention would be supported. We present our results and a road-map for direct management of the invader, should it be undertaken.

^aCo-authors: W. Ian Montgomery & Neil Reid

P.5 Rory Carroll

Natural and anthropogenic drivers of bobcat (*Lynx rufus*) population structure in northeastern United States

Rory Carroll <rorypocarroll@gmail.com>^a
University of New Hampshire, United States

Abstract for poster Population genetic structure results from spatial variation in effective dispersal events and is driven by geographic distance and environmental factors. Anthropogenic disturbances, especially urban areas and high traffic volume roadways, are ubiquitous environmental obstacles for dispersing individuals in the northeastern United States. This is particularly true for wide-ranging carnivores such as the bobcat (*Lynx rufus*). To determine the relative effects of anthropogenic and natural features on bobcat dispersal, we genotyped 300 bobcats at 16 microsatellite loci. Results show division into at least 4 subpopulations. Using the observed genetic structure and GIS-based software packages, we identified putative corridors or barriers and the associated landscape features for each. Our research highlights conservation zones critical for the maintenance of genetically healthy populations of bobcats, a taxon that may function as an umbrella species for sympatric fauna.

^aCo-authors: Marian K. Litvaitis, Brittaney Buchanan, John A. Litvaitis

P.6 Ana Cerveira

Male quality assessment of two house mouse chromosomal races from Madeira Island

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CESAM, Centre for Environmental and Marine Studies, Dept. Biologia Animal, Faculdade de Ciências, Universidade de Lisboa, edif. C2, 1749-016 Lisboa, Portugal

Abstract for poster Opposite patterns of mate preference have been described between Achadas da Cruz (PADC) and Estreito da Calheta (PEDC) house mouse chromosomal races in Madeira Island. Race specific recognition signals, if they exist, do not seem to drive female preference. Here we assess differences in male quality between house mouse PADC and PEDC chromosomal races by analysing urine marking patterns, staging inter-racial male-male encounters and determining each race's urine chemical profile. Preliminary results suggest that PADC males have a higher dominance level than the south PEDC population. Additionally, given the differences found in marking behaviour between south and north PEDC males, our results suggest that dominance levels do not seem to be related with the chromosomal race but could instead be the result of differences in population density, habitat quality or genetic background.

^aCo-authors: Joaquim, S. Tapisso, Sofia I. Gabriel, Graça Ramalhinho, Maria L. Mathias

P.7 Derya Çetintürk

Phylogenetic Relationships of Guentheri Group Species of the genus *Microtus* (Rodentia: Muridae) in Turkey based on mitochondrial COX1 Gene

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Abstract for poster Three species of Guentheri Group Voles: *Microtus guentheri* (Southeastern Anatolia), *Microtus lydius* (Central and Western Anatolia) and *Microtus hartingi* (Turkish Thrace) in Turkey were investigated due to enlight their suspected taxonomic status and phylogenetic relationships. By using 63 specimens from 17 localities, approximately 720 bp sequences of COX1 gene were obtained and analysed. It was found that nucleotide diversity (Pi) was 0.03934, haplotype diversity (Hd) was 0.9457 and number of haplotypes was 31. The highest genetic diversification was between *M. guentheri* and *M. hartingi* while the lowest genetic diversification was between *M. lydius* and *M. hartingi*. Based on Tamura-3 parameter, Maximum Likelihood and Maximum Parsimony dendrograms formed the distinct clades for *M. guentheri* and *M. hartingi*, even *M. lydius* established a separate clade, some samples were positioned in *M. guentheri* clade that proved the close relationships between these taxa.

^aCo-authors: Nuri Yiğit (Ankara University), Ercüment Çolak (Ankara University), Fulya Saygılı Yiğit (Niğde University)

P.8 Andrea Corradini

Comparison of wolf (*Canis lupus*) and lynx (*Lynx lynx*) signs of presence in the Carpathian Mountains (Romania)

Andrea Corradini <corradini.andre@gmail.com>^a

University of Florence, Italy

Abstract for poster The relationship between wolf (*Canis lupus*) and lynx (*Lynx lynx*) in the Romanian Carpathians is still unclear. To date, no studies have been made but, due to the high cost of radio tracking, preliminary studies based on signs of presence can provide useful information. This study, located in the Eastern Carpathian Mountains (Romania), was carried out by the WOLFLIFE project (LIFE13 NAT/RO/000205) covering an area of 1.200 km² (12 squares 10x10 km, EU grid). The study area was surveyed over 119 days of consecutive snow cover during a total of 179 days of wolf monitoring. It used transects (n 57) of different lengths (mean 9,2 km), covering 522,9 km. A total of 69 wolf tracks and 48 lynx tracks were found. Analysis was performed using GIS. The spatial overlap of the signs of presence for both species was compared, considering variables such as land cover and altitude. Contingency tables based on presence/absence in 1-km and 500-m transect segments were also used.

^aCo-authors: Gabriella Rizzardini, Teodora Sin, Viorel Popescu, Ioan-Mihai Pop, Silviu Chiriac, Andrea Gazzola

P.9 Gonçalo Curveira-Santos

Drivers of badger occupancy in Northern Scotland

Gonçalo Curveira-Santos <goncalo-cs@hotmail.com>^a

Centre for Ecology, Evolution and Environmental Changes, Faculty of Sciences, University of Lisbon, Campo Grande, 1749-016 Lisbon, Portugal, Portugal

Abstract for poster Scottish badger (*Meles meles*) populations face an environment characterized by high climatic heterogeneity. We aimed to understand what environmental and anthropic factors drive badger inter and intra-area occupancy variability in Northern Scotland. We applied occupancy models to a comprehensive camera-trapping data set of 11 study areas. Aiming to emphasize the effect of intra-area factors, we clustered study areas into two topo-climatic groups, as temperature and altitude were the main determinants of inter-area variability of occupancy probability. In lower temperature and higher altitude, occupancy likelihood was related to agriculture patches, while in warmer but lower altitude areas, human disturbance (distance to settlements and roads) was the key driver of occupancy. Under predictions of increasing temperature and human population density, our results indicate that human activities will be an increasingly important factor in determining badger occupancy in Scotland.

^aCo-authors: André P. Silva, Kerry Kilshaw, Chris Newman, David W. Macdonald, Luciana Simões, Luís M. Rosalino

P.10 Miguel Delibes-Mateos

The importance of prey subspecies: predator distribution and European rabbits in their native range

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Abstract for poster The European rabbit *Oryctolagus cuniculus* is native to the Iberian Peninsula, where it serves as prey for more than 30 predator species. Two rabbit subspecies are recognized, which differ in morphology, genetic and behaviour. *O.c. algirus* is present in south-western Iberia, while *O.c. cuniculus* is found in north-eastern Spain. Using information from atlas of mammals and birds, we assessed whether species richness of predators that consume regularly rabbits varied between the distribution areas of both rabbit subspecies. The species richness of facultative and specialist predators on rabbits was slightly higher in the *O.c. algirus* distribution area. Also, 70% of the 10x10km grids inhabited by the highly endangered Iberian lynx *Lynx pardinus* and/or the Spanish Imperial Eagle *Aquila adalberti* were found in the *O.c. algirus* distribution area. These findings reveal the key role of this rabbit subspecies, endemic in the Iberian Peninsula, for predator conservation, namely the top-predators

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P.11 Jakub Drimaj

Preliminary findings on the reproductive biology of wild pigs (*Sus scrofa* L.) in the Czech Republic

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Abstract for poster Wild Boar is an autochthonous species in Central Europe, which in recent decades has increased its abundance, in response to favorable environmental conditions of intensively used cultural landscapes and inappropriate methods of hunting management. In order to better understanding of the population explosion of pigs was initiated research aimed at obtaining actual knowledge of their reproductive biology, in different parts of the Czech Republic. Collecting of reproductive organs was performed on common hunts from September 2014 to January 2015. There were collected a total 327 of reproductive organs, uteri were 55.4% of them. The proportion of pregnant females was 9% in piglets, among yearlings and adult sows was pregnant every second individual. Further analyzes and long-term research will contribute for the better understanding of the reproductive biology of populations of wild pigs.

