

BOOK OF ABSTRACTS

Borowski Z. (Ed) 2019



ECM8

8th European Congress of Mammalogy

23 - 27 September 2019, Warsaw, Poland

www.ecm8.org

BOOK OF ABSTRACTS

Borowski Z. (Ed) 2019



ECM8

8th European Congress of Mammalogy

23 - 27 September 2019, Warsaw, Poland

www.ecm8.org

EDITOR:

Borowski Z. (ed) 2019. The 8th European Congress of Mammalogy –
Book of Abstracts (liczba stron) ISBN

ORGANIZERS:

Forest Research Institute
Mammal Research Institute Polish Academy of Sciences
Faculty of Biology, University of Warsaw
Centre of New Technologies, University of Warsaw
The Committee of Environmental and Evolutionary Biology,
Polish Academy of Sciences
University of Warsaw Botanic Garden
Museum and Institute of Zoology Polish Academy of Sciences
European Bison Friends Society

SCIENTIFIC COMMITTEE:

Zbigniew Borowski – Forest Research Institute, Poland
Magdalena Niedziałkowska - Mammal Research Institute, PAS, Poland
Marek Konarzewski - University of Białystok, University of Warsaw, Poland
Karol Zub - Mammal Research Institute, PAS, Poland
Wiesław Bogdanowicz - Museum and Institute of Zoology, PAS, Poland
Michał Kozakiewicz - Faculty of Biology, University of Warsaw, Poland
Rafał Kowalczyk - Mammal Research Institute, PAS, Poland
Danijela Popović - Centre of New Technologies, University of Warsaw, Poland
Mateusz Baca - Centre of New Technologies, University of Warsaw, Poland
Frank Zachos - Natural History Museum Vienna, Austria
Boris Krystufek - Slovenian Museum of Natural History, Slovenia
Elena Buzan - University of Primorska, Slovenia
Astrid Vik Stronnen - University of Ljubljana, Slovenia
Urmas Saarma - University of Tartu, Estonia
Heikki Henttonen - Natural Resources Institute Finland (Luke), Finland
Karen Marie Mathisen - Inland Norway University of Applied Sciences, Norway
Dries Kuijper - Mammal Research Institute, PAS, Poland
Nuria Selva Fernandez – Institute of Nature Conservation PAS, Poland

LOCAL ORGANISING COMMITTEE:

Zbigniew Borowski (Chair) - Forest Research Institute, Poland
Alek Rachwald - Forest Research Institute, Poland
Adam Wójcicki - Forest Research Institute, Poland
Anna Tereba - Forest Research Institute, Poland
Wanda Olech - European Bison Friends Society
Magdalena Niedziałkowska - Mammal Research Institute, PAS
Joanna Stojak - Mammal Research Institute, PAS
Maciej Sykut - Mammal Research Institute, PAS
Karolina Doan, Museum and Institute of Zoology, PAS
Agnieszka Kloch - Faculty of Biology, University of Warsaw, Poland
Marcin Brzeziński - Faculty of Biology, University of Warsaw, Poland
Danijela Popović - Centre of New Technologies, University of Warsaw, Poland
Mateusz Baca - Centre of New Technologies, University of Warsaw, Poland

This publication will be available at:

www.ibles.pl and <https://ibs.bialowieza.pl/en/>

ISBN (paperback) - 978-83-955277-0-8

ISBN (PDF) - 978-83-955277-1-5

Printed in Poland by

„Convention+ Spółka z ograniczoną odpowiedzialnością”Warsaw Sp. k.

PREFACE

Dear ECM8 Attendee,

It is my great pleasure to welcome you in Warsaw on the European Congress of Mammalogy (ECM8). The Polish Forest Research Institute, Mammal Research Institute Polish Academy of Sciences and University of Warsaw are proud to have the opportunity to provide a forum for 200 delegates from 36 European and also non-European countries. I hope that relaxed and friendly atmosphere of this congress provides an excellent opportunity to hear and discuss the latest developments in various fields of mammalogy.

This is our eighth meeting on this most important European convention of theriologists, after successful congresses in Lisboa (1991), Southampton (1995), Jyväskylä (1999), Brno (2003), Siena (2007), Paris (2011) and Stockholm (2015). Now it is the turn of a Central European country again to host this exciting event and to invite mammalogists to the 8th European Congress of Mammalogy (ECM8) in Warsaw, Poland.

A quick look at our schedule will show you a program comprising a broad range of research perspectives covering all fields of current theriology. We have contributed papers identified by topic and grouped into 13 thematic symposia, such as e.g.: squirrel ecology, conservation genetics, predator-prey interactions, predator ecology, phylogeography and biogeography, climate change, ungulates, paleoecology, behavioural and evolutionary ecology and mammals in anthropogenic landscape.

I hope that this meeting will provide a unique opportunity to share research experience and expertise, and to develop new and closer contacts with colleagues from different countries. I believe that you will also find some time to relax and enjoy what the beautiful city of Warsaw has to offer.

The organisers of the meeting thankfully acknowledge the financial support provided by their home institutions, as well as by the Polish Academy of Sciences.

I would like to extend my sincerest gratitude for great work to the members of the local organizing and scientific committee, especially to Heikki Henttonen who is the godfather of this meeting. I am thankful to the plenary speakers, session chair people and all the presenters.

Finally, a big thank you to all of you for coming, for your support for our meeting and for helping us to make the ECM8 success. I wish us all a great conference.

Enjoy the meeting and have a fun in Warsaw!

*Warsaw, 4th September 2019
Zbigniew Borowski, chair of ECM8*

PROGRAM

SUNDAY, 22.09.2019

17:00 - 20:00

REGISTRATION

MONDAY, 23.09.2019

08:00 - 09:00

REGISTRATION

09:00 - 09:15

OPENING

09:15 - 10:15

PLENARY
WILD MIGRATIONS: ANIMAL MOVEMENT, ANTHROPOGENIC BARRIERS, AND CORRIDOR
CONSERVATION IN THE AMERICAN WEST
MATTHEW KAUFFMAN

10:15 - 10:35

LAURENT SCHLEY: EMMA2: UPDATING THE ATLAS OF EUROPEAN MAMMALS

10:35 - 11:05

COFFEE BREAK

11:05 - 13:15

HALL A
CONSERVATION AND POPULATION GENETICS:
LAURA IACOLINA, ALAIN FRANTZ

HALL B
SQUIRRELS:
JOHN KOPROWSKI

11:05 - 11:35

Conservation in the 21st century, technological advances and their challenges
Laura Iacolina

Conservation of squirrels on the ground and in the trees: the value of the Sciuridae
John Koprowski

11:35 - 11:55

Genome-wide analyses of population structure in a highly mobile carnivore, the gray wolf (*Canis lupus*), across Eurasia
Astrid Vik Stronnen

Hidden interactions between alien and native species: new insights in the grey-red squirrel paradigm
Lucas Wauters

11:55 - 12:15

The impact and origin of wolves immigrating to a recently established population on the Scandinavian Peninsula
Mikael Åkesson

Game of Cones – The changing fortunes of red and grey squirrels in Ireland
Colin Lawton

12:15 - 12:35

Wolves at the crossroad: Fission–fusion range biogeography in the Western Carpathians and Central Europe
Barbora Cerna Bolfikova

Cost and benefits of living in the city – comparing two populations of Warsaw red squirrels
Agata Kostrzewa

12:35 - 12:55

Demographic history of an isolated and endangered wolf population
Raquel Godinho

Whistling at the Tower of Babel: geographic variability in alarm calls of the European ground squirrel
Irena Schneiderová

12:55 - 13:15

Demographic and genetic effects of translocation a captive breeding project in the endangered arctic fox (*Vulpes lagopus*)
Johan Wallén

When intraspecific competition is an important cue in animal settlement
Marina Morandini

13:15 - 14:45

LUNCH

14:45 - 16:35		HALL A CONSERVATION GENETICS: <i>FRANK ZACHOS, ELENA BUZAN</i>	HALL B PREDATOR-PREY INTERACTIONS <i>HANNU YLONEN, MARKO HAAPAKOSKI</i>
14:45 - 15:15	Landscape heterogeneity in landform and land use provides functional resistance to gene flow in continuous Asian black bear populations <i>Naoki Ohnishi</i>	New insights to predator-prey interaction with voles and weasels <i>Hannu Ylönen</i>	
15:15 - 15:35	Hybrid identification and admixture time detection in European wildcat populations through genome-wide procedures <i>Federica Mattucci</i>	Communicating Fear: The Role of Alarm Pheromones in a Bank Vole <i>Marko Haapakoski</i>	
15:35 - 15:55	Taming of the wild: a new tool for cross study RNA-seq analysis applied to behavioural traits in dogs and tame foxes <i>Diana Lobo</i>	Secondhand horror: effects of direct and indirect predator cues on behavior and reproduction of the bank vole <i>Thorbjörn Sievert</i>	
15:55 - 16:15	Diversity of the MHC class II DRB alleles in chamois populations <i>Sunčica Stipoljev</i>	Is the wild rabbit (<i>Oryctolagus cuniculus</i>) shaping geographical distribution patterns of its predator's community in the Iberian Peninsula? <i>Patricia H. Vaquerizas</i>	
16:15 - 16:35	Harnessing the potential of environmental DNA (eDNA) metabarcoding for monitoring mammalian communities in temperate and neotropical regions <i>Allan McDevitt</i>	A risky niche: among-individual differences in landscapes of fear <i>Melanie Dammhahn</i>	
16:35 - 17:05	COFFEE BREAK		
17:05 - 17:25	Inbreeding depression and genetic rescue in a cyclic mammal population <i>Karin Norén</i>	Taking risks for food: effects of the landscape of fear at low trophic levels <i>Clara Mendes Ferreira</i>	
17:25 - 17:45	Last chance to see? Status and distribution of the Vojvodina blind mole rat revisited <i>Attila Németh</i>	Using by-catch data from camera-trapping studies aimed at carnivores to study their prey <i>Tim R. Hofmeister</i>	
17:45 - 18:05	Population genetics as a tool for conservation biology: defining management units for the greater horseshoe bat <i>Orianne Tourmayre</i>	Effect of predation on hunting quotas, hunter observations and moose harvest in two countries with an increasing wolf population during 22 years <i>Camilla Wikenros</i>	
18:05 - 18:25	Which primer set(s) for your bat diet metabarcoding study? Application to two insectivorous bat species sharing maternity roosts <i>Orianne Tourmayre</i>	The resource dispersion hypothesis – a test with a cyclic mesopredator <i>Rasmus Erlandsson</i>	
18:25 - 18:45	Effects of habitat fragmentation in the social behaviour of the Cabrera vole: insights from genetic non-invasive sampling <i>Paulo Célio Alves</i>		
20:00	WELCOME PARTY (UNIVERSITY OF WARSAW BOTANIC GARDEN)		

TUESDAY, 24.09.2019

08:30 - 08:35 OPENING

PLENARY
 08:35 - 09:35 EVOLUTION AND ECOLOGY OF PLAGUE: A DISEASE OF TODAY WHICH CHANGED OUR HISTORY
NILS CHR. STENSETH

	HALL A PHYLOGEOGRAPHY AND BIOGEOGRAPHY: <i>ETTORE RANDI</i>	HALL B CLIMATE CHANGE AND POPULATION DYNAMICS: <i>BODIL ELMHAGEN</i>	HALL C WORKSHOP
--	---	--	---------------------------

09:45 - 10:15	Biogeography and Phylogeography: Toolkits for the conservation of biodiversity <i>Ettore Randi</i>	Climate – and mammal community - change <i>Bodil Elmhagen</i>	Wildlife telemetry technologies
---------------	---	--	---------------------------------

10:15 - 10:35	Inferring the evolutionary history of wolf expansion through Beringia land bridge <i>Carolina Pacheco</i>	Impacts of climate change on the Eurasian otter <i>Lutra lutra</i> <i>Anna Loy</i>	Wildlife telemetry technologies
---------------	--	---	---------------------------------

10:35 - 10:55	Next-generation phylogeography resolves post-glacial colonization patterns in the red fox (<i>Vulpes vulpes</i>) in Europe <i>Allan McDevitt</i>	Capturing a cascade in a changing world. How do predator recolonization, community complexity and climate driven shift in prey species influence species interactions in northern ecosystems? <i>Malin Aronsson</i>	Wildlife telemetry technologies
---------------	---	--	---------------------------------

10:55 - 11:15	Is there any adaptive variability of TLR2 gene across bank vole populations from two mtDNA lineages in NE Poland? <i>Ewa Tarnowska</i>	Climate change affects vole population dynamics and plant-herbivore interactions <i>Zbigniew Borowski</i>	Wildlife telemetry technologies
---------------	---	--	---------------------------------

11:15 - 11:35 COFFEE BREAK

11:35 - 11:55	Genetic diversity of two mitochondrial DNA genes in <i>Spirometra erinaceieuropaei</i> (<i>Cestoda: Diphyllobothridae</i>) from Poland <i>Joanna Stojak</i>	An object-oriented modelling of a mammal population <i>Miłosława Sokół</i>	Wildlife telemetry technologies
---------------	--	---	---------------------------------

11:55 - 12:15	An update on the Robertsonian (Rb) chromosomal variability in the natural populations of the house mouse, <i>Mus musculus domesticus</i> , based on the simultaneous study of the three Rb systems of Greece. <i>George P. Mitsainas</i>	Urban rats in Helsinki: seasonal variation in population size and parasite prevalence <i>Tuomas Aivelo</i>	Wildlife telemetry technologies
---------------	---	---	---------------------------------

12:15 - 12:35	Chromosomal variability of the common shrew (<i>Sorex araneus L.</i>) in Central and Eastern Siberia <i>Boris Sheftel</i>	Seasonal models to predict population dynamics of Australian mice <i>Jennifer Paola Correa Cuadros</i>	Wildlife telemetry technologies
---------------	--	---	---------------------------------

12:35 - 12:55	The role of post-glacial demography in shaping variation of innate immunity genes in a free-living rodent <i>Agnieszka Kloch</i>	New RFID technology for small mammal research <i>Sarah Knowles</i>	Wildlife telemetry technologies
---------------	---	---	---------------------------------

13:00 - 14:00 LUNCH

14:00 MID-CONFERENCE EXCURSION

WEDNESDAY, 25.09.2019

08:55 - 09:00	OPENING		
09:00 - 10:00	PLENARY ON THE MOVE: LESSON LEARNED FROM 15 YEARS OF MOVEMENT ECOLOGY ON EUROPEAN MAMMALS <i>FRANCESCA CAGNACCI</i>		
10:10 - 17:20	HALL A PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT: <i>KAROL ZUB</i>	HALL B UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT: <i>MARCO APOLLONIO</i>	HALL C WORKSHOP
10:10 - 10:40	Effect of intensive grasslands management on the abundance of weasels <i>Karol Zub</i>	Future challenges in ungulate conservation and management in Europe <i>Marco Apollonio</i>	Wildlife aquatic
10:40 - 11:00	Paws without claws? Ecological impact and conservation of wolves in Europe's human-dominated landscapes <i>Dries Kuijper</i>	The relative effect of large carnivores, hunter harvest, and climate on ungulate productivity in Sweden <i>Aimee Tallian</i>	
11:00 - 11:20	Wolf at your door: movement of established and disperser wolves and kill sites distribution in relation to human infrastructures <i>David Carricondo-Sanchez</i>	Forest roads modify ungulates' landscape of fear <i>Karen Marie Mathisen</i>	
11:20 - 11:40	A standardized method for conducting and analysing experimental human approaches on wolves <i>Ane Eriksen</i>	Factors influencing red deer bark stripping on spruce: plant diversity, crop intake and temperature <i>Anna Widén</i>	
11:40 - 12:10	COFFEE BREAK		
12:10 - 12:30	The effects of wolves returning to forest ecosystems <i>Adam Wójcicki</i>	The asymmetric share of moose as prey for humans and wolves <i>Barbara Zimmermann</i>	
12:30 - 12:50	Conservation strategies for the arctic fox <i>Anders Angerbjörn</i>	Spatial patterns of immunogenetic and neutral variation influence on selected fitness parameters in roe deer <i>Elena Bužan</i>	
12:50 - 13:10	Using habitat suitability modelling to inform proposed reintroductions of European wildcat <i>Felis silvestris</i> to England and Wales <i>Stephen Carter</i>	The ratios of stable isotopes of carbon and nitrogen in bone collagen: variations within individuals and within populations of modern red deer (<i>Cervus elaphus</i>) <i>Maciej Sykut</i>	
13:10 - 13:30	How do european wildcats (<i>Felis silvestris silvestris</i>) manage to settle in a heavily fragmented landscape <i>Mathias Herrmann</i>	Roads, forestry, and wolves interact to drive moose browsing behavior in Scandinavia <i>Anne Loosen</i>	
13:30 - 15:00	LUNCH		

15:00 - 15:20	Diet of foxes in Warsaw – comparison of the results from three different methods of assessment <i>Mateusz Jackowiak</i>	Diet overlap among red deer, roe deer and moose during winter in forest ecosystems, NE Poland <i>Mirosław Ratkiewicz</i>
15:20 - 15:40	Variations in the interspecific relationships of sympatric carnivores in a fluctuating prey scenario in a boreal ecosystem <i>Rocio Cano-Martinez</i>	Alien vs. native – influence of fallow deer <i>Dama dama</i> introduction on roe deer <i>Capreolus capreolus</i> population <i>Jakub Gryz</i>
15:40 - 16:00	Comparison of grey wolves and red foxes diet in habitats of different quality <i>Zuzanna Wikar</i>	Rusa deer, an invasive species : inter & intra-population ecology, diet and dental microwear <i>Emilie Berlioz</i>
16:00 - 16:20	Fossoriality in a risky landscape: wolves drive badger denning behaviour in Białowieża Primeval Forest <i>Tom Diserens</i>	Composition and diet fluctuations of a reintroduced population of the Atlas Deer <i>Cervus elaphus barbarus</i> (Bennett, 1833) in the Akfadou forest (Algeria). <i>Nora Khammes-Elhoms</i>
16:20 - 16:40	Martens in a changing world – body size variation over space and time <i>Anna Wereszczuk</i>	Impact of wild boar rooting on ectomycorrhizal fungi in boreal forests of Sweden <i>Lars Hillström</i>
16:40 - 17:00	Detecting methods for an opportunistic and expanding mesocarnivore in SW Europe: the Egyptian mongoose (<i>Herpestes ichneumon</i>) <i>Esther Descalzo</i>	Habitat use by Asian elephants: Context matters <i>Dinesh Neupane</i>
17:00 - 17:20	Evidence of urbanization of the Arctic fox near Reykjavik capital <i>Ester Rut Unnsteinsdóttir</i>	Distribution and abundance of wildlife in Europe: Towards harmonization and development of new strategies in the collection and use of data in wildlife management <i>Karolina Petrović</i>
17:20 - 17:50	COFFEE BREAK	
17:50 - 19:20	POSTER SESSION	

THURSDAY, 26.09.2019

08:55 - 09:00	OPENING
09:00 - 10:00	PLENARY: THE EVOLUTION OF THE MAMMALIAN BRAIN FROM LIFE HISTORY PERSPECTIVE <i>MAREK KONARZEWSKI</i>

	HALL A	HALL B
10:10 - 13:10	BEHAVIOURAL AND EVOLUTIONARY ECOLOGY: <i>LESZEK RYCHLIK, BORIS SHEFTEL</i>	MAMMAL PALEOECOLOGY: IMPLICATIONS FOR CONSERVATION AND RESTORATION: <i>HERVÉ BOCHERENS, RAFAŁ KOWALCZYK</i>
10:10 - 10:40	Summer and winter diets of <i>Neomys fodiens</i> and <i>Sorex minutus</i> (Soricidae): Can the weakly expressed Dehnel's phenomenon in these species be explained by high availability of their prey in winter? <i>Leszek Rychlik</i>	Mammal paleoecology: Implications for conservation and restoration <i>Hervé Bocherens</i>

10:40 - 11:00	Looking after energy budget: Ranging behaviour and habitat use of the desert hedgehog <i>Nobuyuki Yamaguchi</i>	Adapt or die Response of large herbivores to environmental changes in Europe during the Holocene <i>Rafał Kowalczyk</i>
11:00 - 11:20	Does Animal Personality Affect Movement in Habitat Corridors? Experiments with Common Voles (<i>Microtus arvalis</i>) using Different Corridor Widths <i>Gabriele Joanna Kowalski</i>	Holocene extinction of autochthonous mammals in the Carpathian Basin (Central Europe) and its ecological consequences <i>Attila Németh</i>
11:20 - 11:40	Do common shrews <i>Sorex araneus</i> (Soricidae) of Novosibirsk and Tomsk chromosomal races differ in behavioural syndromes? <i>Leszek Rychlik</i>	Conceptual reconstruction of Late Pleistocene large mammal communities on the Palaeo-Agulhas Plain reveals resilience to climate change but vulnerability to modern human predators <i>Jan Venter</i>
11:40 - 12:10	COFFEE BREAK	
12:10 - 12:30	Synchronization of rodent reproduction and tree fructification in oak communities <i>Victoria A. Vekhnik</i>	Conservation paleoecology of Southeast Asian gorals (<i>Nemorhedus</i>) and serow (<i>Capricornis</i>) through stable isotopic tracking since 400,000 years <i>Hervé Bocherens</i>
12:30 - 12:50	Can we get along? The role of competitive interactions and forest management in shaping a guild of terrestrial rodents <i>Stefania Gasperini</i>	The NW Iberian brown bear diet from Upper Pleistocene to nowadays: an study on stable isotopes <i>Ana García-Vázquez</i>
12:50 - 13:10	Effects of a simulated seasonal dietary shift on the wood mouse gut microbiota; from the lab to the wild <i>Kirsty Marsh</i>	Ecological niche of red deer (<i>Cervus elaphus</i>) and changes in its range in Europe and the Ural Mountains since the Late Pleistocene <i>Magdalena Niedziałkowska</i>
13:10 - 14:40	LUNCH	
<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="width: 45%;"> <p>HALL A</p> <p>BEHAVIOURAL AND EVOLUTIONARY ECOLOGY: <i>LESZEK RYCHLIK, BORIS SHEFTEL</i></p> </div> <div style="width: 45%;"> <p>HALL B</p> <p>PALEOGENETICS: <i>AXEL BARLOW</i></p> </div> </div>		
14:40 - 15:10	Trophic niche partitioning and dietary competition in small rodents, measured using stable isotopes <i>Piotr Chibowski</i>	Middle Pleistocene genome calibrates the evolutionary history of cave bears <i>Axel Barlow</i>
15:10 - 15:30	Acoustic signals accompanying direct contact in two rodent species: the bank and the root voles <i>Alek Rachwald</i>	Diverse responses of common vole (<i>Microtus arvalis</i>) populations to Late Glacial and Early Holocene climate changes – evidence from ancient DNA <i>Mateusz Baca</i>
15:30 - 15:50	Think before you speak! Using thermal imaging for detecting intention and preparation to vocalize <i>Vlad Demartsev</i>	Highly divergent population of narrow-headed vole from the Late Pleistocene Europe <i>Danijela Popović</i>
15:50 - 16:10	Activity patterns and thermoregulation in male parti-colored bats <i>Vespertilio murinus</i> <i>Zuzanna Hałat</i>	Neolithic revolution triggered demographic expansion of an African opportunistic carnivore <i>Rita Rocha</i>
16:10 - 16:30	The importance of multi-species bat roosts: host-parasite relationships between bats and bat flies of South-Eastern Europe <i>Áron Péter</i>	
16:30 - 16:50	Adaptive differences in host selection and seasonality of bat-specialist ticks in Europe <i>Attila D. Sándor</i>	
20:00	CONFERENCE DINNER	

FRIDAY, 27.09.2019

08:55 - 09:00	OPENING	
09:00 - 10:00	PLENARY ECOLOGY OF RODENT-BORNE PATHOGENS IN EUROPE <i>HEIKKI HENTTONEN</i>	
10:00 - 10:30	COFFEE BREAK	
10:30 - 14:10	HALL A MAMMALS IN ANTHROPOGENIC LANDSCAPE: <i>DUŠKO ČIROVIĆ, ASTRID VIK STRONNEN</i>	HALL B GENERAL SESSION: <i>FRANCK COURCHAMP</i>
10:30 - 11:00	Carnivores in anthropogenic landscapes <i>Duško Čirović</i>	The economic cost of invasive mammals <i>Franck Courchamp</i>
11:00 - 11:20	Resistance modelling infers physical and behavioural gene flow barriers to the red fox (<i>Vulpes vulpes</i>) across the Berlin metropolitan area <i>Alain Frantz</i>	Parasitological investigations of raccoons from several locations in Germany and Luxemburg <i>Natalia Osten-Sacken</i>
11:20 - 11:40	Red fox population dynamics in habitats of different anthropopression levels <i>Dagny Krauze-Gryz</i>	Know your enemy: A molecular approach identifies multiple key factors driving a small mammal invasion-extinction event on an island <i>Samuel Browett</i>
11:40 - 12:00	How does anthropogenic noise impact the behaviour of a keystone species? <i>Graeme Shannon</i>	Multispecies reservoir of <i>Spirometra erinaceieuropaei</i> (Cestoda: Diphyllobothridae) in wild mammalian hosts in NE Poland <i>Marta Kołodziej-Sobocińska</i>
12:00 - 12:30	COFFEE BREAK	
12:30 - 12:50	Evaluation of human influence on the activity of medium – large mammals in Myanmar forests <i>Giacomo Cremonesi</i>	Combining questionnaire survey and biogeographic models to update and forecast the distribution of the only mongoose species in Europe <i>Miguel Delibes-Mateos</i>
12:50 - 13:10	Linking biodiversity to ecosystem services: The small mammal community of NE Portugal agroecosystems <i>Joana Paupério</i>	Spatial variables associated with the geographical range shift of European hamster (<i>Cricetus cricetus</i>) in Poland <i>Aleksandra Zarzycka</i>
13:10 - 13:30	Behavioural adjustments of non-commensal rodents to urban environments <i>Valeria Mazza</i>	The beaver facilitates species richness and abundance of terrestrial and semi-aquatic mammals <i>Janne Sundell</i>
13:30 - 13:50	Do natural margins of arable fields support small mammal populations? <i>Grete Tõnisalu</i>	Mammal mapping in Russia <i>Andrey Lissovsky</i>
13:50 - 14:10	Community Assembly Rules of Insectivorous Bat Species in Man-made plantations in Israel <i>Claudia Allegrini</i>	Networking at sea: unraveling mixed-species cetacean sightings <i>Mridula Srinivasan</i>
14:10 - 14:30		Predators and megaherbivores have contrasting impacts on nitrogen and phosphorus stoichiometry in an African savanna <i>Elizabeth le Roux</i>
14:30 - 15:50	LUNCH	
15:50 - 16:00	CLOSING CEREMONY	
16:00	END OF CONFERENCE	

Contents

PREFACE.....	3
PROGRAM	4
PLENARY TALKS.....	26
Wild Migrations: Animal Movement, Anthropogenic Barriers, and Corridor Conservation in the American West	26
<i>Matthew Kauffman</i>	
Evolution and ecology of plague: a wildlife disease of today which changed our history	27
<i>Nils Chr. Stenseth</i>	
On the move: lesson learned from 15 years of movement ecology on European mammals	28
<i>Francesca Cagnacci</i>	
The Evolution of the mammalian brain from Life History perspective	29
<i>Marek Konarzewski</i>	
ORAL PRESENTATIONS.....	31
EMMA2: Updating the Atlas of European Mammals	31
<i>Laurent Schley, Tony Mitchell-Jones, Giovanni Amori, Boris Krystufek, Andrey A. Lissovsky, Ferdia Marnell, Svetlana Miteva, Friederike Spitzenberger, Johan Thissen, Vladimir Vohralik</i>	
SQUIRRELS	32
Conservation of squirrels on the ground and in the trees: the value of the Sciuridae	32
<i>John Koprowski</i>	
Hidden interactions between alien and native species: new insights in the grey-red squirrel paradigm	33
<i>Lucas Wauters, Maria Vittoria Mazzamuto, Francesca Santicchia, Claudia Romeo, Nicola Ferrari, Damiano Preatoni, Adriano Martinoli</i>	
Game of Cones – The changing fortunes of red and grey squirrels in Ireland	34
<i>Colin Lawton, Colin Guilfoyle, Victoria Molloy, Conor McKinney, Ruth Hanniffy</i>	
Cost and benefits of living in the city – comparing two populations of Warsaw red squirrels	35
<i>Agata Kostrzewa, Dagny Krauze-Gryz, Karolina Jasińska, Jakub Gryz</i>	
Whistling at the Tower of Babel: geographic variability in alarm calls of the European ground squirrel	36
<i>Irena Schneiderová, Lucie Štefanská, Lukáš Kratochvíl</i>	
When intraspecific competition is an important cue in animal settlement	37
<i>Marina Morandini, John Koprowski</i>	

CONSERVATION AND POPULATION GENETICS.....38

Conservation in the 21st century, technological advances and their challenges	38
Laura Iacolina	
Genome-wide analyses of population structure in a highly mobile carnivore, the gray wolf (<i>Canis lupus</i>), across Eurasia	39
Astrid Vik Stronnen, Atidzhe Ahmed, Giorgio Binelli, Duško Ćirović, Mihajla Djan, Helena Sif Ericson, Elena Fabbri, Ancuta Fedorca, Marco Galaverni, Astghik Ghazaryan, Raquel Godinho, Pavel Hulva, Bogumila Jędrzejewska, Natia Kopaliani, Josip Kusak, Federica Mattucci, Carsten Nowak, Kamila Plis, Dmitri Politov, Ettore Randi, Urmas Saarma, Tomaž Skrbinšek, Dragana Šnjegota, Mikael Åkesson, Romolo Caniglia	
The impact and origin of wolves immigrating to a recently established population on the Scandinavian Peninsula	40
Mikael Åkesson, Olof Liberg, Håkan Sand, Petter Wabakken, Øystein Flagstad, Ilpo Kojola, Jouni Aspi	
Wolves at the crossroad: Fission–fusion range biogeography in the Western Carpathians and Central Europe	41
Barbora Cerna Bolfikova, Pavel Hulva, Vendula Woznicova, Milena Jindrichova, Marketa Benesova, Robert Mysłajek, Sabina Nowak, Maciej Szewczyk, Natalia Niedźwiecka, Michal Figura, Atila Sandor, Vladimír Zyka, Dusan Romportl, Miroslav Kutal, Slavomir Findo, Vladimír Antal	
Demographic history of an isolated and endangered wolf population	42
Raquel Godinho, Rita Rocha, Pedro Silva, Raquel Pedra, Diana Castro, Francisco Álvares, José Vicente López-Bao	
Demographic and genetic effects of translocation from a captive breeding project in the endangered arctic fox (<i>Vulpes lagopus</i>)	43
Johan Wallén, Karin Norén, Anders Angerbjörn	
Landscape heterogeneity in landform and land use provides functional resistance to gene flow in continuous Asian black bear populations	44
Naoki Ohnishi, Takeshi Osawa	
Hybrid identification and admixture time detection in European wildcat populations through genome-wide procedures	45
Federica Mattucci, Marco Galaverni, Leslie A. Lyons, Paulo C. Alves, Ettore Randi, Edoardo Velli, Luca Pagani, Romolo Caniglia	
Taming of the wild: a new tool for cross study RNA-seq analysis applied to behavioural traits in dogs and tame foxes	46
Diana Lobo, Raquel Godinho, John Archer	
Diversity of the MHC class II DRB alleles in chamois populations	47
Sunčica Stipoljev, Elena Bužan, Laura Iacolina, Toni Safner, Andrea Rezić, Sandra Potušek, Krešimir Krizanović, Ana Galov, Ferdinand Bego, Georgi Markov, Haritakis Papaioannou, Attila Farkas, Massimo Scandura, Dragana Milošević, Vladimir Maletić, Elmar Babaev, Dragan Gačić, Peter Lazar, María Cruz Arnal, Hüseyin Ambarlı, Nikica Šprem	
Harnessing the potential of environmental DNA (eDNA) metabarcoding for monitoring mammalian communities in temperate and neotropical regions	48
Allan McDevitt, Lynsey Harper, Naiara Sales	
Inbreeding depression and genetic rescue in a cyclic mammal population	49
Karin Norén, Malin Hasselgren, Johan Wallén, Rasmus Erlandsson, Anders Angerbjörn	
Last chance to see? Status and distribution of the Vojvodina blind mole rat revisited	50
Attila Németh, Gábor Csorba, Levente Laczkó, Edvárd Mizsei, Judit Bereczki, Gábor Sramkó	

Population genetics as a tool for conservation biology: defining management units for the greater horseshoe bat	51
<i>Orianne Tournayre, Jean-Baptiste Pons, Maxime Leuchtman, Raphael Leblois, Sylvain Piry, Ondine Filippi-Codaccioni, Anne Loiseau, Jeanne Duhayer, Inazio Garin, Fiona Mathews, Sébastien Puechmaille, Nathalie Charbonnel, Dominique Pontier</i>	
Which primer set(s) for your bat diet metabarcoding study? Application to two insectivorous bat species sharing maternity roosts	52
<i>Orianne Tournayre, Maxime Leuchtman, Marine Trillat, Sylvain Piry, Ondine Filippi-Codaccioni, Dominique Pontier, Nathalie Charbonnel, Maxime Galan</i>	
Effects of habitat fragmentation in the social behaviour of the Cabrera vole: insights from genetic non-invasive sampling	53
<i>Clara Ferreira, Dinora Peralta, Tiago Mendes, Teresa Vaz Freire, Helena Sabino-Marques, Frederico Mestre, Soraia Barbosa, Sara M Santos, Russell Alpizar-Jara, Pedro Beja, António Mira, Xavier Lambin, Jeremy B Searle, Paulo Célio Alves, Joana Paupério, Ricardo Pita</i>	

PREDATOR-PREY INTERACTIONS.....54

New insights to predator-prey interaction with voles and weasels	54
<i>Hannu Ylönen, Marko Haapakoski, Sonny Bleicher, Thorbjörn Sievert</i>	
Communicating Fear: The Role of Alarm Pheromones in a Bank Vole	55
<i>Marko Haapakoski, Thorbjörn Sievert, Hannu Ylönen</i>	
Secondhand horror: effects of direct and indirect predator cues on behavior and reproduction of the bank vole	56
<i>Thorbjörn Sievert, Marko Haapakoski, Rupert Palme, Helinä Voipio, Hannu Ylönen</i>	
Is the wild rabbit (<i>Oryctolagus cuniculus</i>) shaping geographical distribution patterns of its predator's community in the Iberian Peninsula?	57
<i>Patricia H. Vaquerizas, Francisco Díaz-Ruiz, Jesús Olivero, Miguel Delibes-Mateos, Rafael Villafuerte</i>	
A risky niche: among-individual differences in landscapes of fear	58
<i>Melanie Dammhahn</i>	
Taking risks for food: effects of the landscape of fear at low trophic levels	59
<i>Clara Mendes Ferreira, Jana A. Eccard, Melanie Dammhahn</i>	
Using by-catch data from camera-trapping studies aimed at carnivores to study their prey	60
<i>Tim R. Hofmeester, Neri H. Thorsen, Joris P.G.M. Cromsigt, Jonas Kindberg, Henrik Andrés, John D.C. Linnell, John Odden</i>	
Effect of predation on hunting quotas, hunter observations and moose harvest in two countries with an increasing wolf population during 22 years	61
<i>Camilla Wikenros, Barbara Zimmermann, Håkan Sand, Johan Månsson, Erling Maartmann, Ane Eriksen, Petter Wabakken</i>	
The resource dispersion hypothesis – a test with a cyclic mesopredator	62
<i>Rasmus Erlandsson, Malin Hasselgren, Anders Angerbjörn, Karin Norén</i>	

PHYLOGEOGRAPHY AND BIOGEOGRAPHY63

Biogeography and Phylogeography: Toolkits for the conservation of biodiversity	63
<i>Ettore Randi</i>	
Inferring the evolutionary history of wolf expansion through Beringia land bridge	64
<i>Carolina Pacheco, Astrid Vik Stronnen, Bogumiła Jędrzejewska, Raquel Godinho</i>	

Next-generation phylogeography resolves post-glacial colonization patterns in the red fox (<i>Vulpes vulpes</i>) in Europe	65
Allan McDevitt , Ilaria Coscia , Samuel Browett , Mark Statham , Aritz Ruiz-González , Iwona Ruczyńska , Joanna Stojak , Ben Sacks , Cino Pertoldi , Ettore Randi , Rafal Kowalczyk , Jan Wójcik	
Is there any adaptive variability of TLR2 gene across bank vole populations from two mtDNA lineages in NE Poland?	66
Ewa Tarnowska , Magdalena Niedziałkowska , Joanna Stojak , Bogumiła Jędrzejewska	
Genetic diversity of two mitochondrial DNA genes in <i>Spirometra erinaceieuropaei</i> (Cestoda: Diphyllbothridae) from Poland	67
Marta Kołodziej-Sobocińska , Joanna Stojak , Eliza Kondzior , Iwona Ruczyńska , Jan Wójcik	
An update on the Robertsonian (Rb) chromosomal variability in the natural populations of the house mouse, <i>Mus musculus domesticus</i> , based on the simultaneous study of the three Rb systems of Greece	68
George P. Mitsainas	
Chromosomal variability of the common shrew (<i>Sorex araneus L.</i>) in Central and Eastern Siberia	69
Boris Sheftel , Svetlana Pavlova	
The role of post-glacial demography in shaping variation of innate immunity genes in a free-living rodent ...	70
Agnieszka Kloch , Aleksandra Biedrzycka	

CLIMATE CHANGE AND POPULATION DYNAMICS71

Climate – and mammal community – change	71
Bodil Elmhagen	
Impacts of climate change on the Eurasian otter <i>Lutra lutra</i>	72
Anna Loy , Broenniman Olivier , Cianfrani Carmen , Sara Diamente , Mirko Di Febbraro , Antoine Guisan	
Capturing a cascade in a changing world. How do predator recolonization, community complexity and climate driven shift in prey species influence species interactions in northern ecosystems?	73
Malin Aronsson , Bodil Elmhagen , Harto Lindén , Katja Holmala	
Climate change affects vole population dynamics and plant-herbivore interactions.....	74
Zbigniew Borowski , Karol Zub , Marcin Sulwiński , Małgorzata Suska-Malawska , Marek Konarzewski	
An object-oriented model of a mammal population	75
Miłostawa Sokół , Alicja Gryczyńska , Tomasz Gortat , Robert Meronka , Michał Kozakiewicz	
Urban rats in Helsinki: seasonal variation in population size and parasite prevalence	76
Tuomas Aivelo	
Seasonal models to predict population dynamics of Australian mice	77
Jennifer Paola Correa Cuadros , Sergio Estay , Peter Brown , Wendy Ruscoe , Mauricio Lima	
New RFID technology for small mammal research	78
Curt Lamberth , Aura Raulo , Tim Coulson , Sarah Knowles ,	

UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT79

Future challenges in ungulate conservation and management in Europe	79
Marco Apollonio	

The relative effect of large carnivores, hunter harvest, and climate on ungulate productivity in Sweden	80
Aimee Tallian	
Forest roads modify ungulates' landscape of fear	81
Karen Marie Mathisen, Zbigniew Borowski	
Factors influencing red deer bark stripping on spruce: plant diversity, crop intake and temperature	82
Anna Widén	
The asymmetric share of moose as prey for humans and wolves	83
Barbara Zimmermann, Håkan Sand, Camilla Wikenros, Ane Eriksen, Petter Wabakken	
Spatial patterns of immunogenetic and neutral variation influence on selected fitness parameters in roe deer	84
Elena Bužan, Katarina Flajšman, Boštjan Pokorny	
The ratios of stable isotopes of carbon and nitrogen in bone collagen: variations within individuals and within populations of modern red deer (<i>Cervus elaphus</i>)	85
Maciej Sykut, Sławomira Pawełczyk, Bogumiła Jędrzejewska, Magdalena Niedziałkowska	
Roads, forestry, and wolves interact to drive moose browsing behavior in Scandinavia	86
Anne Loosen, Olivier Devineau, Barbara Zimmermann, Joris Cromsigt, Sabine Pfeffer, Christina Skarpe, Karen Marie Mathisen	
Diet overlap among red deer, roe deer and moose during winter in forest ecosystems, NE Poland	87
Miroslaw Ratkiewicz, Eric Coissac, Magdalena Świsłocka, Magdalena Czajkowska, Pierre Taberlet, Marta Czernik, Rafał Kowalczyk	
Alien vs. native – influence of fallow deer <i>Dama dama</i> introduction on roe deer <i>Capreolus capreolus</i> population	88
Jakub Gryz, Dagny Krauze-Gryz	
Rusa deer, an invasive species : inter & intra-population ecology, diet and dental microwear	89
Emilie Berlioz, Gildas Merceron, Marc Colyn	
Composition and diet fluctuations of a reintroduced population of the Atlas Deer <i>Cervus elaphus barbarus</i> (Bennett, 1833) in the Akfadou forest (Algeria).....	90
N Khammes-Talbi, Nora Khammes-Elhomsj, Stéphane Aulagnier	
Impact of wild boar rooting on ectomycorrhizal fungi in boreal forests of Sweden	91
Lars Hillström, Antonio Carpio, Marta Garcia Moreno, Mikael Lönn, Guillermo Bueno	
Habitat use by Asian elephants: Context matters	92
Dinesh Neupane, Youngsang Kwon, Thomas Risch, A. Christy Williams, Ronald Johnson	
Distribution and abundance of wildlife in Europe: Towards harmonization and development of new strategies in the collection and use of data in wildlife management	93
Karolina Petrović, Joaquin Vicente Baños, Jose Antonio Blanco, Marco Apollonio, Ramon Sorriquer, Francesca Brivio, Ezio Ferroglio, Patrick Jansen, Oliver Keuling, Carmen Ruiz Rodrigues, Massimo Scandura, Graham Smith, Nikica Šprem, Nera Fabijanić, Stefania Zanet, Tomasz Borowik, Tomasz Podgórski	