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P.12 Francisco Díaz-Ruiz

Assessing the influence of predator control on target and non-target carnivore populations using occupancy models

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Abstract for poster Understanding the effects of lethal predator control on predator communities is of great interest for the conservation and wildlife management. We used camera traps and occupancy models to assess the influence of predator control on red fox (*Vulpes vulpes*, target species) and stone marten (*Martes foina*, non-target species) populations across 12 localities of central Spain. Results show that the intensity of fox control (IFC) was not associated with fox occupancy, but it was negatively related to fox detectability. On the contrary, the IFC was positively related to stone marten occupancy, but unrelated to its detectability. Habitat composition and prey availability were more closely associated with site occupancy of both species than predator control. We provide valuable information on the ecological consequences of fox control often employed as a management tool in many European game estates.

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P.13 Simon Engelberger

Behavioural response of Geoffroy's bats (*Myotis emarginatus*) to a predating tawny owl

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Abstract for poster Bats of the temperate zone seem to be comparatively unaffected by nocturnal avian predators even though many species congregate in large, stable maternity roosts, potentially making them a predictable and well exploitable prey for owls. However, relatively few such cases are known. Effective predation-avoidance behaviour of bats may explain this apparent contradiction. Here, we report on direct observations of a maternity colony (c. 600 individuals) of *M. emarginatus* in Austria predated upon by a tawny owl. No direct behavioural responses to the attacking owl were observed. However, during the predation phase, each night fewer bats returned to the roost. Afterwards, the colony regained almost its initial size. A short visit to the roost without attacking caused again a decrease of the colony size. Possible explanations for this behavioural response will be discussed.

P.14 Alan Fredy Eriksson

Influence of bat *Artibeus Planirostris* abundance on the ectoparasites prevalence in a tropical wetland

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Abstract for poster We analyzed the effect of the bat *Artibeus planirostris* local abundance on the prevalence of its ectoparasites, *Megistopoda aranea* and *Aspidoptera phyllostomatis* in a tropical wetland in South America. The bat abundance and the prevalence of ectoparasites were estimated at 30 sample sites spread over three different flooding intensities regions. We use a hierarchical analysis which showed that the local abundance of *A. planirostris* did not influence the prevalence of the ectoparasites. However ectoparasites prevalence was distinct between the regions. The two species of ectoparasites showed the same pattern, with higher prevalence in areas with higher intensity of flooding. Although it is expected that the density and abundance of host influence the prevalence of parasites, environmental characteristics such as humidity and rainfall are important to strebilidae prevalence in tropical regions and can be the factors that are determining the prevalence patterns in the studied sites.

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P.15 Mariya Erofeeva

Teratospermia affects reproductive success in domestic cat

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Abstract for poster The domestic cat is less subject to teratospermia than other cats. Their life strategies (sociality, high density, promiscuity) suggest that competition between males during the breeding season should be very high. In such a situation, the males with low sperm quality probably just have smaller chance to sire offspring. The study was performed at the biological station Tchernogolovka on 8 females and 10 males of a domestic cat. We used 5 males with expressed teratospermia (number of intact sperm below 40%) and 5 with higher percent of normal sperm. During the mating season males were paired with the female one by one. Reproductive success was higher in normospermic cats. Twice more kittens were received from them on average. And the percentage of the impregnated females was also higher for normospermic males (83% against 54%). These data shows that teratospermia per se may have negative effect on male's reproductive success. Supported by grants of RFBR (13-04-01465-a, 15-04-07845-a).

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P.16 Maria Fominykh

Relationship between dental microwear patterns and diet in *Cl. glareolus* in a natural population and in two feeding experiments

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Abstract for poster Dental microwear, the pattern of marks on the tooth surface, is an important basis for understanding the diets of mammals. We study the microwear patterns on the flat occlusal surface of *Cl. glareolus* molars from a natural population in the Middle Urals (Russia) and dietary variation during four seasons (in winter, spring, summer and autumn) based on the analysis of stomach content data. The enamel surfaces were examined using a SEM TESCAN VEGA3. As a result, the relationship between the seasonal dietary preferences and number of microwear patterns was revealed. Also we carried out two experimental studies with fixed diet composition (monodiet with one type of food and composite diet consisting of different food items) to determine the correspondence between food components and enamel microwear of voles. Taken together, these results will allow us to improve the accuracy the reconstruction of vole diet. The study is supported by RFBR grants 14-04-32179, 14-04-32018.

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P.17 Maria Fominykh

Clethrionomys and Craseomys species in Quaternary faunas of the Urals

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Abstract for poster Arvicolinae rodents are extensively used in Quaternary studies. *Clethrionomys* and *Craseomys* species related to nemoral and boreal forests and their proportions in fossil faunas may serve as indicators of forest biotopes. The Pleistocene and Holocene sites are located in different landscape zones in the Urals. It allows to analyze the distribution and proportion as well as the variability of red-backed voles in the gradient of environmental conditions. It was shown that they expanded the ranges to the north since Late Pleistocene to Holocene. Their molars are retained the roots that may characterize their relative age. It was studied the age structure of fossil *C. rufocanus* and *Cl. rutilus* from the different layers in Holocene sites and found the differences in proportions of age stages which are related with the process of remains accumulation due to the available age group of voles for the predator in different seasons. The study is supported by RFBR grants 14-04-32179, 13-04-00847.

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P.18 Emma Grocutt

Fitness consequences of arctic fox cub personality

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Abstract for poster To date, there have been few studies of wild carnivore personality, despite its potential impact on fitness. During conservation trapping, I recorded the behaviour of wild arctic fox cubs in wire traps in Sweden and used principal component analysis to determine whether the cubs have personality traits. One personality trait ('fearfulness') was found to be repeatable. To determine whether the fearfulness of cubs affects their survival, a general linear model will be constructed to investigate which factors (such as size, sex, and presence/absence of parents during trapping) predict fearfulness in cubs, and whether survival at 2–3 months is correlated significantly with fearfulness. This study is important because conservation projects such as reintroduction programs may need to take into account cub personality when selecting animals for release. In subsequent years, it may be possible to study how breeding success and long-term survival correlate with personality in the arctic fox.