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT94

Effect of intensive grasslands management on the abundance of weasels	94
Karol Zub, Anna Andruszkiewicz	
Paws without claws? Ecological impact and conservation of wolves in Europe's human-dominated landscapes	95
Dries Kuijper, Marcin Churski, Jakub Bubnicki	

Wolf at your door: movement of established and disperser wolves and kill sites distribution in relation to human infrastructures	96
David Carricondo-Sanchez , Barbara Zimmermann , Petter Wabakken , Ane Eriksen , Milleret Cyril , Andrés Ordiz , Ana Sanz-Perez , Håkan Sand , Camilla Wikenros	
A standardized method for conducting and analysing experimental human approaches on wolves	97
Ane Eriksen , Erik Versluijs , Boris Fuchs , Barbara Zimmermann , Petter Wabakken , Léa Bouet , Andrés Ordiz , Kristoffer T. Nordli , David Carricondo-Sanchez , Peter Sunde , Håkan Sand , Lucrezia Gorini , Frank Michler , Camilla Wikenros , Benjamin Gillich , Siegfried Rieger	
The effects of wolves returning to forest ecosystems	98
Adam Wójcicki , Zbigniew Borowski	
Conservation strategies for the arctic fox.....	99
Anders Angerbjörn , Karin Norén , Johan Wallén	
Using habitat suitability modelling to inform proposed reintroductions of European wildcat <i>Felis silvestris</i> to England and Wales	100
Jenny Macpherson , Sébastien Devillard , Sandrine Ruetten , Michael Hudson , Stephen Carter	
How do european wildcats (<i>Felis silvestris silvestris</i>) manage to settle in a heavily fragmented landscape?	101
Mathias Herrmann	
Diet of foxes in Warsaw – comparison of the results from three different methods of assessment	102
Mateusz Jackowiak , Jakub Gryz , Dagny Krauze-Gryz	
Variations in the interspecific relationships of sympatric carnivores in a fluctuating prey scenario in a boreal ecosystem	103
Rocio Cano-Martinez , David Carricondo-Sanchez , Olivier Devineau , Morten Odden	
Comparison of grey wolves and red foxes diet in habitats of different quality	104
Zuzanna Wikar , Adrian Zwolicki , Maciej Szewczyk	
Fossoriality in a risky landscape: wolves drive badger denning behaviour in Białowieża Primeval Forest	105
Tom Diserens , Marcin Churski , Jakub Bubnicki , Esmee Schutgens , Kira Rokx , Rafał Kowalczyk , Dries Kuijper	
Martens in a changing world – body size variation over space and time	106
Anna Wereszczuk , Sim Broekhuizen , Alexander Csanády , Tomislav Dumić , Tim R. Hofmeester , József Lanszki , Aksel Bo Madsen , Gerard Müskens , Malamati A. Papakosta , Iñigo Zuberogoitia , Andrzej Zalewski	
Detecting methods for an opportunistic and expanding mesocarnivore in SW Europe: the Egyptian mongoose (<i>Herpestes ichneumon</i>)	107
Esther Descalzo , Miguel Delibes-Mateos , Francisco Díaz-Ruiz , José Jiménez , Pablo Ferreras	
Evidence of urbanization of the Arctic fox near Reykjavík capital	108
Ester Rut Unnsteinsdóttir	

MAMMAL PALEOECOLOGY: IMPLICATIONS FOR CONSERVATION AND RESTORATION.....109

Mammal paleoecology: Implications for conservation and restoration	109
Hervé Bocherens , Rafał Kowalczyk	

Adapt or die—Response of large herbivores to environmental changes in Europe during the Holocene	110
<i>Emilia Hofman-Kamińska, Hervé Bocherens, Dorothée G. Drucker, Ralph M. Fyfe, Witold Gumiński, Daniel Makowiecki, Martina Pacher, Giedrė Piličiauskienė, Tomasz Samojlik, Jessie Woodbridge, Rafał Kowalczyk</i>	
Holocene extinction of autochthonous mammals in the Carpathian Basin (Central Europe) and its ecological consequences	111
<i>Attila Németh, Annamária Bárány, Piroska Pazonyi, Enikő Magyari, József Pálffy</i>	
Conceptual reconstruction of Late Pleistocene large mammal communities on the Palaeo-Agulhas Plain reveals resilience to climate change but vulnerability to modern human predators	112
<i>Jan Venter, Christopher Brooke, Curtis Marean, Herve Fritz, Charles Helm</i>	
Conservation paleoecology of Southeast Asian gorals (<i>Naemorhedus</i>) and serow (<i>Capricornis</i>) through stable isotopic tracking since 400,000 years	113
<i>Kantapon Suraprasit, Rasmi Shoocongdej, Jean-Jacques Jaeger, Yaowalak Chaimanee, Hervé Bocherens</i>	
The NW Iberian brown bear diet from Upper Pleistocene to nowadays: an study on stable isotopes	114
<i>Ana García-Vázquez, Ana C. Pinto Llona, José Vicente López-Bao, Fernando Ballesteros, Aurora Grandal-d'Anglade</i>	
Ecological niche of red deer (<i>Cervus elaphus</i>) and changes in its range in Europe and the Ural Mountains since the Late Pleistocene	115
<i>Magdalena Niedziałkowska, Karolina Doan, Maciej Sykut Marcin Górný, Krzysztof Stefaniak, Natalia Piotrowska, Bogumiła Jędrzejewska, Bogdan Ridush, Sławomira Pawełczyk, Paweł Mackiewicz, Ana Stanković</i>	

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY 116

Summer and winter diets of <i>Neomys fodiens</i> and <i>Sorex minutus</i> (Soricidae): Can the weakly expressed Dehnel's phenomenon in these species be explained by high availability of their prey in winter?	116
<i>Leszek Rychlik, Klaudia Kępka, Paweł Kardynia</i>	
Acoustic signals accompanying direct contact in two rodent species: the bank and the root voles	117
<i>Alek Rachwałd, Andrzej Kołaczyński, Zbigniew Borowski</i>	
Looking after energy budget: Ranging behaviour and habitat use of the desert hedgehog	118
<i>Carly Pettett, Afra Al-Hajri, Hayat Al-Jabiry, David Macdonald, Nobuyuki Yamaguchi</i>	
Does Animal Personality Affect Movement in Habitat Corridors? Experiments with Common Voles (<i>Microtus arvalis</i>) using Different Corridor Widths	119
<i>Gabriele Joanna Kowalski, Volker Grimm, Antje Herde, Anja Guenther, Jana A. Eccard</i>	
Do common shrews <i>Sorex araneus</i> (Soricidae) of Novosibirsk and Tomsk chromosomal races differ in behavioural syndromes?	120
<i>Leszek Rychlik, Boris Sheftel, Philipp Tumasian</i>	
Synchronization of rodent reproduction and tree fructification in oak communities	121
<i>Victoria A. Vekhnik, Vladimir P. Vekhnik, Olga A. Rozentsvet, Elena S. Bogdanova</i>	
Can we get along? The role of competitive interactions and forest management in shaping a guild of terrestrial rodents	122
<i>Stefania Gasperini, Alessio Mortelliti, Paola Bartolommei, Cristina Bencini, Andrea Bonacchi, Carlo Cinque, Emiliano Manzo, Roberto Cozzolino</i>	
Effects of a simulated seasonal dietary shift on the wood mouse gut microbiota; from the lab to the wild ...	123
<i>Kirsty Marsh, Aura Raulo, Sarah Knowles</i>	

Trophic niche partitioning and dietary competition in small rodents, measured using stable isotopes	124
<u>Piotr Chibowski, Marcin Brzeziński, Małgorzata Suska-Malawska</u>	
Think before you speak! Using thermal imaging for detecting intention and preparation to vocalize	125
<u>Vlad Demartsev, Glenn Tattersall, Ariana Strandburg-Peshkin, Marta Manser</u>	
Activity patterns and thermoregulation in male parti-coloured bats <i>Vespertilio murinus</i>	126
<u>Zuzanna Hałat, Marcin Zegarek, Ireneusz Ruczyński</u>	
The importance of multi-species bat roosts: host-parasite relationships between bats and bat flies of South-Eastern Europe	127
<u>Áron Péter, Levente Barti, István Csósz, Alexandra Corduneanu, Mihály Földvári, Gábor Földvári, Sándor Hornok, Andrei D. Mihalca, Attila D. Sándor</u>	
Adaptive differences in host selection and seasonality of bat-specialist ticks in Europe	128
<u>Attila D. Sándor, Alexandra Corduneanu, Áron Péter, Andrei Daniel Mihalca, Levente Barti, István Csósz, Krisztina Szőke, Sándor Hornok</u>	

PALEOGENETICS 129

Middle Pleistocene genome calibrates the evolutionary history of cave bears	129
<u>Axel Barlow, Johanna L. A. Paijmans, Federica Alberti, Boris Gasparian, Guy Bar-Oz, Ron Pinhasi, Elena Belyaeva, Irina Foronova, Martina Pacher, Love Dalén, Gennady Baryshnikov, Michael Hofreiter</u>	
Diverse responses of common vole (<i>Microtus arvalis</i>) populations to Late Glacial and Early Holocene climate changes – evidence from ancient DNA	130
<u>Mateusz Baca, Danijela Popović, Katarzyna Baca, Anna Lemanik, Karolina Doan, Ivan Horáček, Juan Manuel López-García, Sandra Bañuls-Cardona, Piroska Pazonyi, Emmanuel Desclaux, Evelyne Crégut-Bonnoure, Claudio Berto, Jadranka Mauch Lenardić, Barbara Miękina, Xabier Murelaga, Gloria Cuenca-Bescós, Magdalena Krajcarz, Zoran Marković, Alexandru Petculescu, Jarosław Wilczyński, Monika Vlasta Knul, John R. Stewart, Adam Nadachowski</u>	
Highly divergent population of narrow-headed vole from the Late Pleistocene Europe	131
<u>Mateusz Baca, Danijela Popović, Anna Lemanik, Katarzyna Baca, Ivan Horáček, Adam Nadachowski</u>	
Neolithic revolution triggered demographic expansion of an African opportunistic carnivore	132
<u>Rita Rocha, Ahmed Eddine, Noureddine Mostefai, Yamna Karssene, Koen De Smet, José Carlos Brito, Dick Klees, Casten Nowak, Berardino Cocchiararo, Susana Lopes, Peter Van Der Leer, Raquel Godinho</u>	

MAMMALS IN ANTHROPOGENIC LANDSCAPE 133

Carnivores in anthropogenic landscapes	133
<u>Duško Ćirović</u>	
Resistance modelling infers physical and behavioural gene flow barriers to the red fox (<i>Vulpes vulpes</i>) across the Berlin metropolitan area.....	134
<u>Alain Frantz, Sophia Kimmig</u>	
Red fox population dynamics in habitats of different anthropoppression levels	135
<u>Dagny Krauze-Gryz, Jakub Gryz, Karolina Jasińska, Mateusz Jackowiak</u>	
How does anthropogenic noise impact the behaviour of a keystone species?	136
<u>Graeme Shannon, Lisa Angeloni, Kevin Crooks, Megan McKenna, Kurt Frstrup, George Wittemyer</u>	

Evaluation of human influence on the activity of medium – large mammals in Myanmar forests	137
<u>Giacomo Cremonesi, Francesco Bisi, Lorenzo Gaffi, Alessandra Gagliardi, Lucas Armand Wauters, Damiano Giovanni Preatoni, Adriano Martinoli</u>	
Linking biodiversity to ecosystem services: The small mammal community of NE Portugal agroecosystems	138
<u>Joana Paupério, João Queirós, João Alexandre Cabral, Hélia Vale-Gonçalves, António Mira, Sara M Santos, Sandra Aresta, Paulo Célio Alves, Ricardo Pita</u>	
Behavioural adjustments of non-commensal rodents to urban environments	139
<u>Valeria Mazza, Melanie Dammhahn, Annika Schirmer, Claudia Götttsche, Jana A. Eccard</u>	
Do natural margins of arable fields support small mammal populations?	140
<u>Grete Tõnisalu, Ülo Väli</u>	
Community Assembly Rules of Insectivorous Bat Species in Man-made plantations in Israel	141
<u>Claudia Allegrini, Carmi Korine, Boris Krasnov</u>	

GENERAL SESSION.....142

The economic cost of invasive mammals	142
<u>Franck Courchamp, Christophe Diagne, Anne-Charlotte Vaissiere, Juliette Baron</u>	
Parasitological investigations of raccoons from several locations in Germany and Luxemburg	143
<u>Natalia Osten-Sacken</u>	
Know your enemy: A molecular approach identifies multiple key factors driving a small mammal invasion-extinction event on an island	144
<u>Samuel Browett, Rachael Antwis, Naiara Sales, Thomas Curran, Denise O'Meara, Kevin Bown, Joseph Jackson, Jon Yearsley, Ian Montgomery, Jeremy Searle, Allan McDevitt</u>	
Multispecies reservoir of <i>Spirometra erinaceieuropaei</i> (Cestoda: Diphyllbothridae) in wild mammalian hosts in NE Poland	145
<u>Eliza Kondzior, Małgorzata Tokarska, Rafał Kowalczyk, Andrzej Zalewski, Iwona Ruczyńska, Ewelina Hapunik, Marta Kołodziej-Sobocińska</u>	
Combining questionnaire survey and biogeographic models to update and forecast the distribution of the only mongoose species in Europe	146
<u>Esther Descalzo, Francisco Díaz-Ruiz, José Jiménez, María Martínez-Jauregui, Mario Soliño, Ana Luz Márquez, Miguel Ángel Farfán, Raimundo Real, Miguel Delibes-Mateos, Pablo Ferreras</u>	
Spatial variables associated with the geographical range shift of European hamster (<i>Cricetus cricetus</i>) in Poland	147
<u>Aleksandra Zarzycka, Katarzyna Bińkowska, Marcin Brzeziński</u>	
The beaver facilitates species richness and abundance of terrestrial and semi-aquatic mammals	148
<u>Janne Sundell, Wenfei Liao, Ophélie Huet, Erminia Scarpulla, Petri Nummi</u>	
Mammal mapping in Russia	149
<u>Andrey Lissovsky, Valery Stakheev, Alexander Saveljev, Boris Sheftel, Oleg Ermakov, Dmitri Smirnov, Sergey Titov</u>	
Networking at sea: unraveling mixed-species cetacean sightings	150
<u>Mridula Srinivasan</u>	
Predators and megaherbivores have contrasting impacts on nitrogen and phosphorus stoichiometry in an African savanna	151
<u>Elizabeth le Roux, Laura S. van Veenhuisen, Graham I.H. Kerley, Joris P.G.M. Cromsigt</u>	

POSTER PRESENTATIONS.....153

SQUIRRELS153

- P1 Search for bornavirus and other viruses in squirrels 153
[Vanessa Schulze](#), [Nicola Ferrari](#), [Claudia Romeo](#), [Peter W. W. Lurz](#), [Michael A. Steele](#), [Shealyn Marino](#), [Kore Schlottau](#), [Martin Beer](#),
[Rainer G. Ulrich](#), [Bernhard Ehlers](#)
- P2 The identification of re-invasion pathways following eradication of the grey squirrel (*Sciurus carolinensis*) using genetic and genomic data 154
[Rebecca Synnott](#), [Allan McDevitt](#), [Samuel Browett](#), [Naiara Sales](#), [Craig Shuttleworth](#), [David Everest](#), [Catherine O'Reilly](#), [Denise O'Meara](#)
- P3 Bridging the gap between conservation genetics and red squirrel (*Sciurus vulgaris*) conservation management 155
[Rebecca Synnott](#), [Colin Lawton](#), [Catherine O'Reilly](#), [David. G. Tosh](#), [Denise O'Meara](#)
- P4 Development and characterization of new polymorphic microsatellite markers for Eurasian ground squirrel, the yellow ground squirrel, *Spermophilus fulvus* 156
[Olga Batova](#), [Sergey Titov](#), [Nina Vasilieva](#), [Liudmila Savinetskaya](#), [Andrey Tchabovsky](#)
- P5 Fast explorers: the first experience of GPS tracking in yellow ground squirrels 157
[Nina Vasilieva](#), [Liudmila Savinetskaya](#), [Nikita Vasiliev](#)

CONSERVATION AND POPULATION GENETICS.....158

- P6 Revealing the diet of the Lesser Horseshoe bat (*Rhinolophus hipposideros*) in Ireland via DNA Metabarcoding 158
[Thomas Curran](#), [Samuel Browett](#), [Denise O'Meara](#), [David O'Neill](#), [Catherine O'Reilly](#), [Andrew Harrington](#), [Allan McDevitt](#)
- P7 Sequencing de novo Y chromosome reference genome of the dog 159
[Maris Hindrikson](#), [Raquel Godinho](#), [Pedro Silva](#)
- P8 Potential role of a Y chromosome in posthitis disease etiology in the European bison males 160
[Sazia Kunva](#), [Małgorzata Tokarska](#)
- P9 Noninvasive monitoring of a critically endangered neotropical primate 161
[Mariane Kaizer](#), [Naiara Sales](#), [Thiago Alvim](#), [Fabiano Melo](#), [Karen Strier](#), [Jean Boubli](#), [Robert Young](#), [Allan McDevitt](#)
- P10 Automatic microsatellite genotyping from noninvasive genetic sampling in wolves 162
[Isabel Salado](#), [Alberto Fernández-Gil](#), [Carles Vilà](#), [Jennifer Leonard](#)
- P11 Landscape genetics of urban environment, exemplified by *Apodemus* model 163
[Tomasz Gortat](#), [Robert Rutkowski](#), [Alicja Gryczyńska](#), [Robert Meronka](#), [Miłosława Sokół](#), [Michał Kozakiewicz](#)
- P12 Identification of management units for wolves in Poland using population genetic data 164
[Maciej Szewczyk](#), [Sabina Nowak](#), [Natalia Niedźwiecka](#), [Michał Figura](#), [Patrycja Tomczak](#), [Przemysław Stachyra](#),
[Tomasz Zwijacz-Kozica](#), [Kinga M. Stępiak](#), [Robert W. Mysłajek](#)

PHYLOGEOGRAPHY AND BIOGEOGRAPHY165

- P13 Detection of hybridization in European hedgehogs 165
[Kristýna Eliášová](#), [Ignacio Lucas](#), [Miroslava Loudová](#), [José Grau](#), [Pavel Hulva](#), [Barbora Černá Bolfíková](#)

P14 Geographical variation of skulls of the northern and common tree shrew complex	166
Hideki Endo, Truong Son Nguyen, Dinh Duy Nguyen, Tatsuo Oshida, Masaharu Motokawa	
P15 New data on the northeastern border of the distribution of the yellow-necked mouse (<i>Apodemus flavicollis</i>) in the Middle Urals	167
Tatyana Fadeeva, Leonid Lvovskiy, Vladimir Isakov	
P16 Challenging the model of the Iberian Peninsula as a refugium for the brown bear (<i>Ursus arctos L.</i>) in the Last Glacial Maximum	168
Ana García-Vázquez, Gloria González-Fortes, Ana C. Pinto Llona, Aurora Grandal-d'Anglade	
P17 Where does the root vole from Eastern Poland come from? Genetic evidence for a criptic high-latitude refugium in Poland.....	169
Elżbieta Jancewicz, Ewa Falkowska, Mirosław Ratkiewicz	
P18 The history of the landscape affects the genetic structure of hygrophilous species: the case study of the root vole from Eastern Poland	170
Ewa Falkowska, Elżbieta Jancewicz	
P19 Different interactions at different areas along the contact zone of Robertsonian chromosomal races of <i>Mus musculus domesticus</i> (Rodentia: Muridae) with monobrachial homology.....	171
Nikolitsa Loukatou, Akylina Skoura, Konstantina Chorba, George Mitsainas	
P20 Intra- and interspecific phylogeny of genus <i>Cervus</i> based on complete mitochondrial genomes	172
Maciej Matosiuk, Magdalena Świsłocka, Frank E. Zachos, Magdalena Czajkowska, Anetta Borkowska, Ghaiet M. Hajji, Zbigniew Borowski, Alexander P. Saveljev, Ivan V. Seryodkin, Tarlan Farahvash, Hamidreza Rezaei, Rasoul Vaez Torshizi, Stefano Mattioli, Mirosław Ratkiewicz	
P21 Phylogenetic signal of small mtDNA amplicons to study the <i>Mazama americana</i> complex through noninvasive genetic sampling	173
Pedro Henrique Peres, Eluzai Sandoval, Márcio Oliveira, José Mauricio Duarte	

CLIMATE CHANGE AND POPULATION DYNAMICS 174

P22 Non-forest patches inside a continuous forest: small mammals in the mid-forest clearings of the Białowieża Primeval Forest	174
Elżbieta Jancewicz	
P23 Population Viability Analysis of the Italian otter population	175
Anna Loy, Sara Diamente, Mirko Di Febbraro	
P24 Estimating Cabrera vole abundance based on presence sign counts: An evaluation using genetic non-invasive sampling	176
Dinora Peralta, Teresa Vaz Freire, Tiago Mendes, Clara Ferreira, Sara M Santos, Paulo Célio Alves, António Mira, Pedro Beja, Joana Paupério, Ricardo Pita	
P25 Factors regulating activity and daily torpor in <i>Crocidura suaveolens</i> (Soricidae) under changing temperate climate – research project and first results	177
Kamila Grossmann, Leszek Rychlik,	

UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT 178

- P26 Monitoring of impact of European bison on habitats –a preliminary results 178
[Daniel Klich](#), [Axel Schwerk](#), [Bartłomiej Popczyk](#), [Wanda Olech](#)
- P27 The projects realized for wisent protection in Poland 179
[Wanda Olech](#), [Zuzanna Nowak-Życzyńska](#), [Wojciech Bielecki](#), [Daniel Klich](#), [Krystyna Cielniak](#)
- P28 Managing behavior, not numbers– investigating drivers behind ungulate impact on forestry and agriculture 180
[Anna Widén](#)

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT 181

- P29 The best way to identify the African painted dogs: first trial of computer-aided identification 181
[Kanako Ake](#), [Tadatoshi Ogura](#), [Gregory Rasmussen](#), [Yayoi Kaneko](#)
- P30 Habitat use of the endangered Scandinavian arctic foxes 182
[Rasmus Erlandsson](#), [Anders Angerbjörn](#), [Helen Rebane](#)
- P31 Effect of inbreeding on cubs' body mass in Eurasian lynx (*Lynx lynx*) 183
[Mariya Erofeeva](#), [Sergey Naidenko](#)
- P32 Eurasian lynx *Lynx lynx* in western Poland – current status and prospects of population development 184
[Iga Kwiatkowska](#), [Robert W. Mysłajek](#)
- P33 Recovery of the Eurasian otter (*Lutra lutra*) in central and southern Italy: a new hope 185
[Simone Giovacchini](#), [Antonio Antonucci](#), [Giuseppina De Castro](#), [Giovanna Di Domenico](#), [Mirko Di Marzio](#), [Maurizio Marrese](#), [Anna Loy](#)
- P34 The Mostela: an adjusted camera-trapping device, a promising monitoring tool to study common weasel (*Mustela nivalis vulgaris*) 186
[Jeroen Mos](#), [Tim Hofmeester](#)
- P35 A genetic look at scent marking behaviour in wolves *Canis lupus* 187
[Kinga Magdalena Stępniaik](#), [Maciej Szewczyk](#), [Natalia Niedźwiecka](#), [Robert W. Mysłajek](#)
- P36 Morphological and histological study of the bear vomeronasal organ 188
[Jumpei Tomiyasu](#), [Daisuke Kondoh](#), [Hideyuki Sakamoto](#), [Naoya Matsumoto](#), [Shingo Haneda](#), [Motozumi Matsui](#)

MAMMAL PALEOECOLOGY: IMPLICATIONS FOR CONSERVATION

AND RESTORATION..... 189

- P37 Small mammals from Early Neolithic sites in the Central Zagros 189
[Jeremy Herman](#), [Mel Morlin](#), [Robin Bendrey](#)
- P38 The impact of major warming at ca. 14.7 ka cal BP on environment at local scale (Orawa-Nowy Targ Basin, Western Carpathians, Poland) on the basis of the succession of vertebrate communities 190
[Anna Lemanik](#), [Mateusz Baca](#), [Krzysztof Wertz](#), [Paweł Socha](#), [Danijela Popović](#), [Teresa Tomek](#), [Grzegorz Lipecki](#), [Barbara Miękina](#), [Aleksandra Żeromska](#), [Andrea Peresviet-Soltan](#), [Zbigniew Szyndlar](#), [Paweł Mackiewicz](#), [Adam Nadachowski](#)

P39 Phylogeography, genetic diversity and habitat use of moose (<i>Alces alces</i>) in Eurasia in Late Pleistocene and Holocene - introduction to an on-going project	191
Magdalena Niedziałkowska , Danijela Popović , Mateusz Baca , Krzysztof Stefaniak , Maciej Sykut , Piotr Chibowski , Małgorzata Suska-Malawska , Paweł Mackiewicz	
P40 Differentiation of Pleistocene and recent <i>Saiga</i> in time and space based on morphometric study of cranial remains	192
Urszula Ratajczak , Krzysztof Stefaniak , Aleksandra Żeromska , Przemysław Gagat , Paweł Mackiewicz	

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY 193

P41 Do our neighbors make us stronger?	193
Galina Alekseeva , Polina Klyuchnikova , Sergey Naidenko	
P42 Automatic Transponder Readers – a new tool for studying activity and movement of small mammals	194
Zbigniew Borowski , Karol Zub , Jan Boratyński	
P43 Plasticity in daily activity patterns of a key prey species to reduce predation risk	195
Esther Descalzo , Jorge Tobajas , Rafael Villafuerte , Rafael Mateo , Pablo Ferreras	
P44 Does the time matter? Individual variation in the onset of active season in edible dormice	196
Karolina Iwińska , Jan S. Boratyński , Kateryna Fyałkowska , Zbyszek Boratyński , Zbigniew Borowski	
P45 Effect of fire on small mammal foraging behaviour	197
Marina Morandini	
P46 The food of the Yellow-Necked Mouse (<i>Apodemus flavicollis</i>) and the Bank Vole (<i>Clethrionomys glareolus</i>) in laboratory experiments	198
Peter Mühlböck , Frantisek Sedlacek , Bozena Sera	
P47 Differentiation of activity rhythms between two competing water shrew species, <i>Neomys anomalus</i> and <i>Neomys fodiens</i> , under laboratory conditions	199
Leszek Rychlik , Oliwia Sęk , Roula Al Belbeisi	

MAMMALS IN ANTHROPOGENIC LANDSCAPE 200

P48 Does the traffic noise affect foraging in small mammals?	200
Paula Antonina Bednarz , Karolina Grzelak , Rafał Zwolak	
P49 Distribution of dens and behaviour analysis of Eurasian badger (<i>Meles meles</i>) inhabiting the area of Warsaw – preliminary studies	201
Izabella Zapędowska , Mateusz Jackowiak , Jakub Gryz , Dagny Krauze-Gryz	
P50 Populations of small mammals in urbanization gradient	202
Gortat Tomasz , Alicja Gryczyńska , Robert Meronka , Miłosława Sokół , Michał Kozakiewicz	
P51 <i>Borrelia miyamotoi</i> infections in urban-inhabiting <i>Apodemus</i> mice	203
Alicja Gryczyńska , Miłosława Sokół , Tomasz Gortat , Michał Kozakiewicz , Maciej Kowalec	
P52 Attacked from two fronts: combined effects of anthropogenic and biotic disturbances generate complex movement patterns	204
Salvatore Valente , Anna Skarin , Paolo Ciucci , Alessia Uboni	

P53 Green-blue spaces of metropolitan Helsinki as habitats for the raccoon dog and red fox	205
Mia Vehkaoja , Milla Niemi , Veli-Matti Väänänen	
P54 Attitudes towards mammal reintroductions in southern Europe correlate with species involved, people's wildlife value orientations and relationship with hunting	206
Rafael Villafuerte , Fernando E. Garrido , Miguel Delibes-Mateos	

GENERAL SESSION.....207

P55 When research and management meet: how to solve pollution from invasive alien species	207
Panzeri Mattia , Francesco Bisi , Maria Vittoria Mazzamuto , Damiano Giovanni Preatoni , Lucas Armand Wauters , Adriano Martinoli	
P56 How coarse woody debris and forest undergrowth vegetation impact the area usage of bank voles? ...	208
Emilia Kielan , Michał Kołakowski , Piotr Zegadło , Elżbieta Jancewicz	
P57 Factors affecting spread of sparganosis in a carnivore community in NE Poland – preliminary results	209
Eliza Kondzior , Marta Kołodziej-Sobocińska , Rafał Kowalczyk	
P58 Identifying new potential areas for the establishment of the invasive raccoon (<i>Procyon lotor</i>) in Europe	210
Adrián Martín-Taboada , David Romero , José María García-Carrasco , Antonio Román Muñoz , L. Javier Palomo , Francisco Díaz-Ruiz	
P59 Some new data on the melanistic population of the common hamster <i>Cricetus cricetus</i> in the northern edge of its range	211
Alexander Saveljev , Natalia Feoktistova , Pavel Bogomolov , Alexey Surov	
P60 Implementing Payments for Ecosystem Services – the case of beavers	212
Stella Thompson , Mia Vehkaoja , Jani Pellikka , Petri Nummi	
P61 The Wind in the Willows: Influence of beaver constructions on activity of other mammals and interactions among them - preliminary results	213
Zuzanna Wikar , Mateusz Ciechanowski , Adrian Zwolicki	
P62 Ecology and ecological roles of long-tailed marmots in an extreme habitat in Eastern Pamir	214
Marcin Zegarek , Aleksandra Zarzycka , Piotr Chibowski , Małgorzata Suska-Malawska	

AUTHORS.....215

PLENARY TALKS

PLENARY TALKS

WILD MIGRATIONS: ANIMAL MOVEMENT, ANTHROPOGENIC BARRIERS, AND CORRIDOR CONSERVATION IN THE AMERICAN WEST

Matthew Kauffman

U.S. Geological Survey Wyoming Cooperative Fish and Wildlife Research Unit Department of Zoology and Physiology University of Wyoming, USA

The American West harbors vast landscapes still capable of supporting long-distance ungulate migrations. Herds move across rugged landscapes up to 150 miles to access important seasonal habitats. Such movements present a conservation challenge because they require animals to cross multiple-use lands, some of which are changing rapidly. Recent research on ungulate migrations has enhanced our understanding of the benefits of migration and the threats they currently face. In particular, detailed movement analyses indicate that migrating mule deer track ephemeral pulses of forage, a phenomena referred to as „surfing the green wave“. New work is also emerging that quantifies the foraging and potential fitness benefits of surfing and the intrinsic and extrinsic factors that influence surfing success across multiple taxa. A final thread to this work is the role of memory and learning, which is increasingly understood to be necessary for migration. Importantly, these scientific advances are being incorporated into conservation. New research, new conservation tools, and new ways of communicating science our bringing people, agencies, and NGOs together to make such journeys easier for migrating ungulates.

EVOLUTION AND ECOLOGY OF PLAGUE: A WILDLIFE DISEASE OF TODAY WHICH CHANGED OUR HISTORY

Nils Chr. Stenseth

University of Oslo

Summary: Plague is a disease caused by the bacterium *Yersinia pestis*. It is first and foremost a wildlife disease which occasionally spills over to the human populations. At present a couple of thousand human cases are reported. In the past plague has caused three big human epidemics, the Justinian plague (from about 541 AD), the Black Death (from about 1330 AD) and the third plague pandemic (from about 1880 AD). During the Black Death about 50% of the European human population was killed. The lecture will provide an overview of the ecology and evolution of the plague illustrating the mutual interaction between ecology and evolution (with partly a focus on the dynamics in the wildlife hosts (rodents) as well as between the wildlife host and humans and within the human population); it will discuss how the bacterium is spread from human to human (mostly by human fleas and lice); it will discuss how the bacterium most likely came to Europe in several waves during the Black Death – using both ecological and genetic data; finally the lecture will discuss how genetic changes in the bacterium change the behavior of the fleas making it, through evolution, be as effective as possible in spreading the bacterium from one (wildlife) host to another host.

ON THE MOVE: LESSON LEARNED FROM 15 YEARS OF MOVEMENT ECOLOGY ON EUROPEAN MAMMALS

Francesca Cagnacci

Fondazione Edmund Mach, Trento, Italy

Movement is key to all ecological processes, from resource acquisition, to avoidance of unfavorable abiotic conditions and predators, to reproduction- thus ultimately affecting individual fitness and population dynamics. In Europe, animals move in a highly anthropic context, where habitat fragmentation and limited ecological connectivity combines with other sources of anthropic pressure, such as human presence and disturbance on the landscape, management practices, and global issues i.e. climate change. In this talk, we analyze these components on several species (mainly ungulates and large carnivores), at different spatio-temporal scale, making use of large movement datasets, to disentangle some of the challenges and adaptations of European mammals, and derive indications to limit human impact on the European mammal community.

THE EVOLUTION OF THE MAMMALIAN BRAIN FROM LIFE HISTORY PERSPECTIVE

Marek Konarzewski

Institute of Biology of University of Białystok and Faculty of Liberal Arts of University of Warsaw

Encephalization, i.e., brain mass/size in relation to an animal's total body mass has increased in homeotherms as compared to ectotherms. Enlarged brains of mammals and birds brought them behavioral advantages, but also incurred energy expenditures of an order of magnitude higher than in their ectothermic predecessors. What are the benefits of larger, energetically expensive brains, culminating in an energetically extravagant human brain? I will discuss those benefits from life history perspective to shed light on the mechanisms of evolution of this remarkable organ.

ORAL PRESENTATIONS

ORAL PRESENTATIONS

EMMA2: UPDATING THE ATLAS OF EUROPEAN MAMMALS

Laurent Schley¹, Tony Mitchell-Jones¹, Giovanni Amori², Boris Krystufek³, Andrey A. Lisovsky⁴, Ferdia Marnell⁵, Svetlana Miteva¹, Friederike Spitzenberger⁶, Johan Thissen¹, Vladimir Vohralík⁷

¹European Mammal Foundation

²Institute of Ecosystem Study ISE, Rome, Italy

³Slovenian Museum of Natural History, Vertebrate Department, Ljubljana, Slovenia

⁴Lomonosov Moscow State University, Moscow Russia,

⁵Government of Ireland National Parks & Wildlife Service, Dublin, Ireland

⁶Museum of Natural History Vienna, Vienna, Austria

⁷Charles University in Prague, Prague, Czechia

In 2016, the European Mammal Foundation launched its new long term and large-scale project, European Mammals on Maps 2. The objectives of the project are:

1. to determine the distribution of around 270 mammal species in Europe, covering an area of 11.442.500 km², and, using these data, publish the Atlas of European Mammals (2nd edition) in 2024. In the Atlas, for each species, there will be a color photograph, a distribution map and a short text with interesting information on the species, written by a specialist. Knowing the distribution of species is essential for their protection.

2. at the same time, to stimulate an increase in scientific research on mammals in Europe.

The project is managed by a Steering Group of 11 professional scientists and conservation managers, coordinating the work of the National Coordinators in 42 countries. The National Coordinators oversee the work carried out at the national level, mainly mammal surveying. Thousands of people throughout Europe are thus contributing to the data collection.

SQUIRRELS

CONSERVATION OF SQUIRRELS ON THE GROUND AND IN THE TREES: THE VALUE OF THE SCIURIDAE

John Koprowski

University of Arizona

The conservation of biodiversity has been described as our greatest environmental challenge for the remainder of the current century. Squirrels have been suggested to be excellent indicators of global change and have been used in this role with some success. With about 300 species recognized and a nearly cosmopolitan distribution that covers all continents except Antarctica and Australia, the squirrels can provide significant insight into how environments are changing. Squirrels also have great value in the other ecosystem services that they provide. Some such as the black-tailed prairie dog (*Cynomys ludovicianus*) are considered to be a keystone species in the vast grasslands that they inhabit. Others such as the scatterhoarding members of the genus *Sciurus* are known to disperse and plant the majority of seeds produced by trees. Flying squirrels in the genus *Glaucomys* are important in the inoculation of soil with hypogeous fungi that improves nutrient uptake and plant survival in forests. Forests and grasslands are among the habitats that are most threatened across the globe and harbor the vast majority of the world's squirrel diversity. An appreciation of the values of the Sciuridae is necessary in order to develop effective conservation strategies. International congresses that promote fruitful collaboration among research groups also increase our knowledge and enhance the efficacy of conservation efforts.

SQUIRRELS

HIDDEN INTERACTIONS BETWEEN ALIEN AND NATIVE SPECIES: NEW INSIGHTS IN THE GREY-RED SQUIRREL PARADIGM

Lucas Wauters¹, Maria Vittoria Mazzamuto¹, Francesca Santicchia¹, Claudia Romeo², Nicola Ferrari², Damiano Preatoni¹, Adriano Martinoli¹

¹Department of Theoretical and Applied Sciences, University of Insubria

²Department of Veterinary Medicine, Università degli Studi di Milano

Invasive alien species are a major threat to biodiversity. Replacement competition of native red squirrels (*Sciurus vulgaris*) by introduced grey squirrels (*Sciurus carolinensis*) in Europe, occurs mainly through competition for limited resources and, on the British Isles, through disease-mediated competition (squirrel poxvirus). However, recent comparative studies in Italy, showed that other, more hidden, mechanisms might be involved. We compared behaviour (personality), parasite infections and physiological stress of red squirrels between control areas (only red squirrels) and experimental areas (both red and grey squirrels) and explored the hypothesis that grey squirrel presence increases the red squirrels' hormonal stress response and that higher levels of chronic stress make reds more susceptible to infection by helminths. We further predicted that interspecific competition will influence the adaptiveness and hence the relative occurrence of different personality traits in the target species. We studied red squirrels by capture-mark-recapture and arena tests [Open Field (OFT) test and the Mirror Image Stimulation (MIS) test] in three control sites (red-only), and three experimental sites (red-grey). Tape tests and faecal samples were used to determine infection status by a "native" and an introduced (through spillover from grey squirrels) helminth. Faecal samples were also collected for extraction and quantification of faecal glucocorticoid metabolites (FGM), an integrated measure of physiological stress. Here I will illustrate the main findings and discuss the importance of understanding the processes underlying competition between ecologically similar species, since they can have implications for character displacement and community structuring.

SQUIRRELS

GAME OF CONES – THE CHANGING FORTUNES OF RED AND GREY SQUIRRELS IN IRELAND

Colin Lawton¹, Colin Guilfoyle¹, Victoria Molloy¹, Conor McKinney², Ruth Hanniffy³

¹Zoology, School of Natural Sciences, Ryan Institute, NUI Galway

²Ulster Wildlife

³Vincent Wildlife Trust

There are two species of squirrel in Ireland, the native Eurasian red squirrel *Sciurus vulgaris* and the invasive eastern grey squirrel *Sciurus carolinensis*. The grey squirrel was introduced and became established on the island of Ireland in the early 20th century, and its spread from the one-off introduction point to cover much of the eastern half of Ireland has been documented through early anecdotal reports, and later dedicated surveys. The spread of the invasive species was mirrored by a loss of the native red squirrel, which is impacted by exploitative competition and the squirrel pox virus. The most recent surveys, however indicated that the grey squirrel had started to disappear once again from certain areas, a loss that has been attributed to the regional recovery of the native carnivore, the pine marten *Martes martes*. In this talk we will review the successive distribution surveys carried out on the two squirrel species and the pine marten, and present the results from the latest survey conducted throughout 2019. The 2019 survey is a cross-border initiative involving research teams and NGOs in Northern Ireland and the Republic of Ireland. Records of the animals have been collected through a citizen science survey, conducted through social media, and utilising the web platforms of the National Biodiversity Data Centre (Rep. Ireland) and CEDaR (N. Ireland). Further records and validation of sightings have been obtained using non-invasive monitoring techniques such as hair-tubes and trail cameras.