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P.19 Klaus Hackländer

Stress responses in snowshoe hares facing mismatch of coat colour and their environment

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Abstract for poster With decreasing duration of snow cover due to global warming, species under-going seasonal colour moults show a colour mismatch with their environment. As this results in increasing predation pressure for white-coloured individuals in periods free of snow, one should expect adaptations to avoid a higher risk of mortality. In this study we aimed at analyzing the stress response to colour mismatch in snowshoe hares (*Lepus americanus*). We collected faecal samples of individuals hares with known coat colour dwelling in habitats of known snow cover. Faecal samples were homogenized and dried at 60–80 degree C. We extracted 0.15 g with 5.0 ml of methanol (80%). After shaking on a hand vortex (1 min) and centrifugation (2,500 g, 15 min) the amounts of GCM were determined in the supernatant of the extracts with an 11-oxo-aetiocholanolone-EIA. We discuss these preliminary data in the light of climate change, phenotypic plasticity within a population and evolutionary adaptation of the species.

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P.20 Jenni Harmoinen

Unequal sampling can bias population genetic studies; an example from North American canids

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Abstract for poster A recently published article (Cronin et al., Journal of Heredity (2014), 106: p.26–36) studying the population structure of North American canids with the use of Illumina 170K CanineBeadChip did not produce convincing results; e.g. their ADMIXTURE results were noisy and to some extent contradicting to previous results of wolf taxonomy in the area. Our interest was to re-analyze the online available dataset using more strict criteria for quality checking and compare the results with results obtained by a subset of SNPs that overlap with a previously published Affymetrix canine array dataset by vonHoldt et al. (2011). Our findings suggest that using a different SNP array or more strict quality filtering of SNPs did not have a big impact on the results; instead the results were biased because of very high relatedness of individuals and unequal sampling of populations. This illustrates the importance of study design, despite the ever increasing genotyping capacity.

P.21 Tomohiko Hori

Dental microwear morphology of the Japanese dormice (*Glirulus japonicus*)

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Abstract for poster Japanese dormice (*Glirulus japonicus*) are endemic to Japan and are thought to be the most primitive species in the Gliridae family. Fossils of this species have been uncovered from the Pleistocene fauna in Japan. However, there is also uncertainty regarding the form of the molars, as there is less morphological information available for comparison with fossils. Using the skull of extant species, with a focus on microwear, premolar and molar teeth were studied and compared with other Japanese rodents. Many variations in the microwear patterns were confirmed for Japanese dormice as compared with those for any other rodents. It is possible that chewing patterns and diet are more diverse for this species than for other rodents. This observation is considered to be useful for fossil, function and ecological studies. In the future, there is a need for comparison with Gliridae species in Europe and Asia (fossil and extant).

P.22 Ivan Horáček

Pleistocene/Holocene transition in Central Europe: small mammals in a high-resolution fossil record

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Abstract for poster The Holocene apochoric elements compose about one third of contemporary mammal fauna of Central Europe. Most of them demand a warm open ground habitats, which were established by the postneolithic landscape rearrangements. A rich fossil record obtained from continuous sedimentary sequences in the Czech Republic and Slovakia (900 community samples, 30,000 MNI) show that at least some of these elements appeared in Central Europe prior to the Neolithic stage. This possibility is robustly supported by the record obtained from the 10m thick sedimentary sequence in Byci skala cave (Moravian karst), covering 21 horizons and 4525 MNI of 52 mammalian spp and a period from 12 to 8.5 ky BP. The record convincingly demonstrates that most of the apochoric elements appeared, against expectancy, already at time of the Pleistocene/Holocene transition. Their early expansion performed the unique features of the Holocene faunal development in Central Europe independently upon the anthropogenic effects.

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P.23 Saher Islam

Population estimation and genetic inferences of Markhor (*Capra falconeri*) in Chitral, Pakistan using non-invasive sampling

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Abstract for poster The wild goat markhor (*Capra falconeri*) is national animal of Pakistan and IUCN Caprinae Specialist Group considers markhor as endangered due to continuing decline rate estimated at 20% over two generations. So, this study will address major threats to markhor using non-invasive genetic sampling techniques. Host species will be confirmed by designing species specific primers. The goal of such an experimental validation is to distinguish markhor species feces from those of others, potentially occurring in the study area. Extracted DNA will further be amplified using microsatellite markers to genetically count their individuals. Survival of most endangered wild goats may depend on breeding programs where sex identification plays an important role. Sex-linked DNA markers can also provide significant insights into demographic history and phylogenetic relationships among populations. In particular, polymorphic Y chromosome markers are useful in tracing paternal lineages in wild populations.

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P.24 Iris Kempter

Seed predation and seed dispersal by small mammals in central European mixed forest ecosystems

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Abstract for poster Seeds of European beech are favored food sources for many small mammals in European forest ecosystems and high interactions and dependence exists between population dynamics of seed predators and masting of trees. In this study we investigated seed fate (i.e. predation and dispersal) of beech nuts using two different seed tagging methods (radio-transmitters and flag tags) on different study plots in the Wilderness Area Dürrenstein and in the Biosphere Reserve Vienna Woods. The tagging method did not affect the acceptance behavior of seeds by predators but transport distances and final seed fate. Seeds marked with radio-transmitters were transported over larger distances and experienced more transport events than seeds marked with flag tags. Seed fate was also affected by microsite structures corresponding to habitat preferences of rodent species. Finally, none of the cached seeds germinated and no facilitating effect of rodents' seed dispersal on forest tree germination were observed.

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P.25 Sang-In Kim

Range-wide skull morphogeographic variation of red fox in the Northern Hemisphere

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Abstract for poster Red fox is one of most widely distributed carnivores in the Northern Hemisphere. Its high adaptability to various environments may be related to the polymorphic characteristics. Although many regional-scaled morphometric study of this species have been carried out, the geographic pattern throughout the Northern Hemisphere is still unclear. To demonstrate morphogeographic variation of red fox, we conducted morphometric analyses on the skull specimens from East Asia, Middle East, Europe and North America. Specific pattern with the larger skull size in the northern population was observed except for the Japanese populations. In the Eurasian red foxes, population from Spain and Middle East might have substantially small body size. Significant separations among Eurasian, Japanese and North American populations were observed in the skull height and skull width. Both of specific environmental conditions and phylogenetic differences might influence morphological variation of red fox.

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P.26 Andrew Kitchener

The Atlas of European Mammals, 2nd Edition?

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Abstract for poster It is now almost 15 years since the Atlas of European Mammals was published, completing a project that began in 1988. Much has changed since then; is it time for a second edition? Our aim is to broaden the previous project to include the whole of geographical Europe, roughly doubling the total area. We envisage a cooperative multi-year project, involving all the mammal societies or recording schemes of Europe and are now seeking views on whether this project is both desirable and feasible.

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P.27 Markéta Knitlová

The Holocene history of *Apodemus flavicollis* in Central Europe

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Abstract for poster Although the genus *Apodemus* represents the dominant component of extant mammals communities in Central Europe, its Holocene history is not known, because of a lack discrimination criteria for particular species. Using a sample of recent species we analyzed variation pattern and interspecific overlaps for a large set of metric and nonmetric dental variables and establish the criteria enabling a reliable species identification of fragmentary fossil record. The studied fossil material of the genus (4479 items; 1822 MNI) coming from 25 continuous sedimentary series from the Czech Republic and Slovakia representing 145 community samples from LGM to Recent. *Apodemus flavicollis* was found to be the most frequent species of the genus throughout the early and middle Holocene. The detailed morphometric analysis demonstrated a pronounced stabilization of the phenotype variation during the Boreal stage but dramatic fluctuation in phenotype variables along the Pleistocene/Holocene boundary.