SQUIRRELS

COST AND BENEFITS OF LIVING IN THE CITY – COMPARING TWO POPULATIONS OF WARSAW RED SQUIRRELS

Agata Kostrzewa¹, Dagny Krauze-Gryz¹, Karolina Jasińska¹, Jakub Gryz²

¹*Faculty of Forestry, Warsaw University of Life Sciences*

²*Forest Research Institute, Department of Forest Ecology*

Animals, thanks to their behavioural plasticity, are able to adjust to urban environment. The red squirrel (*Sciurus vulgaris*) is one of the species that has adapted well to very specific conditions in cities. In our study we focus on two populations of red squirrels inhabiting the same city (Warsaw) but utterly different habitat: one population lives in a very popular, located in the centre, urban park, where squirrels are commonly fed by visitors and the second lives in urban forest with highly limited access of people. The study started in July 2018 and will last till spring 2021, with live-trapping sessions conducted every two months in both areas. This will allow us to compare two populations in terms of health and body condition (body mass, presence of parasites and dermatophytes), percentage of males and females being sexually active, time of breeding period and behavioural measures (i.e. struggle time, breath rate). Additionally, 20 individuals were radio-tagged in urban park in February 2019 (next 20 will be tagged in September 2019) to compare their behaviour in two periods, one when natural food is scarce and the other with plenty of seeds. This allow to differentiate between feeding strategies (taking food from visitors vs. using mostly natural food) of certain individuals and to combine this with their condition and breeding performance. Here, we would like to present trapping data collected in the first year of the study and radiotometry data collected in the first period (late winter/early spring to summer).

SQUIRRELS

WHISTLING AT THE TOWER OF BABEL: GEOGRAPHIC VARIABILITY IN ALARM CALLS OF THE EUROPEAN GROUND SQUIRREL

Irena Schneiderová¹, Lucie Štefanská², Lukáš Kratochvíl³

¹Department of Animal Science and Food Processing, Czech University of Life Sciences in Prague; Prague Zoo

²Nature Conservation Agency of the Czech Republic

³Department of Ecology, Faculty of Science, Charles University in Prague

Geographic variability has been documented in calls of many mammals. The European ground squirrel (*Spermophilus citellus*) is critically endangered in the Czech Republic, and currently distributed in 38 colonies. Most of these colonies have been isolated from each other for a longer time period, while others are interconnected. Artificial colonies established from individuals originating from several different colonies can also be found in the Czech Republic. Thus, the current distribution of the European ground squirrel in the Czech Republic provides a unique opportunity to explore the emergence of geographic variability in alarm calls of this rodent species. We recorded alarm calls of 82 individuals from five natural colonies (Raná, Raná Hrádek, Mohelno, Velká Dobrá, Vyškov) and of 24 individuals from an artificial semi-natural colony located at the Prague Zoo. Founders of this colony originated from four different colonies in the Czech Republic. General linear model (GLM) as well as discriminant function analysis (DFA) showed that some of the colonies manifest high acoustic differentiation. The correct classification success ranged from 37.5% to 73.7%. Surprisingly, the artificial colony achieved a relatively high classification success of 58.3%. It remains to be tested how ground squirrels react to alarm calls of individuals from different colonies. Results are also discussed with respect to reintroduction programmes that have been successfully implemented in the Czech Republic for several years.

SQUIRRELS

WHEN INTRASPECIFIC COMPETITION IS AN IMPORTANT CUE IN ANIMAL SETTLEMENT

Marina Morandini¹, John Koprowski¹

¹*University of Arizona*

Animals disperse into a new area as a consequence of natal or breeding dispersal, after catastrophic events, or after a translocation carried out for management reasons. Food, shelters, water are typically resources that can affect the decision of an animal to settle in a new area. However, the presence of other animals (predators, competitors) can be an important factor in an animal's settlement. With our project, we assessed the importance of food and conspecifics as cues for the settlement response of a territorial tree squirrel. We translocated 22 red squirrels (*Tamiasciurus fremonti*) in the White Mountains (AZ, USA) and we studied their space use and subsequent settlement in the new environment. Using areas that were at least 5 km apart, we translocated 10 animals in the fall and 12 in winter. The preliminary results showed lower retention in the release site during the fall because all the squirrels were chased away by juveniles. Only 3 animals were able to settle in a territory in the fall, and the distance from the release site was between 700 and 2500 m. In winter, squirrels spent more time in the release site and only 20% of them was chased by adult squirrels. Eight animals settled in the release site, 7 between 0 and 500 m, and 1 at 1500 m from it. The two seasons are characterized by different food availability and intraspecific competition. While the fall is characterized by large food resources available that would allow squirrels to easily settle in most of the areas around the release site, it is also the season with the high intraspecific competition due to juveniles' dispersal. This study shows how intraspecific competition must be considered by management actions that use translocation, due to its key role in the settlement of animals.

CONSERVATION AND POPULATION GENETICS

CONSERVATION IN THE 21ST CENTURY, TECHNOLOGICAL ADVANCES AND THEIR CHALLENGES

Laura Iacolina

University of Zagreb, Faculty of Agriculture Department of Fisheries, Apiculture, Wildlife Management and special Zoology, Zagreb, Croatia

Over the past few decades, we observed increased use of genomic approaches. Initially mostly in domesticated species and model organisms but, thanks to technological advances that led to decrease in price, genomic methods are gaining popularity in wildlife conservation as well. These new approaches allow us to investigate an unprecedented amount of information at once. Just to make few examples, we can now investigate the whole genome of individuals or, at a smaller scale, the mitogenome instead of fragments, but we can also better detect local environmental selection and differences in hybridization effect across genomics regions or non-invasively investigate diet preferences. However, it is no bed of roses, the approaches present several challenges, methodological, computational and economical. At the same time, we should not forget the importance of historical data already collected with previous methodologies. Additionally, being well established, such methods are better understood and accepted by practitioners making it easier to implement them in monitoring activities. Such methods, despite their limitations and shortcomings, are still a valuable tool for the monitoring of wild populations and their conservation. Now, more than ever, the choice of the methodological approach should be based on a good understanding of the advantages and pitfalls of the different methods, in order to select the one that better suits the research question. Additionally, we need to involve and increase practitioners' awareness of the distinctions and benefits of the different techniques to improve communication, understanding, and planning for the benefit of conservation actions.

CONSERVATION AND POPULATION GENETICS

GENOME-WIDE ANALYSES OF POPULATION STRUCTURE IN A HIGHLY MOBILE CARNIVORE, THE GRAY WOLF (*Canis lupus*), ACROSS EURASIA

Astrid Vik Stronnen¹, Atidzhe Ahmed², Giorgio Binelli³, Duško Ćirović³, Mihajla Djan⁴, Helena Sif Ericson⁵, Elena Fabbri⁶, Ancuta Fedorca⁷, Marco Galaverni⁸, Astghik Ghazaryan⁹, Raquel Godinho¹⁰, Pavel Hulva¹¹, Bogumila Jędrzejewska¹², Natia Kopaliani¹³, Josip Kusak¹⁴, Federica Mattucci⁶, Carsten Nowak¹⁵, Kamila Plis¹², Dmitri Politov¹⁶, Ettore Randi¹⁷, Urmaz Saarma¹⁸, Tomaž Skrbinšek¹, Dragana Šnjegota¹⁹, Mikael Åkesson²⁰, Romolo Caniglia⁶

¹University of Ljubljana, Slovenia; ²Bulgarian Academy of Sciences, Bulgaria; ³Insubria University, Italy; ³University of Belgrade, Serbia; ⁴University of Novi Sad, Serbia; ⁵Aalborg University, Denmark; ⁶Istituto Superiore per la Protezione e la Ricerca Ambientale, Italy; ⁷National Institute for Research and Development in Forestry "Marin Dracea", Romania; ⁸WWF Italia, Italy; ⁹Yerevan State University, Armenia; ¹⁰CIBIO/InBIO, Portugal; ¹¹Charles University, Czech Republic; ¹²Mammal Research Institute Polish Academy of Sciences, Poland; ¹³Iliia State University, Georgia; ¹⁴University of Zagreb, Croatia; ¹⁵Senckenberg Research Institute and Natural History Museum, Germany; ¹⁶Vavilov Institute of General Genetics, Russia; ¹⁷University of Bologna, Italy; ¹⁸University of Tartu, Estonia; ¹⁹University of Banja Luka, Bosnia and Herzegovina; ²⁰Swedish University of Agricultural Sciences, Sweden

Background: Large carnivores are wide-ranging organisms capable of dispersing hundreds of kilometers, yet they sometimes show population genetic structure consistent with local ecological and environmental gradients. For such species we expect gene flow across Eurasia to be higher in the east-west direction than for north-south, owing to generally more similar environmental conditions across latitudinal than longitudinal gradients. We thus expect limited isolation-by-distance in the east-west direction and will test this prediction by analysing profiles from the gray wolf (*Canis lupus*). Methods: We analysed profiles from more than 700 wolves genotyped on the Illumina CanineHD BeadChip with over 170,000 single nucleotide polymorphism (SNP) loci. Wolves were sampled in Europe from Scandinavia to the southern Balkans, Iberia, and Italy, plus Caucasus, central and eastern Russia. After quality screening of data and filtering for loci in Hardy-Weinberg and linkage disequilibrium, we evaluated population genetic structure by principal component analyses and maximum-likelihood methods. Results: The most divergent population across our study area was Italian. We observed other population clusters in central and eastern Russia, Caucasus, Iberia, northcentral Europe, Scandinavia, the Carpathian Mountains, and the Dinaric-Balkan region. The population clusters extending through central and eastern Russia, and northcentral Europe, indicate relatively high gene flow across these geographic regions. This contrasts with finer-scale genetic structure in other areas such as Italy, the Dinaric-Balkan region and the Carpathian Mountains. With time, recolonization of historic ranges could increase gene flow between presently divergent populations such as Dinaric-Balkan and Italian wolves.

CONSERVATION AND POPULATION GENETICS

THE IMPACT AND ORIGIN OF WOLVES IMMIGRATING TO A RECENTLY ESTABLISHED POPULATION ON THE SCANDINAVIAN PENINSULA

Mikael Åkesson¹, Olof Liberg¹, Håkan Sand¹, ²Petter Wabakken, Øystein Flagstad³, Ilpo Kojola⁴, Jouni Aspi⁵

¹*Swedish University of Agricultural Sciences,*

²*Inland Norway University of Applied Sciences Search*

³*Norwegian Institute for Nature Research*

⁴*Finnish Game and Fisheries Research Institute*

⁵*University of Oulu*

Small and recently founded populations need immigration of unrelated individuals in order to counteract genetic drift, accompanied with increased inbreeding and potentially increased genetic load and reduced evolutionary potential. The Scandinavian wolf population was founded in 1983. The population is separated from the Finnish-Russian population by a 600 km land bridge with very restricted national policies for wolf presence. With DNA samples collected during the genetic monitoring of the Scandinavian population from 1977 to 2014, we identified 22 wolves that were determined to have a non-Scandinavian origin based on 26 microsatellite loci and the use of a near complete pedigree. Our aim was to study the impact that the immigrants had on the genetic variation of the Scandinavian wolf population the geographical origin of the immigrants in relation to the genetic variation among wolves sampled in Finland ($n = 64$) and Russian Karelia ($n = 23$) the genetic relatedness among the immigrants First, the genetic contribution of five breeding immigrants resulted in an increase in genetic diversity in Scandinavia between 1983 and 2014, but it still has not reached the levels of wolves in Finland and Russian, with 43% fewer microsatellite alleles and $> 18\%$ lower heterozygosity. Second, microsatellite DNA revealed that 6 of 20 immigrants most likely originated from Finland and 12 of 20 from Russian Karelia. Interestingly, two immigrants did not assign to any of the areas, maybe indicating a third differentiated population of origin. Third, the average relatedness among the immigrants was $R = 0.043$ and 11 of 190 pairs were closely related ($R > 0.25$). We therefore suggest that predictions about the genetic impact of immigration henceforth take immigrant relatedness into account.

CONSERVATION AND POPULATION GENETICS

WOLVES AT THE CROSSROAD: FISSION–FUSION RANGE BIOGEOGRAPHY IN THE WESTERN CARPATHIANS AND CENTRAL EUROPE

Barbora Cerna Bolfikova¹, Pavel Hulva², Vendula Woznicova¹, Milena Jindrichova¹, Marketa Benesova², Robert Myslajek³, Sabina Nowak⁴, Maciej Szewczyk³, Natalia Niedźwiecka³, Michal Figura⁴, Atila Sandor⁵, Vladimir Zyka², Dusan Romportl², Miroslav Kutal⁶, Slavomir Findo⁷, Vladimir Antal⁸

¹*Czech University of Life Sciences Prague*

²*Charles University Prague*

³*University of Warsaw*

⁴*Association for Nature "Wolf"*

⁵*University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca*

⁶*Mendel University*

⁷*National Forest Centre*

⁸*State Nature Conservancy of Slovak Republic*

Population fragmentation represents a leitmotif of conservation biology, but the impact of population reconnection is less well studied. The recent recolonization of large carnivores in Europe is a good model for studying this phenomenon. We aim to show data regarding distribution and population genetic structure of the grey wolf in Central Europe, a region considered as a crossroad and contact zone of different phylogeographic lineages. Integrating the landscape genetics and biogeography enabled the identification of transitions in population architecture. Genetic differentiation mirrors population isolation and recognized environmental clusters. The east-west split in the Western Carpathians likely represents the signature of range fragmentation during bottlenecks in the 20th century. Mitochondrial variability is more depleted than nuclear variability, indicating founder-flush demography. Microsatellites show finer-scale differentiation in the Carpathians compared to the European plain, corresponding to topographic heterogeneity. Long-range dispersal of a Carpathian wolf (300 km), the establishment of enclaves originated from the lowland population and admixture with mountain wolves were ascertained. Carpathian wolves are characterized by periods of population and range decline due to eradication, facilitating refugial role of alpine habitats and peripatric effects, followed by expansions and fusions probably caused by forest transition, population adaptation and efforts in conservation management. New occurrence and hybridization events predict further contacts between formerly isolated populations, with potential opposing effects of heterosis and outbreeding depression. Population recovery might be hindered due to isolation by environment and anthropogenic impacts.

CONSERVATION AND POPULATION GENETICS

DEMOGRAPHIC HISTORY OF AN ISOLATED AND ENDANGERED WOLF POPULATION

Raquel Godinho¹, Rita Rocha¹, Pedro Silva¹, Raquel Pedra¹, Diana Castro, Francisco Álvares¹, José Vicente López-Bao²

¹*CIBIO/InBio - Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto*

²*Research Unit of Biodiversity UO/CSIC/PA, University of Oviedo*

Range fragmentation and demographic declines can heavily impact genetic diversity and population viability. At the beginning of the past century wolves ranged over most of Portugal and have since then experienced a steep demographic decline especially pronounced in the South of Douro river in Portugal, where a very small population remains isolated. We have assembled distribution maps with current and historical presence records to understand the evolution of fragmentation and to estimate the probability of persistence for a population fragment over time. We have also genotyped historic and modern samples for 224 SNPs to compare differences in genetic diversity and population structure, and to test demographic scenarios to understand the time and intensity of bottlenecks. The compilation of presence records showed a drastic decline to 11% of the original wolf range in the South of Douro river since 1900, with the emergence of small and isolated fragments over time. We detected a positive relationship between fragment size and the probability of fragment persistence. We observed a general increase in homozygosity over time and a differentiation into an historical and two contemporary genetic clusters. Contemporary populations split during the second half of the 20th century, concurring with habitat fragmentation, and an historical bottleneck was inferred between the 14th and the 18th century, potentially associated with an increase of firearms and venom availability in Iberian Peninsula. Estimates of effective population size for this population ranged between 7 and 30. Our results present an historical perspective of population contraction and loss of population viability, highlighting the current dramatic status of the South of Douro river wolf population in Portugal.

CONSERVATION AND POPULATION GENETICS

DEMOGRAPHIC AND GENETIC EFFECTS OF TRANSLOCATION FROM A CAPTIVE BREEDING PROJECT IN THE ENDANGERED ARCTIC FOX (*Vulpes lagopus*)

Johan Wallén¹, Karin Norén¹, Anders Angerbjörn¹

¹Department of Zoology, Stockholm University

The small population paradigm describes how demographic, genetic and stochastic factors, operate at both individual and population levels. Under extremely low densities, a population can be drawn into an extinction vortex. An immigrating individual can, given that gene flow occurs, promote a genetic rescue effect by numerically increase the population and introduce new genetic variation. New individuals can appear in a population naturally or with human help (i.e. translocation from a captive breeding project). The Fennoscandian arctic fox (*Vulpes lagopus*) exists in a small peripheral population, fragmented in smaller subpopulations with little to no contact, which has made the population demographically vulnerable and exposed to inbreeding depression. In 2008/2009, releases of Norwegian captive bred arctic foxes with the intention of re-establishing the arctic fox in an empty area was initiated. The summer of 2011, there were observations of released foxes immigrating into one of the Swedish core populations, but the extent of immigrants and gene flow is however unknown. Here, we try to answer how many individuals have established in the Swedish population and how this have affected inbreeding levels, demographics and the genetic composition of the population.

CONSERVATION AND POPULATION GENETICS

LANDSCAPE HETEROGENEITY IN LANDFORM AND LAND USE PROVIDES FUNCTIONAL RESISTANCE TO GENE FLOW IN CONTINUOUS ASIAN BLACK BEAR POPULATIONS

Naoki Ohnishi¹, Takeshi Osawa²

¹*Forestry and Forest Products Research Institute, Japan,*

²*Tokyo Metropolitan University, Japan*

Genetic diversity is one of the most important facets of biological diversity, and changes in the spatial pattern of habitats, often modified by human activity, are believed to have affected the genetic diversity of resident natural populations. We undertook a landscape genetic analysis in order to determine which landscape features influence gene flow within Asian black bear populations and to identify the underlying processes. In our evaluation of gene flow, we estimated four parameters of resistance with regard to landscape elevation: the mean, the difference between the highest and lowest, the standard deviation, and the coefficient of variation of elevation among individuals. We then examined the resistance effect of different land-use types. With the exception of mean elevation, we found that all parameters showed a significant relationship with genetic distance, indicating that unevenness in elevation provides functional resistance to gene flow. Although we found no evidence of landscape barriers (isolation-by-barrier), there was an indication of landscape resistance (isolation-by-resistance). Urban area and farmland are suggested to be strong factors contributing to the resistance to gene flow, even though isolation-by-distance was also detected. When we examined gene flow for pairs of males and pairs of females, both isolation-by-distance and isolation-by-resistance were stronger in order of female pairs, male pairs, all individual pairs. We conclude that landscape resistance was detectable with a high contrast in landscape heterogeneity and they are more influential on females than males.

CONSERVATION AND POPULATION GENETICS

HYBRID IDENTIFICATION AND ADMIXTURE TIME DETECTION IN EUROPEAN WILDCAT POPULATIONS THROUGH GENOME-WIDE PROCEDURES

Federica Mattucci¹, Marco Galaverni², Leslie A. Lyons³, Paulo C. Alves⁴, Ettore Randi⁵, Edoardo Velli¹, Luca Pagani⁶, Romolo Caniglia¹

¹ISPRA

²WWF Italia

³University of Missouri

⁴CIBIO

⁵University of Bologna

⁶University of Padua

Background: Cross-breeding between wild and domestic cats offers a remarkable anthropogenic hybridization case-study. Accurate hybrid detection, introgression quantification and their demographic and ecological determinants are needed for developing appropriate wildcat conservation plans. Methods: We genotyped 182 European wildcats, domestic cats and known or putative admixed cats from a large part of the European wildcat distribution range with the Illumina Infinium iSelect 63k DNA cat array. Genotypes were analyzed with multivariate, Bayesian and gene-search tools to evaluate i) admixture levels, ii) admixture timing and ancestry proportions, iii) track the origin (wild or domestic) of the genomic blocks carried by admixed cats, and iv) define a reduced panel of ancestry informative markers (AIMs) for routinely population structure and hybridization monitoring projects. Results: On average, 17% of the analyzed putative admixed wildcats show genomic domestic ancestry which likely originated from hybridization events occurring between 6 to 22 generations in the past. Approximately more than 600 coding genes with an excess of wild or domestic ancestry were identified in the admixed wildcats. These genes were significantly enriched for Gene Ontology categories mainly related to behavior, adaptive processes (wild-like genes), cognition and neural crest development (domestic-like genes), or immune system functions and lipid metabolism (parental-like genes). The selected AIMs reliably distinguished individuals, admixed wildcats, and the substructure of European wildcat macro-populations. Genomic ancestry analyses could be reliably applied to unravel admixture dynamics and design more efficient conservation plans in European wildcats and other hybridizing populations.

CONSERVATION AND POPULATION GENETICS

TAMING OF THE WILD: A NEW TOOL FOR CROSS STUDY RNA-SEQ ANALYSIS APPLIED TO BEHAVIOURAL TRAITS IN DOGS AND TAME FOXES

Diana Lobo¹, Raquel Godinho¹, John Archer²

¹CIBIO/InBIO - FCUP/UP

²CIBIO/InBIO

Animal domestication has led to a shared spectrum of behavioural changes, including taming. Patterns of gene expression in the brain of domestic animals may answer if tameness is controlled by a common set of genes. With the advance of RNA-seq, it is now possible to use several transcriptomic data at an inter-study level, however, it is fundamental to reduce background noise within gene expression profiles. Here, we present a new method for the removal of transcripts that display high intra-condition variation within normalized read count profiles at an inter-study level, which relies on pairwise distances between read counts for each transcript across all samples of a given condition. We applied it to RNA-seq data from brain samples of dogs, wolves and two strains of foxes (tame and aggressive) and perform subsequent expression analysis between wolves vs dogs and aggressive vs tame foxes in order to identify common genes associated with both independent domestication events. We observed that after removing transcripts harbouring the top percentage of intra-condition variation, the number of differentially expressed transcripts increased when compared to the unfiltered reference. Using these filtered sets, we found 50 common over expressed genes in the brain of dogs and tame foxes, including those involved in brain development, neuronal connectivity, learning and memory capabilities and immunity, factors known to be involved in domestication. We provide the method as a freely available tool, to aid in the integration and analysis of transcriptomic data from multiple studies and demonstrated its use in the identification of novel genes involved in tame behaviour, which seems to have played a crucial role as a primary selective target during the canine domestication.

CONSERVATION AND POPULATION GENETICS

DIVERSITY OF THE MHC CLASS II DRB ALLELES IN CHAMOIS POPULATIONS

Sunčica Stipoljev¹, Elena Bužan², Laura Iacolina¹, Toni Safner¹, Andrea Rezić¹, Sandra Potušek², Krešimir Križanović¹, Ana Galov¹, Ferdinand Bego³, Georgi Markov⁴, Haritakis Papaioannou⁵, Attila Farkas⁶, Massimo Scandura⁷, Dragana Milošević⁸, Vladimir Maletić⁹, Elmar Babaev¹⁰, Dragan Gačić¹¹, Peter Lazar¹², María Cruz Arnal¹³, Hüseyin Ambarlı¹⁴, Nikica Šprem¹

¹University of Zagreb

²University of Primorska

³University of Tirana

⁴Bulgarian Academy of Sciences

⁵University of Ioannina

⁶University of Sopron

⁷University of Sassari

⁸University of Montenegro

⁹Ss. Cyril and Methodius University

¹⁰Caspian Institute of Biological Resources

¹¹University of Belgrade

¹²University of Veterinary Medicine and Pharmacy

¹³Universidad de Zaragoza

¹⁴Düzce University

The genes of the major histocompatibility complex (MHC) code for receptors that recognize and bind antigens in order to present them to T cells, thus they have a major role in determining the immune response. MHC region includes some of the most variable loci in the vertebrate genome, reflecting the strong association between MHC diversity and resistance/susceptibility to disease. With their well-characterized function and exceptional diversity, they are a key genetic marker for studying the processes of species adaptive evolution. The goal of our study was to examine spatial distribution of allelic diversity at exon 2 of MHC class II DRB locus across the majority of distribution range of the genus *Rupicapra* using next generation approach (Ion Torrent S5, Thermo Fisher). We identified 20 alleles in 96 individuals. Twelve alleles had been previously identified in chamois while the remaining 8 are novel. The number of variable nucleotide sites in detected alleles was 23 (10%) and the number of variable amino acid positions in translated sequences was 11 (14%). Out of 20 identified alleles, 18 translated into different amino acid sequences. The number of alleles per individual ranged from 1 to 6 (mean = 3.1), indicating the presence of at least 3 loci resulting from gene duplication events. The most frequent allele, Ruru-DRB*01, was identified in 68 individuals (71%) while 5 alleles were present only in a single individual each. Our results provide evidence of multiple co-amplifying copies, showing that MHC class II DRB is a complex multilocus system with a high level of polymorphism in chamois. Finally, our study represents the first assessment of immunogenetic map of chamois populations that can be used in future conservation management of this species.

CONSERVATION AND POPULATION GENETICS

HARNESSING THE POTENTIAL OF ENVIRONMENTAL DNA (EDNA) METABARCODING FOR MONITORING MAMMALIAN COMMUNITIES IN TEMPERATE AND NEOTROPICAL REGIONS

Allan McDevitt¹, Lynsey Harper², Naiara Sales¹

¹University of Salford

²University of Hull

The application of environmental DNA (eDNA) metabarcoding as a biomonitoring tool has greatly increased in the last decade. This involves the simultaneous identification of multiple taxa using DNA extracted from an environmental sample (e.g. water and soil) using short amplicon sequences. However, the vast majority of studies have focused on aquatic macroorganisms in temperate areas (e.g. fishes). In the first instance, we evaluated eDNA metabarcoding of pond and riverine water for monitoring semi-aquatic and terrestrial mammals in the UK and compared it against more conventional survey techniques such as camera trapping and field signs. In rivers/streams, water voles, field voles and red deer were readily detected through eDNA in almost all sites where they are known to be present and water-based eDNA provided comparable detection probabilities to camera traps and latrine surveys using occupancy modelling. For ponds, all focal species were detected in captivity. Semi-aquatic and arboreal species produced stronger eDNA signals than ground-dwelling species and eDNA signal strength differed according to behaviours (e.g. swimming, urination) observed at water bodies. Samples were also taken from two biomes in Brazil, the Amazon and the Atlantic Forest. We identified critically endangered (e.g. northern muriqui) and vulnerable (e.g. river dolphin) species. However, it is clear that there is a lack of reference sequences available and many sequences can not be identified to species level in these regions. Overall, we demonstrate that eDNA metabarcoding is a promising tool for conducting biomonitoring of mammals over large spatial and temporal scales but there remain significant challenges for its implementation in different regions and environments.

CONSERVATION AND POPULATION GENETICS

INBREEDING DEPRESSION AND GENETIC RESCUE IN A CYCLIC MAMMAL POPULATION

Karin Norén¹, Malin Hasselgren¹, Johan Wallén¹, Rasmus Erlandsson¹, Anders Angerbjörn¹

¹Stockholm University

The small population paradigm and extinction vortex model are central themes in the field of conservation genetics. According to these, the decline of a small population accelerates through an interplay between demographic and genetic processes and the negative trend can only be reversed through gene flow. The Swedish arctic fox (*Vulpes lagopus*) population went through a population bottleneck in the 19th century and was on the verge of extinction around year 2000, but has since then increased five-fold in response to conservation actions. Based on a long-term data set of individual fitness traits and pedigree information, we use the arctic fox as a model system to demonstrate the impact of inbreeding depression in fundamental traits, followed by a rescue effect mediated by natural immigration from a captive breeding project on both individual and population levels. This presentation highlights the importance of including natural population demography as a crucial factor influencing the outcome of evolutionary processes operating in a small population, but also emphasizes the short-term effect of genetic rescue and its consequences for conservation and management.

CONSERVATION AND POPULATION GENETICS

LAST CHANCE TO SEE? STATUS AND DISTRIBUTION OF THE VOJVODINA BLIND MOLE RAT REVISITED

Attila Németh¹, Gábor Csorba¹, Levente Laczkó², Edvárd Mizsei^{2,3}, Judit Bereczki⁴, Gábor Sramkó⁵

¹*Hungarian Natural History Museum*

²*Department of Botany of the University of Debrecen*

³*Department of Tisza River Research of the Centre for Ecological Research, Hungarian Academy of Sciences*

⁴*Department of Evolutionary Zoology and Human Biology of the University of Debrecen*

⁵*MTA-DE 'Lendület' Evolutionary Phylogenomics Research Group*

Blind mole rats are among the most threatened mammals of Central Europe, and the situation of the critically endangered Vojvodina blind mole rat is the most worrying. The taxon was originally described solely on chromosomal grounds in 1973, based on specimens collected in Serbia. At 2008, it was also discovered along a small section of the Hungarian-Serbian borderline. Later, at 2013 another population of this species was found near Baja, in Hungary. In April 2017, a further, previously unknown population of blind mole rats was discovered in the vicinity of Albertirsa, in North-Central Hungary. We used newly designed primers to specifically amplify the whole mitochondrial cytochrome b region and two nuclear DNA regions to identify the new population. Both mitochondrial and nuclear regions have unequivocally placed the Albertirsa population into the monophyletic lineage of the Vojvodina blind mole rat. However, we are not only identified the fourth known population of an extremely rare rodent taxon, but the results also helped to clarify the distribution area of the taxon heavily affected by data deficiency. As currently understood, Vojvodina blind mole rat is predominantly confined to sandy grasslands of the Danube–Tisza Interfluve in Hungary and Serbia. This distribution range reflects the importance of geographic barriers in the allopatric/peripatric speciation and in shaping the phylogenetic structure of blind mole rats. Based on the recent knowledge this taxon endemic to the central part of the Carpathian Basin and in the phylogenetic reconstructions represents a deeply divergent clade. Based on the so far deepest taxonomic sampling compared this taxon to several other European blind mole-rat taxa, it turned out to be sister to all other studied European *Nannospalax*.

CONSERVATION AND POPULATION GENETICS

POPULATION GENETICS AS A TOOL FOR CONSERVATION BIOLOGY: DEFINING MANAGEMENT UNITS FOR THE GREATER HORSESHOE BAT

Orianne Tournayre, Jean-Baptiste Pons, Maxime Leuchtman, Raphael Leblois, Sylvain Piry, Ondine Filippi-Codaccioni, Anne Loiseau, Jeanne Duhayer, Inazio Garin, Fiona Mathews, Sébastien Puechmaille, Nathalie Charbonnel, Dominique Pontier

The greater horseshoe bat (*Rhinolophus ferrumequinum*) is among the most widespread bat species in Europe but it has experienced severe declines. This species is considered to be highly sensitive to human activities and particularly to habitat fragmentation. In this study we have therefore aimed to understand the population genetic structure and past demography of populations of the greater horseshoe bat in the Western European part of its distribution and propose relevant guidelines for its conservation. We have screened 28 maternity colonies of *R. ferrumequinum* using 17 microsatellite markers. The results of our study indicate high levels of genetic diversity with a large population size on the European mainland but lower estimates in England and Northern France. Our analyses revealed a barrier effect on *R. ferrumequinum* dispersal caused by the English Channel and potentially another by the Mediterranean Sea. Conversely, we did not find any gene flow disruption from both sides of the Western Pyrenees. Our results provide important information for improving the delineation of *R. ferrumequinum* management units in its western range. We suggest that a large management unit corresponding to the European mainland population should be considered. Particular attention should be given to mating territories as they seem to play a key role in maintaining the high levels of genetic mixing between colonies. A smaller management unit corresponding to the Northern France colony should also be implemented. The mainland colonies at the Northern limit of its range could be at higher risk of extinction in the near future.

CONSERVATION AND POPULATION GENETICS

WHICH PRIMER SET(S) FOR YOUR BAT DIET METABARCODING STUDY? APPLICATION TO TWO INSECTIVOROUS BAT SPECIES SHARING MATERNITY ROOSTS

Orianne Tournayre, Maxime Leuchtman, Marine Trillat, Sylvain Piry, Ondine Filippi-Codaccioni, Dominique Pontier, Nathalie Charbonnel, Maxime Galan

European insectivorous bats have high energetic needs especially during the maternity season when they give birth, suckle and rear the young. High energetic expenditures mean that bats require high quality and quantity of prey (up to 70% of their body mass). Yet, because of the massive use of pesticides and anti-parasitic treatments of the cattle, a decline of arthropods biodiversity and biomass has been recorded, as well as a contamination of the prey and their predator through bio-accumulation. It is therefore urgent to assess the diet of bat species, as it could be a major driver of their decline. In this study we have compared different primer set strategies to maximize arthropod detection and identification while identifying the bat species at the same time. We have made a complete comparison in three steps (in silico, mock community and guano samples) of 12 primer sets, for which primer features were tested to determine their effect on taxa detection. Our results showed contrasted performance of the primer sets among the three steps. Degeneracy level and amplicon length were the two main primer characteristics influencing the success of taxa detection for both non-degraded DNA and degraded DNA. The choice of the best primer set(s) varied depending on the type of samples and objectives of the study. Based on our results we accurately described the diet of two insectivorous bat species, throughout the whole maternity period, in seven mixed colonies located in contrasted ecotoxicological landscapes of Western France.

CONSERVATION AND POPULATION GENETICS

EFFECTS OF HABITAT FRAGMENTATION IN THE SOCIAL BEHAVIOUR OF THE CABRERA VOLE: INSIGHTS FROM GENETIC NON-INVASIVE SAMPLING

Clara Ferreira¹, Dinora Peralta², Tiago Mendes², Teresa Vaz Freire³, Helena Sabino-Marques², Frederico Mestre², Soraia Barbosa⁴, Sara M Santos², Russell Alpizar-Jara², Pedro Beja⁵, António Mira², Xavier Lambin⁶, Jeremy B Searle⁷, Paulo Célio Alves⁵, Joana Paupério⁵, Ricardo Pita²

¹*Animal Ecology - University of Potsdam*

²*Universidade de Évora,*

³*Universidade de Lisboa*

⁴*University of Idaho*

⁵*Universidade do Porto*

⁶*University of Aberdeen*

⁷*Cornell University*

Analysing how habitat fragmentation affects within-population processes of spatially structured populations is crucial to predict their ability to persist at local scales. In this study we used genetic non-invasive sampling (gNIS) to assess how habitat fragmentation affects the relatedness, family groups and inbreeding of the Iberian-endemic Cabrera vole in SW Portugal. We sampled fresh vole faeces in 20 patches, with various levels of habitat quality and isolation, during four consecutive days and genotyped a set of 11 microsatellites for individual identification and for assessing genetic diversity. We estimated relatedness for all pairs of individuals in each patch and assessed kinship with the software Colony. We identified a total of 101 individuals (between 1-12 individuals per patch), with mean relatedness per patch varying between low (-0.215) and high values (0.721). We found family groups in 16 out of 20 patches, with 12 family groups displaying genetic monogamy in 11 patches, while in five patches a consensus pedigree could not be obtained for the family groups, and thus polygamous behaviour cannot be ruled out. We explored how habitat variables associated with fragmentation relate to the social behaviour and genetic diversity within patches. The results suggest that in low quality habitats and isolated patches, the probability of monogamous behaviour increases, while genetic diversity is higher in larger patches and in areas with more suitable habitat available. Overall, our study shows that gNIS provides useful insights on the social and reproductive behaviour of rare and elusive small mammals, such as the Cabrera vole, and is valuable for informing management and conservation planning focused on improving species persistence in fragmented landscapes.

PREDATOR-PREY INTERACTIONS

NEW INSIGHTS TO PREDATOR-PREY INTERACTION WITH VOLES AND WEASELS

Hannu Ylönen¹, Marko Haapakoski¹, Sonny Bleicher¹, Thorbjörn Sievert¹

¹University of Jyväskylä, Konnevesi Research station, Finland

Voles and weasels provide a major model system in predator – prey interactions in mammals. This interaction is modified by many factors. We review a series of experiments in bank vole – weasel interaction under experimentally manipulated environmental conditions. We manipulate the indirect cues of weasel risk and, for instance, take into account the unique light-regime of northern latitudes as a factor affecting vole behavior. We propose a new continuum in prey-vole response to long-lasting, conservative predation risk signaled by predator odor or risk cues carried by conspecific alarming on acute high-risk of predator vicinity. We have been verifying either, slowing down reproduction or putting stronger effort for reproduction as a different strategic responses to high predation risk in bank voles. When risk is long-lasting, how the situation in the nature is during high numbers of predators, prey voles can even habituate to it. A direct contact with a predator, however, intensify or “refresh” the behavioral responses of voles to indirect cues of predator.

PREDATOR-PREY INTERACTIONS

COMMUNICATING FEAR: THE ROLE OF ALARM PHEROMONES IN A BANK VOLE

Marko Haapakoski¹, Thorbjörn Sievert¹, Hannu Ylönen¹

¹University of Jyväskylä / Konnevesi Research Station

Fear of being eaten has the power to shape populations and drive evolution. An animal can perceive high predation risk from predators directly either visually, via sound or by smelling the predator odor. Also, conspecifics can warn individuals about high predation risk. Many animals from insects to fish use alarm pheromone to warn conspecifics about the danger. In addition, mice and rats are known to produce alarm pheromones in stressful situations and alarm conspecifics about possible danger. Yet, the ecological and evolutionary significance of alarm pheromones in wild mammals remains unclear. We investigated how alarm pheromones affect the behavior and fitness of wild bank voles (*Myodes glareolus*) in several experiments conducted either in the lab or under semi-natural conditions in large outdoor enclosures. Specifically, we compared the effects of real predator odour and second-hand fear cue transmitted via odour of predator-exposed, scared voles. Control animals were exposed to odour from voles with no predator experience. Besides that, we show the preliminary result on evolution and chemistry of bank vole alarm pheromones. The first results show that bank vole mothers produce more offspring after smelling the AP odors produced by scared males. Furthermore, female voles seem to be attracted to bedding that had been used by predator-exposed male voles. Our results suggest that frightening experience and the important information of danger can be communicated to neighboring individuals in the population, even when the neighbors do not see, smell, or hear an actual predator themselves.

PREDATOR-PREY INTERACTIONS

SECONDHAND HORROR: EFFECTS OF DIRECT AND INDIRECT PREDATOR CUES ON BEHAVIOR AND REPRODUCTION OF THE BANK VOLE

Thorbjörn Sievert¹, Marko Haapakoski¹, Rupert Palme², Helinä Voipio³, Hannu Ylönen¹

¹University of Jyväskylä

²University of Veterinary Medicine, Vienna

³University of Helsinki

Risk recognition by prey is of paramount importance within the evolutionary arms race between predator and prey. Prey species are able to detect direct predator cues like odors and adjust their behavior appropriately. The question arises whether an indirect predation cue, such as the odor of scared individuals, can be detected by conspecifics and subsequently affects recipient behavior. Parents may also transfer their experience with predators to their offspring. In two experiments, we assessed how direct and indirect predation cues affect bank vole (*Myodes glareolus*) foraging behavior, reproduction, and pup fitness. Weasel (*Mustela nivalis*) odor served as the direct cue, whereas the odor of weasel-scared conspecifics, alarm pheromones, was used as an indirect cue and both of those were compared to a control odor, clean wood shavings. Alarm pheromones attracted female voles, measured as time in proximity to the treatment and foraging. Both predator odor and alarm pheromones enhanced reproduction compared to the control odor. Females treated with alarm pheromone had significantly higher pregnancy rates, and pups from predator-treated mothers were significantly heavier at birth. Our study provides two novel ideas. First, the impact of a predator can be socially transmitted. Second, predation risk likely triggers terminal investment in reproduction.

PREDATOR-PREY INTERACTIONS

IS THE WILD RABBIT (*ORYCTOLAGUS CUNICULUS*) SHAPING GEOGRAPHICAL DISTRIBUTION PATTERNS OF ITS PREDATOR'S COMMUNITY IN THE IBERIAN PENINSULA?

Patricia H. Vaquerizas¹, Francisco Díaz-Ruiz², Jesús Olivero³, Miguel Delibes-Mateos¹, Rafael Villafuerte¹

¹Instituto de Estudios Sociales Avanzados IESA-CSIC

²Dpto. Biología Animal, Facultad de Ciencias, Universidad de Málaga

³Dpto. Biología Animal, Facultad de Ciencias, Universidad de Málaga

The wild rabbit (*Oryctolagus cuniculus*), a native species in the Iberian Peninsula, is considered to be both ecologically and economically relevant in its native range for many reasons. Among others, it is part of the diet of more than a score of predator species, including birds of prey and carnivores.

In this study, we explore the existence of assemblages of predator species with similar geographical distribution patterns (i.e. chorotypes) in order to analyze the potential role of wild rabbits in determining the spatial configuration of the predator community. Chorotypes could provide insights about the ecological and geographical differentiation of predators closely related to rabbits, a question that is especially relevant for species subject to important management and conservation challenges.

We analyzed the distribution of 24 rabbit-consumer predator species (15 birds of prey and 9 carnivores) with well-known distributions in the Iberian Peninsula. We used presence/absence data on 10 x 10-km UTM squares, according to available Portuguese and Spanish atlases of mammals and reproductive birds. Our results reveal that species forming part of the same predator guild are clustered in the same chorotypes. Raptors and carnivores keep usually separated in different chorotypes. Only raptors and predators that are highly specialized in the consumption of rabbits are biogeographically clustered together, being restricted to southwestern Iberia. Interestingly, the spatial distribution of this chorotype matches the range of one of the two rabbit subspecies (*O. cuniculus algirus*). Our approach could be useful to design shared management strategies aimed at preserving wildlife species that belong to the same species' assemblage.