^aCo-authors: Ivan Horáček

P.28 Marta Kolodziej-Sobocinska

Parasites of invasive American mink (*Neovison vison*) in Poland: does co-infection induce competition between parasites?

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Abstract for poster The American mink is invasive predator, which is now widespread across Europe. The great invasive success of this species has been explained by many hypotheses, including the enemy release hypothesis. To test this hypothesis we compared prevalence and abundance of intestine track parasites in 245 mink from regions colonized earlier (E Poland) and later (W Poland) in their invasive expansion. The highest number of parasites obtained from examined animals belonged to two species: *Isthmiophora melis* (trematodes) and *Aonchotheca putorii* (nematodes). Males were more infected than females. The mean parasitic load was lower in western Poland, which confirms the parasite-release hypothesis. This relation was more noticeable for trematodes. Most mink were co-infected by two species of parasites and abundance of one was negatively correlated with the abundance of another. This suggests that inter-species competition of parasites is occurring in co-infected hosts. (Grant NCN 2012/05/B/NZ8/01247)

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P.29 Sahila Kudalkar

Habitat Correlates of the Forest Non-volant Small Mammal Community in Northeast India

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Abstract for poster Relatively little is known about non-volant small mammal (NVSM) ecology in the tropical forests of northeast India. We conducted live-trapping by deploying 64 traps in an 8x8 grid over 7 nights per site in 11 sites from November 2014 to May 2015 to study influence of habitat structure on NVSM community. We established 4 vegetation plots per grid to measure tree, bamboo, shrub, herb density, percent rock and logs. We captured 289 individuals: *Niviventer* (commonest), *Rattus*, *Tupaia*, *Mus* and 2 members of unidentified shrew species (rarest). *Niviventer* abundance was positively correlated with rock presence (Pearson's $r:0.63$, $P:0.036$) while *Rattus* abundance was negatively correlated with bamboo ($r:-0.71$, $P:0.015$). Sites with low capture success were generally associated with high bamboo density. Our primary results suggest that whereas higher rock cover is beneficial, the dominant secondary vegetation in the region i.e. bamboo maybe associated with lower NVSM abundance.

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P.30 Elin Lilja

Seals and tourists: A worldwide investigation of codes of conduct for tourist behavior

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Abstract for poster Seal watching is becoming increasingly popular worldwide. Managing such activities is important to ensure protection and conservation, since disturbance can affect the fitness of seals. Providing tourists with codes of conduct for how to behave around animals has been used to regulate wildlife watching and can often be quicker to implement than laws. However, no general worldwide seal watching code exists. This study analysed the content of 33 codes of conducts intended for seal watching. Results show that many areas where seal watching occurs lack guidelines. The content and detail of the codes varied and the guidelines provided were often insufficient to offer adequate protection of seals. Few codes were based on research and a minority were presented in a teleological way. Factors that could be included in a general international code of conduct for seal watching are suggested. More research on the relationships between tourists and seals are needed to improve sealwatching management

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P.31 Yilin Liu

Sequencing of 1000 mtDNA genomes in a single Miseq run

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Abstract for poster The purpose of this project is to analyze mtDNA genomes from thousands of individuals. The sequencing strategy is based on nested and multiplexed PCR amplification with dual index identification tagging, and sequence analysis on Illumina Miseq(2x300 bp). PCR amplification is performed for 32 regions of approximately 550 bp (in eight quadruple plexes), thus covering the whole dog mtDNA genome. The amplifications are performed using an in house produced DNA polymerase, keeping down costs considerably (approximately 34 SEK per mitochondrial genome). After the initial PCR, the eight quadruple plex amplicons are pooled for each individual and then used as template in another PCR introducing index primers. The 32 forward primers and 36 reverse primers combine into 32x36 unique dual index combinations, giving each of 1,152 individuals a unique dual index. The 1,152 samples are then loaded into a single Miseq run, and after sequencing the reads are sorted according to the dual index sequences.

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P.32 Miroslava Loudová

Population genomics of European hedgehogs

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Abstract for poster For studying evolutionary processes in Quaternary period, we choose species *Erinaceus europaeus*, *E. roumanicus* and *E. concolor* due to their sensitivity to climatic oscillations. We aim to describe population structure and infer evolutionary processes affecting speciation. Apart of phylogeography of refugial and island populations, our study is focused on secondary contact zone in the Central Europe. Hybridization in this sympatric area is limited, so the reproductive-isolation mechanisms are probably in late stage of development. For a detail insight into the evolutionary history of the hedgehogs we use a combination of traditional genetic and next-gen sequencing approaches.. RAD-seq assay was used to generate approximately 20.000 sequences representatively covering *Erinaceus* genome. These data provide much more resolution of population structure compared to microsatellite loci and enable us to study introgression, diversification of particular species and other phenomena.

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P.33 Johan Michaux

Molecular phylogeny of all *Apodemus* species based on the complete mitochondrial genome and two nuclear genes

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Abstract for poster The *Apodemus* genus is composed of 20 different species distributed throughout the Palearctic region. It is subdivided into the *Sylvaemus* subgenus corresponding to the majority of the species living in the Western Part of the Palearctic region, and the *Apodemus* subgenus, associating most of the Asian species. Although these rodent species are very common and are spread in many European and Asian habitats, their evolutionary history and their phylogenetic relationships are still largely unknown. The aim of our study was to analyse for the first time in a single research, the totality of the 20 *Apodemus* species, using as genetic markers, the whole mitochondrial genome as well as three nuclear genes. Analyses based on ca. 20 000 unambiguously aligned nuclear and mitochondrial DNA sites provide new insights onto the phylogenetic relationships among extant species

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P.34 Pedro Monterroso

New variant of the rabbit hemorrhagic disease virus in Portugal: Preliminary results of its evolution and impacts in rabbit populations

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Abstract for poster Recently, a new variant of the rabbit hemorrhagic disease virus (RHDV2) emerged, and rapidly spread across the Iberian Peninsula, where the European rabbit is the main prey of several predators. RHDV2 appears to be shaping the demographic patterns of rabbit populations, with strong impacts in the conservation of endangered predators, and at a socio-economical level. Thus, we aimed to assess the impact and epidemiology of RHDV2. For this, we monitored the demography of several rabbit populations. Also, dead rabbits collected in the field were screened for RHDV2 presence, and partial genome sequences were obtained for positive samples. Our results suggest that European rabbit populations in Portugal decreased by over 50%. We found that three different RHDV2 strains are simultaneously circulating in natural rabbit populations. The impact of the disease appears to be density-dependent and varies spatially among population nuclei within the same rabbit population.