PREDATOR-PREY INTERACTIONS

A RISKY NICHE: AMONG-INDIVIDUAL DIFFERENCES IN LANDSCAPES OF FEAR

Melanie Dammhahn

Animal Ecology/University of Potsdam

To eat or to feed - that is one of the most fundamental problems governing animal behaviour. Besides direct predation risk, the mere presence of predators might change prey foraging behaviour. This perceived predation risk varies in space and time creating a landscape of fear, but do all individuals have the same distribution of fear? Here, I test the hypothesis that among-individual differences in exploration and boldness predict the spatio-temporal distribution of perceived predation risk, i.e. individual specialisation in risk niches. In semi-natural enclosures and laboratory conditions I created landscapes varying in avian predation risk and quantified foraging and space use of behaviourally phenotyped bank voles (*Myodes glareolus*). I found that aspects of foraging and space use varied among individuals, were repeatable over time, and predicted by among-individual differences in boldness and exploration. These results suggest that individual variation along a risk-reward trade-off creates individualized landscapes of risk, which might have important consequences for predator-prey interactions.

PREDATOR-PREY INTERACTIONS

TAKING RISKS FOR FOOD: EFFECTS OF THE LANDSCAPE OF FEAR AT LOW TROPHIC LEVELS

Clara Mendes Ferreira¹, Jana A. Eccard¹, Melanie Dammhahn¹

¹*Animal Ecology, Institute for Biochemistry and Biology, University of Potsdam, Potsdam, Germany*

Recent research has revealed the importance of indirect predation effects on prey. The mere fear of predation in a landscape, i.e. the landscape of fear (LoF), can affect forager activity and movement. Less known are the cascading effects of changes in forager behaviour on lower trophic levels. Using an experimental approach, we aimed to test if the perceived predation risk would increase the number of resources left in the landscape and their composition. We also evaluate whether individuals shorten their movement patterns to optimise foraging behaviour under risk. We conducted an arena experiment with 15 captive bank voles (*Myodes glareolus*) using two different perceived predation risks: risky – under light with no cover; and safe – under dark with a net cover. Individuals stayed in the arena for 24h, with a nest box in the centre for shelter. We placed 25 seed trays in a grid pattern, each filled with 500 mL of sand and seven seeds of four different species, varying in size, husk, and caloric content. In risky conditions, foragers decreased their activity and seed consumption but moved further away from their shelter to forage. In safer conditions, individuals foraged in most of the seed trays, and the amount of seeds left was reduced in the arena. In both conditions, foragers showed preference for bigger seeds, regardless of caloric content and husk. Overall, we showed that foraging under risk affects the forager behaviour and giving-up density of seed communities, with movement routes changing due to fear of predation. We hope to expand this experiment to evaluate changes in biodiversity, by studying the effect of the forager a complex landscape with perceived predation risk, independently of predator presence.

PREDATOR-PREY INTERACTIONS

USING BY-CATCH DATA FROM CAMERA-TRAPPING STUDIES AIMED AT CARNIVORES TO STUDY THEIR PREY

Tim R. Hofmeester¹, Neri H. Thorsen², Joris P.G.M. Cromsigt¹, Jonas Kindberg^{2,1}, Henrik Andréén², John D.C. Linnell², John Odden²

¹Swedish University of Agricultural Sciences

²Norwegian Institute for Nature Research

Due to their low population densities, carnivores are often hard to study. The advance of camera trapping technology has led to a great increase in studies using camera traps to study large carnivores. As these cameras can detect any animal that passes, these studies also generate data on prey species, and this data is increasingly used to study predator-prey interactions. However, it is unclear how the camera placement, that is often optimized to capture large carnivores, influences inference on prey populations and predator-prey interactions. We used data from one of the Scandcam project's permanent camera-trapping grids aimed at monitoring Eurasian lynx (*Lynx lynx*) in Hedmark County, Norway, and paired randomly placed cameras at two spatial scales for 38 of the targeted cameras for three months, to study the effect of camera placement on detection of carnivores and their prey. Detection probabilities for most species were higher at the targeted cameras, where the difference was largest for several carnivores, e.g., lynx, and red fox (*Vulpes vulpes*), and smaller for prey species, e.g., mountain hare (*Lepus timidus*). These differences in detection probability between carnivores and prey can be problematic when using uncorrected matrices such as trapping rate. However, the higher detection probability at targeted cameras resulted in more precise site-use predictions for most species when correcting for species-specific detection probabilities in an occupancy framework. In contrast, the lower detection probability at random cameras led to spurious inference of predator-prey interactions. We conclude that by-catch data from camera trapping studies aimed at carnivores can be used to study interactions with their prey, but only after correction for detection bias.

PREDATOR-PREY INTERACTIONS

EFFECT OF PREDATION ON HUNTING QUOTAS, HUNTER OBSERVATIONS AND MOOSE HARVEST IN TWO COUNTRIES WITH AN INCREASING WOLF POPULATION DURING 22 YEARS

Camilla Wikenros¹, Barbara Zimmermann, Håkan Sand¹, Johan Månsson¹, Erling Maartmann², Ane Eriksen², Petter Wabakken²

¹Swedish University of Agricultural Sciences

²Inland Norway University of Applied Sciences

Predation from large predators and harvest are the two most important factors affecting the dynamics of many ungulate populations. Most of the world's habitat that will be available for future colonization by large predators are likely to be strongly influenced by humans. Therefore, human behavioural responses may constitute a key trait that governs the impact of large predators on their prey populations. We used harvest statistics from two countries (Norway and Sweden) that share a population of wolves (*Canis lupus*) and the local moose (*Alces alces*) population in the bordering area, but with differences in both wolf and moose management on national as well as regional levels. Moose is the main prey of wolves and wolf predation mainly includes animals that otherwise would have been available for harvest. We investigated how the distribution of wolves affected moose density (using hunter observations of moose), hunting quotas and harvest, along a landscape gradient (latitude) in different management units during 1995-2017. A change in the number of moose observations during one or several years resulted in a corresponding change in the number of moose harvested the following years. The distribution of wolves affected both the number and the age- and sex composition of observed and harvested moose, as well as hunting quotas. Country, latitude and proportion of agricultural land were also important factors in addition to wolf distribution explaining the variation in the number and composition of moose observed and harvested. Management actions were taken in both countries, but in different ways, in order to reduce the total mortality in the moose population (reduced harvest) as well as maximize productivity in the population (reduced harvest of adult females).

PREDATOR-PREY INTERACTIONS

THE RESOURCE DISPERSION HYPOTHESIS – A TEST WITH A CYCLIC MESOPREDATOR

Rasmus Erlandsson¹, Malin Hasselgren¹, Anders Angerbjörn¹, Karin Norén¹

¹Department of Zoology, Stockholm University

Sociality is prominent among territorial animals, but group living in socially flexible species is expected to change with varying ecological conditions. The Resource Dispersion Hypothesis predicts that group size within a territory changes in response to fluctuations in resource availability, while Hersteinsson's model claims that sociality is also driven by predation pressure. In the arctic fox (*Vulpes lagopus*), group living has been explained by static differences in resources availability and predation pressure. However, no study has accounted for the spatiotemporal fluctuations that are inherent to some cyclic systems, and the two hypotheses make different predictions when basal prey decline. Based on 17-year monitoring of arctic fox and cyclic rodent prey, we tested the Resource Dispersion Hypothesis in time and space and discuss the results in relation to Hersteinsson's model. Group living increased with rodent prey density, from 7.7% (during rodent increase years) to 28% (rodent peak). However, it remained high (44%) despite rodent decrease and instead group living could be explained by an increased predation pressure due to prey switching predators and benefits from cooperative defense. Hence, support for the two hypotheses varied temporally and we suggest that predictions regarding group living should include both fluctuations in resources and predation.

PHYLOGEOGRAPHY AND BIOGEOGRAPHY

BIOGEOGRAPHY AND PHYLOGEOGRAPHY: TOOLKITS FOR THE CONSERVATION OF BIODIVERSITY

Ettore Randi

Department of Biological, Geological and Environmental Sciences, University of Bologna, Bologna, Italy

Biogeography has been born into the heart of modern evolutionary biology. Alfred Russell Wallace (1823 - 1913) is the acknowledged father of zoogeography (the geographic distribution of animal species), and also Charles Darwin (1809 - 1882) gave important contributions to this field. Wallace's zoogeographical regions have been largely validated and are still used nowadays. Recent founder-dispersal models in phylogeography are rooted in Darwin's descriptions of oceanic island colonisation. Thanks to the seminal research by John C. Avise (born 1948), molecular phylogenetic and coalescent approaches began to be rapidly used in population genetics, leading to the birth of intraspecific phylogeography (1987). Phylogeography is essentially an interdisciplinary and integrative activity which in a few decades moved from using a predominant single molecular marker (the mtDNA) to big data sets extracted from entire genome sequences (phylogenomics). Narrative reconstructions based on qualitative overlays of geographical maps and phylogenetic trees evolved in quantitative landscape phylogeographic procedures. Verbal comparisons of simple phylogeographic models evolved in rigorous computer simulations and likelihood testing (statistical phylogeography). Model-based phylogeography can now make full use of big climate and habitat datasets, projecting retrospective inferences into the recent past and future of species and populations evolutionary dynamics. Climate, habitat and genomic quantitative interrelationships, and the inference of causal factors of microevolutionary dynamics, open the way to develop fully predictive tools for the conservation of biodiversity and populations evolvability in the face of the current Anthropocene crisis.

PHYLOGEOGRAPHY AND BIOGEOGRAPHY

INFERRING THE EVOLUTIONARY HISTORY OF WOLF EXPANSION THROUGH BERINGIA LAND BRIDGE

Carolina Pacheco¹, Astrid Vik Stronnen², Bogumiła Jędrzejewska³, Raquel Godinho¹

¹*CIBIO/InBIO - Research Center in Biodiversity, Genetics and Evolution, Porto University*

²*Department of Biology, University of Ljubljana*

³*Mammal Research Institute Polish Academy of Sciences*

In species such as the grey wolf (*Canis lupus*) with complex social system and wide, mostly continuous, geographical distributions, local adaptation to distinct ecosystems and habitats can create conspicuous population structure. Understanding the demographic processes that led to the current observed genetic background is essential to improve our understanding of the patterns of population differentiation and local environmental selection. One of the major past demographic events that has shaped the evolutionary history of many terrestrial species was the crossing of the Bering Strait land bridge, between Eurasia and North America, during the Pleistocene. Here, we test the previously proposed hypothesis that extant North American wolves originate from multiple waves of colonization from Asia. Also, we infer the ancestral contribution of both Asian as well as Continental North American populations to the genetically distinct population of the Alexandre Archipelagos, testing the hypotheses of this population representing the gene pool of an initial expansion wave from Asia. For that we combine new with previously published genomic data, to obtain a dataset of 190 individuals genotyped for ~100k single nucleotide polymorphism (SNP) loci, from Eastern Russia to Southeast Alaska. We explore patterns of haplotype sharing among individuals to infer population differentiation and ancestry. Further demographic inferences were done using a combination of a global search algorithm with the ordinary differential equation to infer the best fitting demographic model to our observed data. Our results do not corroborate the previously suggested hypothesis for the colonization of North America and emphasise the distinctiveness of the Alexandre Archipelagos population.

PHYLOGEOGRAPHY AND BIOGEOGRAPHY

NEXT-GENERATION PHYLOGEOGRAPHY RESOLVES POST-GLACIAL COLONIZATION PATTERNS IN THE RED FOX (*Vulpes vulpes*) IN EUROPE

Allan McDevitt¹, Ilaria Coscia¹, Samuel Browett, Mark Statham, Aritz Ruiz-González, Iwona Ruczyńska, Joanna Stojak, Ben Sacks, Cino Pertoldi, Ettore Randi, Rafal Kowalczyk, Jan Wójcik

¹University of Salford

The advent of next-generation sequencing techniques has the potential to revolutionize our understanding of phylogeographic processes in mammals at continental scales. A total of 524 red foxes were genotyped in 29 populations using genotype-by-sequencing (GBS) and over 15,000 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 in the British Isles. A minimum of seven genomic clusters were identified through Bayesian and Principal Component analyses, with separate island populations in the British Isles, Scandinavian, Iberian, Italian, central European and Russian clusters identified. These corresponded to known refugial populations and recently isolated groups. Approximate Bayesian Computation (ABC) revealed human-mediated colonization of Ireland and multiple waves of colonization of Scandinavia at different time points. This expanded dataset has uncovered phylogeographic patterns not previously revealed by more 'traditional' marker sets and highlights the potential of using thousands of markers to uncover broad scale patterns of genomic structure.

PHYLOGEOGRAPHY AND BIOGEOGRAPHY

IS THERE ANY ADAPTIVE VARIABILITY OF TLR2 GENE ACROSS BANK VOLE POPULATIONS FROM TWO MTDNA LINEAGES IN NE POLAND?

Ewa Tarnowska¹, Magdalena Niedziałkowska¹, Joanna Stojak¹, Bogumiła Jędrzejewska¹

¹*Mammal Research Institute PAS*

One of the factors shaping the genetic pattern of the bank vole (*Myodes glareolus*) populations in the north-eastern Poland might be the differences in vulnerability to *Borrelia afzelli* infection among voles. Some variants of Toll-like receptor 2 (TLR2) gene can play an adaptive role by reducing the risk of infection. We checked if there were any correlations between frequency of different variants of TLR2 in 30 bank vole populations from NE Poland and 1) *Borrelia afzelli* infection rate in the populations belonging to two mtDNA lineages, 2) several environmental factors. We also compared the infection rate between 487 individuals of different sex and age. We detected three TLR2 variants in the studied populations: 83.8% of sequences belonged to C1 variant (high prevalence for *Borrelia afzelli*), 7.6% to C2 (low prevalence), and 8.6% to C3 (unknown prevalence). The frequency of the C3 cluster positively correlated with the frequency of the Carpathian mtDNA lineage of bank vole. However, the distribution of each TLR2 cluster was patchy and we did not detect clear spatial structure of this gene. The infection rate in all studied individuals was 12% and varied from 0 to 37.5% among populations, but did not differ among numbers of infected voles carrying different TLR2 genotypes or between specimens belonging to two mtDNA lineages. Most of the infected voles (47 out of 57) were adults. Males were infected more often than females. There was no association between the frequencies of the TLR2 clusters, the infection rate and environmental factors in the studied populations. We did not support the hypothesis on the adaptive role of TLR2 gene in the analyzed populations. The study was financed by the Polish National Science Centre, project no. 2014/13/N/NZ8/02472.

PHYLOGEOGRAPHY AND BIOGEOGRAPHY

GENETIC DIVERSITY OF TWO MITOCHONDRIAL DNA GENES IN *Spirometra erinacei* (CESTODA: DIPHYLLOBOTHRIDAE) FROM POLAND

Marta Kołodziej-Sobocińska, Joanna Stojak¹, Eliza Kondzior, Iwona Ruczyńska, Jan Wójcik

¹Mammal Research Institute, Polish Academy of Sciences

The tapeworm species *Spirometra erinacei* was documented mainly in Asia and Europe. In recent years, plerocercoid larvae (spargana) of this parasite have been found in different hosts in northeastern Poland. The evolutionary history and way of *S. erinacei* spreading across Eurasia have been not described yet. However, this phenomenon could be closely related to the evolutionary history and migration routes of studied tapeworm host species. We investigated the genetic variability and divergence pattern among *S. erinacei* populations in intermediate and paratenic hosts from north-eastern Poland based on complete mitochondrial sequences of cytochrome b (cytb) and cytochrome c oxidase subunit I (cox1) genes. Analysis of 319 consolidated sequences of these two genes showed no genetic structure across study area. Comparison of sequences from Poland and China showed distinct separation of *S. erinacei* populations from these two regions. They split from their common ancestor approximately 28.6 million years ago. Demographic expansion of Polish population of *S. erinacei* started from glacial refugia approximately 12.5 thousand years ago and recent population expansion has been observed in the tapeworm population from north-eastern Poland. The study was financed by the National Science Centre project no. 2016/21/B/NZ8/02429.

PHYLOGEOGRAPHY AND BIOGEOGRAPHY

AN UPDATE ON THE ROBERTSONIAN (RB) CHROMOSOMAL VARIABILITY IN THE NATURAL POPULATIONS OF THE HOUSE MOUSE, *Mus musculus domesticus*, BASED ON THE SIMULTANEOUS STUDY OF THE THREE RB SYSTEMS OF GREECE

George P. Mitsainas

Laboratory of Zoology, Section of Animal Biology, Department of Biology, University of Patras

The house mouse, *Mus musculus domesticus*, is characterised by the appearance of Robertsonian (Rb) fusions in its karyotype, i.e. biarmed chromosomes formed, because uniarmed chromosomes join at the centromere, reducing the diploid chromosome number from the typical $2n = 40$ down to $2n = 22$. Over a hundred Rb fusions have been recorded in nature, which in turn lead to the formation of many Rb races and complex Rb systems, mostly around Europe. The study of this variability for over more than thirty years in natural house mouse populations from Greece has revealed the existence of three Rb systems, i.e. in Peloponnese, in Ipeiros and in E. Sterea Ellada. This work presents the results that have been gathered over the last years from the systematic study of all three Rb systems simultaneously. Among exciting new findings that will be presented, we point out a) the much larger size of the Rb system of Ipeiros, W. Greece than previously known, which extends for more than 65 km on a N-S direction and is characterized by $2n = 28-39$, distributed over an extended contact zone with the $2n = 40$ population; b) that the Rb system of E Sterea Ellada is also much larger than earlier expected, extending from an area E of Athens, for ca. 140 km on a NW direction and that the Rb race GRT1 with the lowest $2n$ in the Rb system ($2n = 26$), earlier regarded as a rare encounter, is now considered a rather well-established Rb race; c) the study of a very interesting contact zone among the major Rb races in the Rb system of Peloponnese, which has even revealed the occurrence of natural hybrids between Rb races with monobrachial homology; d) a new case of Rb chromosomal variability in SW Sterea Ellada, north of NW Peloponnese, which, however, appears to be somehow related to the Rb system of Peloponnese.

PHYLOGEOGRAPHY AND BIOGEOGRAPHY

CHROMOSOMAL VARIABILITY OF THE COMMON SHREW (*Sorex araneus L.*) IN CENTRAL AND EASTERN SIBERIA

Boris Sheftel¹, Svetlana Pavlova¹

¹*A.N. Severtsov Institute of Ecology and Evolution, Russian Academia of Science*

Analyzing shrew karyotypes from Krasnoyarsk and Irkutsk regions and Sakha Republic (Yakutia), we determined seven chromosomal races in total. The Zima (g/m, hi, jl, k/o, n/q, p/r) and Irkutsk (gk, hi, jl, n/q, m, o, p, r) races were described for the first time (Pavlova et al. 2017). In the Krasnoyarsk region the Tomsk (g/k, hi, jl, mn, q/r, o, p), Novosibirsk (g/o, hn, ik, j/l, m/p, q/r) and Strelka (g/o, hi, jl, k, m, n, p, q, r) races were found, in the Irkutsk region - the Irkutsk and Baikal (g, hi, j/l, k, m, n, o, p, q, r) races. The Zima race was found in both Irkutsk and Krasnoyarsk regions, and the Ilga race (g/k, ho, im, jl, nq, p, r) was detected in the Irkutsk region and the Sakha Republic. We also found that the left bank of the Yenisei River near Krasnoyarsk is occupied by the Tomsk race while the right bank by the Strelka race (the Stolbi Reserve). But then further north the Tomsk race is still distributed on the right bank while the left bank is occupied by the Novosibirsk race. Such race distribution was continued almost till the northern limit of the species range. In comparison with southern race parts, both Novosibirsk and Tomsk races demonstrated higher level of chromosomal polymorphism within these northern parts. In the Irkutsk region, the Baikal and Zima races come into contact and possible hybridise along the left bank of the Angara River. Polymorphic karyotypes were also found among these races as well as among shrews belonging to the Irkutsk race. The Ilga race had stable karyotypes in all three studied places.

Thus we observed: 1) an increase in chromosomal polymorphism in races at the northern limit of species range; 2) very wide the Zima-Baikal hybrid zone, 3) the existence of stable Ilga karyotypes over about 1000 km.

PHYLOGEOGRAPHY AND BIOGEOGRAPHY

THE ROLE OF POST-GLACIAL DEMOGRAPHY IN SHAPING VARIATION OF INNATE IMMUNITY GENES IN A FREE-LIVING RODENT

Agnieszka Kloch¹, Aleksandra Biedrzycka²

¹*University of Warsaw*

²*Institute of Nature Conservation, Polish Academy of Sciences*

Innate immunity system is an evolutionarily older than adaptive immunity and it provides the first line of defence against pathogens. Contrarily to adaptive immune response, the mechanisms of selection affecting genes coding components of innate immunity are still poorly understood. Here, we analyse geographical variation and selection patterns in seven innate immunity genes in free-living bank voles *Myodes glareolus* from 10 localities across species range. Based on mtDNA variation, these populations had been assigned to several mitochondrial lineages corresponding to distinct glacial refugia. We found clear discrepancies between population structure in mtDNA and all studied innate immunity genes. There was no uniform pattern of spatial variation at immunity loci, they differed in the levels of polymorphism, and the results of neutrality tests were not consistent over loci. Each locus comprised a few common haplotypes shared between mitochondrial lineages and studied locations, plus numerous haplotypes unique for each studied site. Our results suggest that the diversity of innate immunity genes cannot be explained solely in terms of demographic processes, and that the observed polymorphism may be attributed to local selection. The strength and direction of selection differed between loci, even within the same gene family, what underlines how crucial it is to take a complex approach while studying the selection patterns acting on immune related genes.