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P.35 Adam Nadachowski

Phylogeography of cave bear from Central and Eastern Europe in the light of ancient DNA studies

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Abstract for poster Genetic analyses of ancient DNA enabled to recognize two main Late Pleistocene forms of cave bear, *Ursus ingressus* and *U. spelaeus*, which previously were regarded as one species. In order to study the evolution and diversity of *U. ingressus* in the north-eastern range of its distribution, we collected more than 70 samples from excavation sites in the territory of Poland, Czech Republic, Slovakia, Moldavia and Ukraine. Studies of mitochondrial control region demonstrated that sequences from Romania grouped together with one sequence from Poland at the base of *U. ingressus* phylogenetic tree. It is possible that an early long-distance migration of the bear from South-eastern Europe beyond the Carpathian arch occurred. A big clade in the tree was created by samples from Poland, which included also single samples from Germany and Ural. It may indicate that the bears migrated from the territory of Poland both to Western and Eastern Europe.

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P.36 Magdalena Niedziałkowska

Habitat preferences of red deer (*Cervus elaphus*) in Late Pleistocene and Holocene in Europe, introduction to the on-going study

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Abstract for poster Red deer is an opportunistic species that can exist in different environmental and climatic conditions. We plan to study habitat selectivity of red deer in Europe in Late Pleistocene and Holocene based on the analyses of stable isotopes of carbon (¹³C) and nitrogen (¹⁵N). The content of these isotopes in tissue of animals allows to reconstruct their environments and diets. Firstly, we will compare the content of the isotopes in tissues of contemporary European red deer living in different environmental conditions and belonging to different mtDNA lineages. The obtained results will be compared with the content of stable isotopes in bones of red deer found in the fossil materials and dated with AMS radiocarbon method, to reconstruct their paleoenvironments and paleodiets. The results of the analyses will be compared to the history of red deer populations, phylogeography of the species, and data on climate and environmental changes in Europe from Late Pleistocene until today.

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P.37 Stefan Prost

Living in Extreme Environments: Genome Adaptation in Arctic, Desert and High-Altitude Foxes (genus: *Vulpes*)

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Department of Integrative Biology, Center for Theoretical Evolutionary Genomics, University of California, Berkeley, USA

Abstract for poster True foxes (*Vulpes*) are small to medium-sized canids that exist naturally in diverse environments through-out the Holarctic, South East Asia and Africa. Their habitats include the extreme cold of the Arctic, dry and hot deserts, urban areas, high altitude regions and even the marine. This near universal distribution is made possible by special adaptations to the environment they live in. While morphological and physiological adaptations have, for some species, been well studied, our current understanding of the underlying genetics is still very poor. In this study we are investigating these adaptations using high-coverage genomes (20x) of the Arctic, the Tibetan, the Kit, the Rueppell's, the Blanford's and the Fennec fox, and low-coverage genomes (1.5x) from 120 Red foxes from different environments. Using comparative analyses (dn/ds based) and population scans (Population Branch Statistic) we are inferring genomic regions under selection in the different species and populations.

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P.38 Joao Queiros

Tuberculosis, fitness and heterozygosity in the red deer

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Abstract for poster Understanding how genetic diversity, infectious diseases and fitness interact in wild populations has become a major challenge in ecology and management. These interactions were addressed by assessing the presence and severity of tuberculosis, and the body condition in red deer populations from central-southern Spain. Heterozygosity-fitness correlation models were constructed taking into account biological, demographic and management determinants. The models allowed not only to better understand the link between genetic diversity and resistance to tuberculosis at individual and population levels, but also to better understand the dynamics of multi-host interaction in the wild. While the presence of tuberculosis on deer was positively modulated by the prevalence of tuberculosis in wild boar, the body condition of animals and heterozygosity at single locus, the ability to control disease progression was positively correlated with the levels of population genetic diversity.

^aCo-authors: Joaquín Vicente, Jose de la Fuente, Christian Gortazar, Paulo C. Alves

P.39 Benjamin Ramassamy

A new long-snouted beaked whale from the Late Miocene of Denmark: evolution of sexual dimorphism in the Ziphiidae

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Abstract for poster A new genus of beaked whale (Odontoceti: Ziphiidae), from the upper Miocene Gram Formation (10 Myr) is the first occurrence of the family in Denmark. A phylogenetic analysis including 25 species and 69 characters placed the new genus in the *Messapicetus* clade as sister taxon of *Messapicetus*. The Gram formation was deposited in a marine environment between 50 and 100 meters. Extant beaked whales are regular deep divers, finding a ziphiid at this depth is unusual. The hypothesis of a regular deep diver can't be discarded as the carcass may have drifted until there. The Gram specimen displays tusks and an ossified rostrum indicators of a male in extant species. Sexual dimorphism was already proposed in fossil species. If correct, the Gram specimen would be a male. Alternatively, like in *Berardius*, the development of tusks could be associated to aggressive intraspecific interactions and present in the two sexes. No definitive conclusion can be given based on this unique specimen.

P.40 Neil Reid

Diversity, extinction, and threat status in Lagomorphs

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Abstract for poster A quarter of all lagomorphs (pikas, rabbits, hares and jackrabbits) are threatened with extinction, including several monotypic genera. Genus species richness correlates with extinction risk in lagomorphs, but not in other mammals. Non-random extinction of small clades disproportionately threatens genetic diversity and phylogenetic history. Phylogenetic analyses suggest that lagomorph threat status was not related to body size, and there was no phylogenetic signal in extinction risk. Extinction risk was greater in areas of higher human population density and negatively correlated with anthropogenically modified habitat. Consistent with this, habitat generalists were less likely to be threatened. Our models did not predict threat status accurately for taxa that experience region-specific threats. Pressure from human populations is so severe and widespread that it overrides ecological, biological, and geographic variation in extant lagomorphs.

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P.41 Alba Rey de la Iglesia

Mitogenomics of red deer (*Cervus elaphus*) in Iberia: insights into the post-LGM colonization of Europe

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Abstract for poster The major climatic oscillations that characterized the Quaternary Period had a great influence on the evolution and distribution of several species. During cold periods the distribution of temperate adapted species became fragmented with a lot of species surviving in southern refugia, such as the Iberian, Italic and Balkan Peninsulas. The red deer was one of the many species that contracted its original range to southern refugia. To test role of Iberia as refugium and its contribution to the current red deer genetic pool, we have generated full mitochondrial genomes for 23 specimens, radiocarbon dated to 38,000 YBP from Spain, as well as for 15 modern individuals spread in Europe. This data was compared to publicly available red deer mitochondrial sequences and mitogenomic data from ancient Danish specimens (4,000–8,000 YBP) also generated in this study. Finally, we have also tested the contribution of past Iberian populations to the Danish red deer genetic pool.

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P.42 Juliana Ribeiro

Isotopic niche of small mammals in a neotropical savanna

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Abstract for poster The knowledge of the niche dimensions of sympatric species allows us to understand mechanisms responsible for the coexistence of species within a community. We evaluated the diets of 22 small-mammal species based on stable isotope analysis (delta13Carbon and delta15Nitrogen) in the Brazilian Cerrado during dry and rainy seasons and in the 3 main vegetation types (grassland, savanna and forest). We evaluated the contribution of 3 main groups (C3 fruit, C4 grasses and invertebrates) in their dietary composition. Most species of small terrestrial mammals demonstrated to be omnivorous, but with distinct groups showing predominantly frugivorous habits or else a more insectivorous diet. For some species, the size and distribution of isotopic niche metrics changed according to season and habitat complexity, with greater trophic niche width in the rainy season compared to the dry season and an increase in more complex environments.

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P.43 Gabriella Rizzardini

Wolf detection using camera trapping: a pilot study in the southern part of the Eastern Carpathians, Romania.

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Freelancer, Italy

Abstract for poster The aim of this study is to present preliminary results achieved during a winter session of camera trapping carried out by the WOLFLIFE project (LIFE13NAT/RO/000205). The study area is 1200 km² and located in the Eastern Carpathians, Romania. 14 camera trapping stations were chosen opportunistically and determined by the spatial distribution of wolf signs collected during monitoring activities (transects and snow-tracking). Camera trapping sessions ranged from 30 to 61 days (a total of 600 trapping days). 409 videos/photos recorded the presence of 13 mammal species. 57% of camera traps detected wolf presence, but the Capture Rate (Number of video/camera-traps x working-days) was low (0.04). 50% of wolf images recorded one individual, 29% recorded two wolves, whilst the maximum number of wolves recorded together was 3 (21%). Camera trapping is useful to detect wolf presence, sex and physical condition, but it is difficult to estimate the size of a wolf pack.

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P.44 Lars Rød-Eriksen

**Generalist species range expansion into alpine regions of
Fennoscandia: the red fox**

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Abstract for poster Over the past century, the red fox (*Vulpes vulpes*) has gradually expanded its range into alpine regions of Fennoscandia. Several drivers of this expansion have been suggested. We performed a pilot-study in Norwegian alpine regions, exploring which factors influence red fox distribution, to better understand the mechanisms behind the expansion. Our results showed that the red fox distribution was positively related to human structures, to presence of ungulates and to local scale landscape productivity, however limited by winter conditions. To disentangle the importance of different drivers contributing to the red fox range expansion we need more quantified data on the actual resource availability for generalist species in Fennoscandian alpine regions.

P.45 Fulya Saygılı

**Genetic Differentiation of *Meriones tristrami* (Mammalia:Rodentia)
Subpopulations in Turkey; Inferring Allozyme Variations**

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Abstract for poster Allozyme variations of *Meriones tristrami* which is distributed in the steppe and semi-arid areas in Turkey were studied by using 24 loci of 83 specimens from 8 locations in Turkey. Seven loci were found to be polymorphic. According to the patterns of allozyme variation, the percentage of polymorphic loci was 12.5. F_{ST} was found to be 0.44 indicating high genetic variations among *M.tristrami*, accordingly N_m value (0.3157) appeared quite low. UPGMA dendrogram based on genetic distance showed that the central and western Anatolian population established very close sub clusters, and south-eastern populations connected to these sub clusters, respectively. As expected, eastern population appeared to be more divergent due to geographic distance. Our findings indicated the genetic isolation among these subpopulations which might be caused metapopulations by means of geographic isolation.

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P.46 Stéphanie Schai-Braun

Spring and autumn habitat preferences of active European hare (*Lepus europaeus*) in a small-scale agricultural area with low hare density

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Abstract for poster Habitat preferences of European hares (*Lepus europaeus*) are known to be affected by hare density, but most studies have been conducted in agricultural areas where hare densities were medium to high. In addition, in agricultural areas field size might influence the hares' habitat selection. However, most studies relate to areas with large field sizes. In this study, we analysed the habitat preferences of active European hares in spring and autumn in an agricultural area with low hare density and small average field size. Our results show that European hares avoided several habitat types which were preferred in other study areas with higher hare densities. Therefore, we assume that hare density has an influence on the species' habitat selection. In contrast, the small average field size of our study area seemed not to have an effect on hare habitat preference. In conclusion, our results imply that studies on habitat preferences have to be conducted in areas with low hare density.

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P.47 Analena Severon

Intrasexual home range overlap, kinship and dispersal in the European wildcat

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Abstract for poster The European wildcat (*Felis silvestris silvestris*) is a solitary living carnivore. In this study, we investigated the correlation of intrasexual range overlap and kinship of males and females. As a prerequisite for sex differences, we further tested whether natal dispersal is male-biased. Telemetry and genetic data were available for 29 male and 36 female intrasexual wildcat dyads from five study areas in Germany and France. Range overlap was calculated with the utilisation distribution overlap index (UDOI). Kinship was based on genetic analyses of 14 microsatellite markers. In order to investigate male-biased dispersal, we tested whether kinship was higher in females than in males within a study area. Additionally, a genetic spatial autocorrelation analysis was conducted. None of the result could support male-biased dispersal. A Mantel test confirmed a positive correlation between kinship and home range overlap only in females in study areas where mother-daughter dyads were present.

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P.48 Aaron B.A. Shafer

The genomic legacy of human exploitation and extreme climatic oscillations in marine mammals

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Abstract for poster Humans have a dramatic impact on the species and ecosystems of Earth. Pinnipeds - seals, sea lions and walruses - have been commercially exploited for centuries (e.g. for hides, oil, meat, other products). Climatic oscillations, particularly El Niño events, also have dramatic negative impacts on many pinniped populations. We ask the question: have these events left a signature on the genome? Genomic data was generated on 15 different pinniped species spanning the globe. Population genomic models – both composite-likelihood and coalescent-based – were used to detect historic changes in effective population size. Preliminary results have been mixed, but events (likely) during or before the last glacial period left the strongest signature on the genome.

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P.49 André Silva

Suitable climatic conditions for the jungle cat and leopard cat after the last-inter-glacial in the Indian subcontinent

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Abstract for poster The biogeography of the Jungle cat (*Felis chaus*) and Leopard cat (*Prionailurus bengalensis*) in India is believed to be closely associated with climate variation across the years. Using ecological niche models and climate models, we first identified the most important environmental variables explaining the current species occurrence and then used the most important climatic variables to explore suitable climatic areas across time. We show that suitable climatic conditions for both species are likely to have fluctuated across the years with an increase of appropriate conditions during the Last Glacial Maximum (22000 years BP) and mid Holocene (6000 years BP) but likely reduction of suitable climatic environment towards current time (1950 -2000). Our results indicate that future (2070) warming is likely to accentuate the reduction of suitable climatic environment and may cause additional constraints to the species occurrence in particular regions of the subcontinent.

^aCo-authors: Mats Björklund, Carlos Fernandes, Shomita Mukherjee

P.50 Mark Statham

Peninsulas and islands in a sea of red: phylogeography and population substructure of the European red fox.

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Abstract for poster Historical climate change during the Quaternary Period caused temperate and arctic adapted species to cycle through periods of range expansion and contraction. Such changes alternately facilitated and constrained gene flow, and resulted in both the evolution of local endemic lineages and in homogenization. Previous investigations of red fox (*Vulpes vulpes*) population substructure within Europe have concluded that there is relatively limited population subdivision evident in mtDNA, while regional microsatellite based studies have found both minimal subdivision and local substructure. Here we examined the continent-wide subdivision of 275 European red foxes examined at two mtDNA regions and 21 nuclear microsatellite markers. We identified distinct populations on peninsulas and on off-shore islands, and a central population derived from multiple sources. Together with population splitting time estimates these findings shed light on the post-glacial colonization history of the species.

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P.51 Janne Sundell

Field stations provide valuable infrastructure for environmental sciences and biology: introduction to UHEL research stations

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Abstract for poster Field stations have been the backbone of research and high level teaching in biology, environmental sciences, physics and geography. Traditionally, these have been the place for hands-on learning in the natural environment, giving students the opportunity to develop the species identification skills and learn about different habitats. Currently these same functions are the key focus in field stations, but many have become multifunctional, cutting-edge research institutes with modern laboratory facilities, extensive experimental systems and high precision measuring devices. Environmental data are gathered for monitoring purposes but also for providing background data on research. Often field stations are away from the main campuses and serve as important representatives of universities having a high impact on society by providing e.g. environmental education. This is also true for the field stations of the University of Helsinki in Kilpisjärvi, Lammi and Tvärminne which are introduced.

P.52 Marta Szurlej

Species composition, sexual structure and phenology of bats foundet by Tricity inhabitants

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Abstract for poster In the area of the Tricity Agglomeration occurrence of 14 species was confirmed. Our knowledge about the bat fauna of Tricity is still very limited, especially in case of those species that do not use underground hibernacula. Starting from 2002, members of the Academic Bat group of the Polish Society of Nature Protection "Salamandra" in Gdansk were regularly provided with bats found by inhabitants of the agglomeration, mainly in places that weren't hibernacula nor daily roosts (street, lawns, flats, balconies, staircases, external walls of buildings, etc.). The aim of the study was to present species composition, sex proportions and phenology of those bats, as well as an attempt to explain reasons for that seasonal occurrences, including their links to particular weather conditions (temperature, precipitation, air pressure) before and at the moment of every finding. In total we received 178 bats from 11 species.

^aCo-authors: dr Mateusz Ciechanowski, Konrad Bidziński

P.53 Joaquim Tapisso

Phenotypic flexibility in the energetic strategy of the greater white-toothed shrew, *Crocidura russula*

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Abstract for poster Little is known about the energetic strategy used by the greater white-toothed shrew (*Crocidura russula*) to cope with seasonal variations under Mediterranean climate conditions. We studied the phenotypic flexibility of the thermogenic capacity, behavioral activity and daily torpor of this species under three different experimental groups: a control group, acclimated to a 12L:12D photoperiod and a constant temperature of 20°C; a winter group and a summer group, acclimatized to winter and summer natural fluctuations of light and temperature, respectively. Comparison between the three groups revealed no flexibility in resting metabolic rate and nonshivering thermogenesis. However, summer acclimatized shrews were more active, particularly at night, while winter acclimatized shrews entered daily torpor more frequently and for shorter periods of time. Our results suggest that *C. russula* relies mostly on behavioral mechanisms to adjust their energetic requirements to seasonal variations.

^aCo-authors: Flávio G. Oliveira, Rita Monarca, Ana M. Cerveira, Maria L. Mathias

P.54 Philipp Tumasian

An experience of development of artificial population of Piebald Shrew (*Diplomesodon pulchellum* Lichtenstein, 1823)

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Abstract for poster Piebald Shrew inhabit in the Turan Lowland east of the Caspian Sea in Turkmenistan and Uzbekistan, the only extant member of the genus *Diplomesodon*. Lifespan of the animal is short, maximum 3 years in captivity. Since 2008 in Moscow Zoo exist stable population of this shrews. During this time, methods of keeping and breeding were developed, we have success breeding each season, more than 200 animals have been born in 10 generations in captivity. Using this population many scientific works have been done, including studying of acoustic, ontogenesis, behavior and influence of domestication. As well as scientific research such population could be used for reintroduction of the species if it is need. Our experience of creation and development of stable artificial population could be used for other species.

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P.55 Kristine Ulvund

Use of supplementary feeding stations by arctic foxes in Norway

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Abstract for poster Since 2006, the Norwegian arctic fox captive breeding program has bred and released young foxes in the wild. To increase the survival rate of released foxes, and aid the recovery of the arctic fox population, supplementary feeding stations equipped with wildlife cameras are installed at each release site. Both wild-born and captive bred foxes use the feeding stations. Data from the wildlife cameras show that the feeding stations likely reduces the competition between the red and arctic fox. This is probably due to the custom-made feeding stations designed to be exclusive for the arctic fox. Data from nine stations with Biomark pit-tag readers provides information on individual foxes and allows examining the social structures of foxes using the feeding stations. This knowledge is important to optimize the localization of supplemental measures. Preliminary findings suggests that although the feeding stations are located near active den sites, the residing couple do not monopolize them.

^aCo-authors: Arild Landa, Nina E. Eide, Lars Rød-Eriksen, Anne-Mathilde Thierry, Øystein Flagstad and Ingrid Ertresvåg

P.56 Nina Vasilieva

Prolonged handling time could affect the blood profile in the wild cat species

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Abstract for poster Obtaining the blood profiles is a standard way to assess the immune function in wild mammals; at the same time, often it is difficult to collect the blood immediately after the capture. Our goal was to estimate the effect of handling time on blood profiles and adrenal activity in the far-east cat (*Prionailurus bengalensis euptilura*), small solitary cat species. The test was conducted in captivity; six individuals were anesthetized, blood samples were collected in 3, 20 and 40 min after the capture; different blood parameters and cortisol level were estimated in the samples. The time of sampling affected significantly the estimated parameters: the cortisol level increased and the number of red and white blood cells decreased in the 20 min samples as compared to 3 min samples. The most stable parameter was the ratio of neutrophils to lymphocytes. Thus, prolonged handling could change the blood profile in the wild cats. Supported by RFBR (15-34-20526).

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P.57 Johan Wallén

Population history and northern recolonization in a generalist carnivore: the Scandinavian red fox

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Abstract for poster Historical events are important factors influencing the present distribution and possibly also the ecological niche of many species and populations. The red fox (*Vulpes vulpes*) is a classical generalist species, distributed from deserts to Arctic tundra. Little is however known about the history of red foxes in Scandinavia, where red foxes are distributed from nemoral forest in the south to Arctic tundra in the north. The Scandinavian Peninsula was covered by ice during the last glacial maximum. Using mitochondrial and Y chromosome data, we investigate where red foxes survived the last ice age and how Scandinavia was recolonized when the ice sheet melted. We specifically test for the occurrence of a southern, eastern or cryptic, northern refugium and discuss its' impact on present ecology.

^aCo-authors: J. Wallén (1), M.J. Statham (2), B.N Sacks (2), K. Norén (1, 2)

P.58 Sergey Zykov

Comparative analysis of dental enamel microstructure in the late quaternary and modern *Microtus gregalis* in the Urals

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Abstract for poster Because of its relatively early divergence (among *Microtus*), rapid evolution, wide distribution and abundant fossil record, the phylogenetic lineage of *Microtus* (*Stenocranius*) *hintoni* - *Microtus* (*S.*) - *gregaloides* - *Microtus* (*S.*) *gregalis* is commonly employed in Quaternary biostratigraphy across northern Eurasia. Evolutionary changes within the terminal taxon - *Microtus gregalis* - appear to be good chronological markers when morphotype characters and measurements of the first lower molar (m1) are considered. Here, we explore the potential usefulness of dental enamel microstructure to reveal evolutionary significant changes within *M. gregalis*. The study aims to investigate the spatio-temporal and ontogenetic patterns of the cheek tooth enamel microstructure variation in *Microtus gregalis* from different parts of the present-day disjunct range and from the Late Pleistocene and Holocene localities of the Middle Urals. The work was supported by the RF President Grant MK-331.2014.4.

^aCo-authors: Tatiana Strukova

Index of authors

A

Ahlgren, Hans, 2
Aivelo, Tuomas, 2
Albrycht, Marzena, 80
Alves, Paulo C. , 3
Andrén, Henrik, 3
Aronsson, Malin, 4

B

Bajwa, Amna Arshad, 81
Bakloushinskaya, Irina, 4
Barnes, Ian, 5
Bartosiewicz, Laszlo, 5
Begall, Sabine, 6
Bergvall, Ulrika A, 6
Berteaux, Dominique, 7
Biffi, Marjorie, 81
Bobek, Boguslaw, 8
Borowski, Zbigniew, 8
Boston, Emma, 9
Brace, Selina, 9
Bruford, Mike, 10

C

Caravaggi, Anthony, 10, 82
Carroll, Rory, 82
Cerna Bolfikova, Barbora, 11
Cerveira, Ana, 11, 83
Çetintürk, Derya, 83
Charbonnel, Anaïs, 12
Chevret, Pascale, 12
Clutton-Brock, Tim, 13
Cooper, David, 13
Corradini, Andrea, 84
Cromsigt, Joris, 14
Curveira-Santos, Gonçalo, 84

D

Dammhahn, Melanie, 14
Danell, Kjell, 15
Díaz-Ruiz, Francisco, 86
de Jong, Joost, 15
Delibes-Mateos, Miguel, 85
Demartsev, Vlad, 16
Doan, Karolina, 16
Drimaj, Jakub, 85
Dures, Simon, 17

E

Eide, Nina E., 17
Ekblom, Robert, 18
Elmhagen, Bodil, 18
Engelberger, Simon, 86
Eriksson, Alan Fredy, 19, 87
Erlandsson, Rasmus, 19
Erofeeva, Mariya, 87
Ersmark, Erik, 20

F

Farida, Khammar, 20
Faurby, Søren, 21
Ferreira, António, 21
Ferrerias, Pablo, 22
Flagstad, Øystein, 22, 23
Fominykh, Maria, 88
Frantz, Laurent, 23, 24

G

Gol'din, Pavel, 24
Goswami, Anjali, 25
Grocutt, Emma, 89

H

Haage, Marianne, 25
Haapakoski, Marko, 26
Hackländer, Klaus, 26, 89
Halliday, Thomas J.D., 27
Halliez, Guillaume, 27
Harmoinen, Jenni, 90
Hawlitschek, Oliver, 28
Hayward, Matt, 28
Heino, Matti, 29
Henttonen, Heikki, 29
Herman, Jeremy, 30
Hertel, Anne, 30
Hill, Russell, 31
Hofman-Kaminska, Emilia, 31
Hofmeester, Tim, 32
Holmala, Katja, 32
Horáček, Ivan, 91
Hori, Tomohiko, 90

I

Islam, Saher, 91

J

Jansen, Patrick, 33

Jensen, Thomas Secher, 33
Johnson, Chris, 34

K

K. Lagerholm, Vendela, 34
Kallio, Eva, 35
Kangas, Veli-Matti, 35
Kempter, Iris, 92
Khalil, Hussein, 36
Kim, Sang-In, 92
Kitchener, Andrew, 36, 93
Knitlová, Markéta, 93
Koivuniemi, Meeri, 37
Kolodziej-Sobocinska, Marta, 37,
94
Kopatz, Alexander, 38
Kotlik, Petr, 38
Kowalczyk, Rafal, 39
Kudalkar, Sahila, 94
Kukekova, Anna, 39

L

Lado, Sara, 40
Lafuente, Regina, 40
Lambin, Xavier, 41
Landa, Arild, 41
Landman, Marietjie, 42
Larson, Greger, 42
Latinne, Alice, 43
le Roux, Liza, 44
Leonard, Jennifer, 43
Levänen, Riikka, 44
Lilja, Elin, 95
Linderholm, Anna, 45
Linnenbrink, Miriam, 45
Liu, Yilin, 95
Lorenzen, Eline, 46
Loudová, Miroslava, 96
Lundkvist, Åke, 47
Luque-Larena, Juan Jose, 46
Lynsdale, Carly, 47

M

Macdonald, David, 47
McDevitt, Allan, 48
Mendes Ferreira, Clara, 49
Michaux, Johan, 49, 96
Michler, Berit Annika, 50
Miller, Christine, 50
Mills, L. Scott, 51

Monterroso, Pedro, 51, 97
Montgomery, Ian, 52
Mozūraitis, Raimondas, 52

N

Nadachowski, Adam, 97
Naderi, Morteza, 53
Niedziałkowska, Magdalena, 53, 98
Niskanen, Alina K, 54
Norén, Karin, 55
Norman, Anita, 54

O

Orlova, Maria, 55
Ozkurt, Sakir Onder, 56

P

Pasanen-Mortensen, Marianne, 56
Pavlova, Ekaterina, 57
Peart, Claire R., 57
Persson, Jens, 58
Persson, Mia, 58
Prost, Stefan, 98

Q

Queirós Neves, Isabel, 59
Queiros, Joao, 99

R

Ramassamy, Benjamin, 99
Rød-Eriksen, Lars, 102
Reid, Neil, 59, 60, 100
Renaud, Sabrina, 60
Rey de la Iglesia, Alba, 100
Ribeiro, Juliana, 101
Rizzardini, Gabriella, 101
Rosengren, Erika, 61
Rowcliffe, Marcus, 61

S

Sacks, Ben, 62
Samelius, Gustaf, 62
Sand, Håkan , 63
Savolainen, Peter, 63
Saygılı, Fulya, 102
Schai-Braun, Stéphanie, 63, 103
Schneiderová, Irena, 64
Seiler, Andreas, 65
Severon, Analena, 103
Shafer, Aaron B.A., 104
Silva, André, 104

Sin, Teodora, 66
Singh, Navinder, 66
Sironen, Tarja, 67
Skarpe, Christina, 67
Statham, Mark, 68, 105
Stojak, Joanna, 68
Street, Sally, 69
Stronen, Astrid Vik, 69
Sundell, Janne, 105
Szurlej, Marta, 106

T

Tallian, Aimee, 70
Tapisso, Joaquim, 70, 106
Tarnowska, Ewa, 71
Thierry, Anne-Mathilde, 71
Thulin, Carl-Gustaf, 72
Tison, Jean-Luc, 72
Tokarska, Malgorzata, 73
Tosh, David, 73
Tumasian, Philipp, 107

U

Uboni, Alessia, 74

Ulvund, Kristine, 107
Unnsteinsdottir, Ester Rut , 74

V

Van Langevelde, Frank, 75
Vasilieva, Nina, 108
Vijay, Nagarjun, 75
Vogt, Kristina, 76
von Merten, Sophie, 80

W

Wallén, Johan, 108
Wallgren, Märtha, 76
Ware, Roselyn, 77
Woodfin, Sarah, 77

Y

Yamaguchi, Nobuyuki, 78
Yoccoz, Nigel, 78

Z

Zimova, Marketa, 79
Zub, Karol, 79
Zykov, Sergey, 109