CLIMATE CHANGE AND POPULATION DYNAMICS

CLIMATE – AND MAMMAL COMMUNITY – CHANGE

Bodil Elmhagen

Stockholm University

Climate change is an increasingly important driver of biodiversity and ecosystem change. Depending on its scale and scope, climate-related research targets everything from direct mechanistic responses in individual animals, to consequential long-term responses reflected in population trends and geographical distribution patterns. Irrespective of the research topic, species interactions are often key as mediating drivers of change. In boreal and alpine Sweden, the transformation of the mammal community since the 19th century includes; (1) Range expansion and/or increasing population trends in southern mammals, such as Eurasian lynx, red fox, badger, roe deer and European hare; (2) Range contractions and/or population declines in northern mammals, such as arctic fox and mountain hare; and (3) Periodic disruptions and a decline over time in the occurrence of 3-5 year cycles in small rodents, which are characteristic for northern ecosystems and have flow-on effects on medium-sized mammals, such as rodent predators and their alternative prey. Climate change is one factor behind these transformations, but climate change has often worked in synergy with other anthropogenic drivers. This has primarily favoured southern species through increased resource availability, facilitating and reinforcing northern expansions. It has been hypothesised that top-down species interactions may stabilise community structure and constrain some effects of climate change. However, this requires compensatory changes in the abundance of top consumers. As climate-driven change in community composition give rise to novel species interactions, top-down regimes may rather respond and adjust, thus contributing to change in the structure and function of mammal communities.

CLIMATE CHANGE AND POPULATION DYNAMICS

IMPACTS OF CLIMATE CHANGE ON THE EURASIAN OTTER *Lutra lutra*

Anna Loy¹, Broenniman Olivier², Cianfrani Carmen², Sara Diamente¹, Mirko Di Febbraro¹, Antoine Guisan²

¹University of Molise

²Université de Lausanne

Climate change (CC) is affecting composition, phenology, and distribution of species, and is expected to deeply impact freshwater ecosystems. Most otter species depend on freshwater ecosystems and are top predators already threatened by habitat degradation and persecution. Thus they are among the mammal guilds most vulnerable to CC. We recently developed a Global Vulnerability Index (GVI) to CC for 11 freshwater otter species, combining climatic niche models, climate change scenarios, human footprint, and protected areas coverage. GVI takes into account both range exposure, and climatic niche sensitivity and marginality. The Eurasian otter *Lutra lutra* is expected to be among the less affected otter species (GVI RCP2.6 2050 = - 2.33; GVI RCP8.5 2070 = - 0.89), as habitat loss in the southern portions of its current range will be compensated by habitat gain in the northern hemisphere. However, severe habitat loss and fragmentation are expected to occur in isolated portions of the species range (e.g. North Africa and Himalayan belt), exposing six over the 11 subspecies to extinction risk. Moreover, effects of CC on freshwaters include changes in the frequencies of extreme events like floods and droughts. While droughts is expected to reduce habitat and feeding resources availability for otters, channel incision related extreme flooding has a detrimental effect on cub survival and on habitat quality at local scale. A Population Viability Analysis run on the Italian otter population showed probability of extinction varying from 14 to 100% in 100 years when these events were included as catastrophes.

CLIMATE CHANGE AND POPULATION DYNAMICS

CAPTURING A CASCADE IN A CHANGING WORLD. HOW DO PREDATOR RECOLONIZATION, COMMUNITY COMPLEXITY AND CLIMATE DRIVEN SHIFT IN PREY SPECIES INFLUENCE SPECIES INTERACTIONS IN NORTHERN ECOSYSTEMS?

Malin Aronsson¹, Bodil Elmhagen^{1,2}, Harto Lindén³, Katja Holmala³

¹Stockholm University

²Swedish Association for Hunting and Wildlife Management

³Natural Resources Institute Finland, Luke,

Ecosystems are shaped by a complex network of interactions, and apex consumers may have far-reaching, top-down cascading effects. It has been suggested that this could stabilise communities and constrain bottom-up responses to climate change, but also and alternatively, that top-down forcing might weaken in more productive and complex systems. We revisit the documented top-down cascade in Boreal Finland; where an apex predator, Eurasian lynx, suppresses a mesopredator, red fox, which indirectly favours the mountain hare. We use three decades of species abundance data, collected over a 700 km north-south climatic gradient, to assess if this top-down cascade is retained through three scenarios: i) temporal differences in apex predator status, ii) increasing community complexity in the Boreal-Temperate ecotone, and iii) climate driven shift in prey species. In the Boreal forest, the mesopredator suppression was supported, with a temporal delay following lynx colonization. The mountain hare decline was reinforced by productivity but not by predators. As mountain hare decrease, a positive relationship with both predators emerges, promoting a bottom-up regime reflecting predator dependence on a keystone prey. Also, the mesopredator mediated cascade was only indicated early in the study period during early lynx colonization, suggesting this to be a passing state. In the Boreal-Temperate ecotone, advancing prey, such as European hare, and increasing community complexity alter ecosystem functioning and facilitate niche separation that reduce both mesopredator suppression and prey dependency, and hence dissolve the cascade. We demonstrate how the bioclimatic regime determines the net outcome of species interactions, as novel interactions arise and top-down regimes adjust.

CLIMATE CHANGE AND POPULATION DYNAMICS

CLIMATE CHANGE AFFECTS VOLE POPULATION DYNAMICS AND PLANT-HERBIVORE INTERACTIONS

Zbigniew Borowski¹, Karol Zub², Marcin Sulwiński³, Małgorzata Suska-Malawska³, Marek Konarzewski⁴

¹*Department of Forest Ecology, Forest Research Institute, Raszyn, Poland*

²*Mammal Research Institute PAS, Białowieża, Poland*

³*Faculty of Biology, Biological and Chemical Research Centre, University of Warsaw, Warsaw, Poland*

⁴*Institute of Biology, University of Białystok, Białystok, Poland*

Weather (the state of the atmosphere at a particular place and time) along with climate change (the change in global/local weather patterns) are the crucial factors affecting animal populations. We analyzed the effect of key weather/climate factors on the root vole population dynamics between 1993-2018 in the Biebrza river valley (NE Poland). For 10 years of this period, we also analyzed changes in Si concentration in sedges consumed by voles. The spring-autumn increase in population density was positively affected by NAO from previous year. However, autumn-spring population decline was affected by previous year autumn vole density only. The Si level in sedges was elevated by both vole population density in a previous year (i.e. herbivory pressure) and groundwater level in spring. Conversely, the vole population density was affected neither by Si content nor water level. These results indicate that recent changes in NAO may be dampening vole cycles not only by snow shortage but also by more complex weather changes, which reduce the effect of plant-herbivore interaction on the root vole population dynamics.

CLIMATE CHANGE AND POPULATION DYNAMICS

AN OBJECT-ORIENTED MODEL OF AN MAMMAL POPULATION

Miłosława Sokół¹, Alicja Gryczyńska¹, Tomasz Gortat¹, Robert Meronka¹, Michał Kozakiewicz¹

¹Faculty of Biology, Biological and Chemical Research Centre

The dynamics of population size in many models is characterized by cyclical fluctuations. It causes that it is not known which models explain this often observed phenomenon for the populations of small mammals. Using object-oriented modelling method and their statistical characteristics named a predicted curve we received models which time is calculated in real units (days). It allowed to prove that fluctuations of the simple population model in discrete time doesn't explain the fluctuations of the small mammals population size. Also the distribution gender population model does not do this. After taking into account in the model the restrictions related to mammalian reproduction (long period of maturation, a relatively long pregnancy and a frequently occurring long infertile period after the birth of the descendants, fertilization treated as random event in different population state than appearance of the offspring) it was found that the dynamics of fast-reproducing mammals may have a tendency to regularly repeated fluctuations. It was not shown by populations with a slower pace of reproduction. The reason of this fluctuations was the spontaneous synchronization of the reproduction. But the periods of this fluctuation were much less than a year. The multiannual fluctuations of the population size appeared when the seasonal disappearance of reproductive activity was introduced to such model. But then the diversity of maximum population sizes during the year was smaller than they were observed in reality. These calculations show how to use the object-oriented models of the population to statistical analysis of the population hypotheses.

CLIMATE CHANGE AND POPULATION DYNAMICS

URBAN RATS IN HELSINKI: SEASONAL VARIATION IN POPULATION SIZE AND PARASITE PREVALENCE

Tuomas Aivelo

University of Helsinki

Brown rats (*Rattus norvegicus*) are one of the most common and ubiquitous mammals living in urban areas around the world. Helsinki Urban Rat Project is a new research program, which aims to look at the effects and consequences of close proximity of rats and humans in multidisciplinary fashion. Here, I describe the results of our citizen science initiative, which has put school students looking for rat tracks over the whole city, and allows for us to look at spatiotemporal rat population dynamics. Furthermore, I have obtained rat carcasses from extermination companies and looked for a number of parasites and pathogens (helminths, *Leptospira*, *Campylobacter*, antibiotic resistant bacteria). My preliminary results suggest that rat population and their parasites undergo substantial seasonal variation due to restriction of rat population sizes and rat movement in wintertime. Especially in areas, with low population densities during the wintertime, parasite levels drop, whereas areas with high densities throughout the year, parasite prevalence stays high. While this effect is clear in every pathogen, it is less pronounced in *Campylobacter* strains, which are usually retained throughout the individual's lifetime and can be acquired from environmental sources. This findings have clear public health indication as we will be expanding our studies also into the rodent viruses. Furthermore, I will discuss the usability of citizen science approach in urban mammal studies.

CLIMATE CHANGE AND POPULATION DYNAMICS

SEASONAL MODELS TO PREDICT POPULATION DYNAMICS OF AUSTRALIAN MICE

Jennifer Paola Correa Cuadros¹, Sergio Estay², Peter Brown³, Wendy Ruscoe³, Mauricio Lima¹

¹*Pontificia Universidad Católica de Chile*

²*Universidad Austral de Chile*

³*Commonwealth Scientific and Industrial Research Organisation CSIRO*

House mice in Australia are an example of an irruptive species that irregularly reach plague numbers and cause considerable damage in cropping systems. We used a 20-year dataset of mouse abundance and various climatic and predator variables to try and understand drivers of the population increase and decrease. Previous analysis has shown that the mouse outbreaks occur in years following good winter rain because of increased crop yield (food supply). We examine the effects of other climatic variables on population growth rates (via their potential effects on soil that might influence the ability for mice to dig burrows) and use bird observation data to examine hypotheses around the role of predators. We also explored whether a dry year followed of a wet year can generate an outbreak due to the production of high-quality food. The rate of increase of mouse populations over the summer breeding season was determined by evaporation in summer and the cumulative winter rainfall (food) in the two years prior to the outbreak. The rate of population decline over winter was best explained by the starting abundance in autumn (density dependence), the previous year's winter rainfall and an index of barn owl abundance during autumn and winter. We conclude that the population dynamics of house mice we studied are complex and that multiple factors are interacting in the system with no single factor sufficient to generate mouse outbreaks.

CLIMATE CHANGE AND POPULATION DYNAMICS

NEW RFID TECHNOLOGY FOR SMALL MAMMAL RESEARCH

Curt Lamberth¹, Aura Raulo¹, Tim Coulson¹, Sarah Knowles¹,

¹Department of Zoology, University of Oxford

Studying small mammals in the wild frequently relies on one of two core methods: capture-mark-recapture methodology, in which traps are set repeatedly in a given area, and radio-tracking to follow animal movements. However, both these methods can have important welfare concerns, with repeated trapping carrying a risk of mortality, and radio-tracking involving the attachment of relatively heavy tags to small animals that may impede their natural behaviour. These welfare concerns in turn limit what is achievable scientifically, as study designs have to work around them. Motivated by these issues, we have recently developed two new RFID-based devices intended for use in small mammal research. These devices are designed to allow trapping and monitoring of small mammals with improved animal welfare, thereby facilitating the use of new study designs in small mammal research. The first of these devices is a “Smart Trap”, that provides researchers with selectively over which animals they trap according to body mass and PIT-tag, and can optionally trap animals overnight or release animals after a pre-specified time period. The second is a low power RFID logger, a set of which can be used to passively monitor the space use and home ranges of a set of PIT-tagged animals without active tracking. Here, we will present these new devices along with pilot data we have acquired trialling them on woodland rodents (*Apodemus* and *Myodes* spp.) in the UK, and discuss their future application in small mammal research.

UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT

FUTURE CHALLENGES IN UNGULATE CONSERVATION AND MANAGEMENT IN EUROPE

Marco Apollonio

Department of Veterinary Medicine, University of Sassari, Italy

Ungulates experienced an uninterrupted increase in Europe from WWII onwards. However, environmental conditions can be changed by several factors, that can all be very effective in reverting this trend. Global change is well known to have deep effects on ungulate population with specific reference to mountain species, however also common and widely distributed species like roe deer and wild boar can be strongly influenced in unexpected directions by the ongoing temperature increase. Large predators, with special reference to wolves, are increasing quite steadily in Central-South Europe in a sometimes largely underestimate fashion. Their impact on ungulate population dynamics is variable in relation to environmental productivity and species biology. However, no definite forecasts on future development of such relationships can be simple or univocal. Land use in Europe was characterized by strong decrease of agricultural land in the last 70 years and the resilience of some agricultural landscapes is linked to strong political decisions. These can be modified in face of changing economic situation, either with the reduction of residual agricultural areas or, on the contrary, turning back to strong exploitation of natural resources. Finally, disease can impact quite strongly not only on single species population dynamics but overall ungulate community. The recent outbreak of African Swine Fever and the potential diffusion of Chronic Wasting Disease can completely change wild boar and deer status in Europe. In conclusion, the favourable present status of European ungulates is far from being assured for the future and a proactive management of these species characterized by a strong scientific input is needed.

UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT

THE RELATIVE EFFECT OF LARGE CARNIVORES, HUNTER HARVEST, AND CLIMATE ON UNGULATE PRODUCTIVITY IN SWEDEN

Aimee Tallian

Norwegian Institute for Nature Research

The relative influence of top-down versus bottom-up processes on wildlife population dynamics and ecosystem function is a long-term debate within the scientific community. Large mammal populations are thought to be primarily driven by bottom-up processes, however, debate continues over the relative role of top-down predation on the population dynamics of large herbivorous mammals, such as ungulates. We used moose observation data collected by hunters over ~20 years in Sweden to evaluate the relative role of recovering large carnivores (i.e., wolves (*Canis lupus*) and brown bears (*Ursus arctos*)), climate, and hunter harvest on moose productivity (i.e., the number of observed calves per female moose). Our results suggest that bottom-up, top-down, and anthropogenic controls were all important to subsequent years' moose productivity. Interestingly, bottom-up processes, such as climate, seemed less important in the region where wolves and bears were sympatric, compared to the regions where they were allopatric. Our results suggests that the assemblage of predators within a landscape may contribute to the relative strength of top-down versus bottom-up processes within an ecosystem.

UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT

FOREST ROADS MODIFY UNGULATES' LANDSCAPE OF FEAR

Karen Marie Mathisen¹, Zbigniew Borowski²

¹*Inland Norway University of Applied Science*

²*Forest Research Institute*

Roads may affect ungulates in many ways, depending on the size and type of road. Major roads may represent a risk of mortality from vehicles, or act as barriers to movement and migration, fragmenting the landscape. However, roads may also increase travelling speed, and create attractive foraging sites on the road verges, due to increased light and disturbance. On the other hand, pollution and dust from gravel roads may decrease forage palatability near roads. Most studies have focused on the effect of major roads, and few on smaller roads, such as forest gravel roads. Forest roads with low traffic intensity, may represent a low risk of collision, and act as corridors for movement of wildlife. In addition, forest roads may represent a predation risk from hunters or natural predators that use roads for travelling. Previous studies indicate that ungulates avoid forest gravel roads, leading to higher browsing pressure far from roads. Hunter's use of forest roads may create predictable corridors of fear for ungulates linked to roads. To test this assumption, we compared habitat use and browsing in relation to forest roads, in an area with high versus low hunting intensity, in southeast Poland. We predicted higher vigilance and less browsing close to road, especially in areas with high hunting pressure. The results show that the effects of roads are complex, and species specific. Red deer (*Cervus elaphus*) avoided roads both at low and high hunting pressure, whilst roe deer (*Capreolus capreolus*) tended to use areas close to road in areas with high hunting pressure. Species-specific effects of forest roads on forage availability and predation pressure may explain these patterns.

UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT

FACTORS INFLUENCING RED DEER BARK STRIPPING ON SPRUCE: PLANT DIVERSITY, CROP INTAKE AND TEMPERATURE

Anna Widén

Wildlife, Fish and Environmental Studies

Red deer increases in distribution and density in many regions of Europe, and may cause severe damage in forestry and agriculture. Bark stripping is the main problem in forests. It is suggested that an imbalance in nutrient intake, especially a diet with high amounts of easily-digestible macronutrients, can lead to increased bark consumption. My aim was to investigate the relationship between oil seed rape intake and bark stripping on Norway spruce by red deer. In addition, influence of air temperature and plant diversity was measured. I did this by a feeding experiment with four groups of captive red deer in southern Sweden. All groups were given spruce logs weekly, but only two groups had access to oil seed rape plants. I found no influence of oil seed rape on bark stripping. However, bark intake was positively related to air temperature and there was a sudden increase in bark intake at the end of April. This increase may have been influenced by several factors driven by air temperature, such as bark adhesiveness to the stem, differences in nutritional value of the bark, switch to a more nutritious and digestible diet. Deer in enclosures with the lowest plant diversity consumed the highest amount of bark, indicating a relationship between diet composition and bark stripping. This finding may be important for Swedish wildlife management since there are signs of decreased diversity and availability of important forage species in Swedish forests. I conclude that to understand and reduce bark stripping by red deer on spruce, several interactive variables must be considered. Obviously, interactions between agriculture and forestry needs to be further studied before we can implement suggestions in wildlife management.

UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT

THE ASYMMETRIC SHARE OF MOOSE AS PREY FOR HUMANS AND WOLVES

Barbara Zimmermann¹, Håkan Sand², Camilla Wikenros², Ane Eriksen¹, Petter Wabakken¹

¹Inland Norway University of Applied Sciences

²Swedish University of Agricultural Sciences

Humans are partly or entirely replacing large carnivores as a regulating factor of many of today's ungulate populations, but the recent carnivore return raises questions about prey partitioning. We studied harvest and predation rates in Scandinavian moose by means of fecal pellet counts, GPS telemetry and hunting statistics in 20 wolf territories. The annual predation rate, i.e. the percentage of available moose after calving killed by wolves, was $7.8\% \pm 1.1\%$ (mean \pm 2 SE) and negatively related with wolf territory size, number of available moose and moose/wolf ratio. Annual harvest rate in the same territories was $15.1\% \pm 2.8\%$ and positively related with the density of moose, but unrelated with the number of available moose and wolf predation rate. We estimated annual mortality of moose to $27.9\% \pm 3.1\%$, with wolves being responsible for about 28%, hunting for 54% and other mortality for 18% of all mortality. Harvest rates were 2.2 ± 0.7 times higher than wolf predation rates. Moose mortality peaked with the onset of the hunting season with a 23 times higher chance for a moose to be killed by a hunter than by a wolf. Moose survival decreased with 18% during three months of hunting (October – December) and 10% during the other nine months of the year. Our results indicate that harvest is a strong regulating factor of the moose population not only in areas without wolves, but also where wolves exert a limiting effect on the moose population. The significant seasonality of the harvest has a profound effect on seasonal moose population dynamics and possibly also on evolutionary adaptations of the species, because moose density is reduced before harsh winter conditions can act as a selective force through intra- and inter-specific competition, predation and disease.

UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT

SPATIAL PATTERNS OF IMMUNOGENETIC AND NEUTRAL VARIATION INFLUENCE ON SELECTED FITNESS PARAMETERS IN ROE DEER

Elena Bužan¹, Katarina Flajšman², Boštjan Pokorny³

¹University of Primorska, Faculty of Mathematics, Natural Sciences and Information Technologies

²Slovenian Forestry Institute

³Environmental Protection College, Slovenian Forestry Institute

Across its pan-European distribution, roe deer (*Capreolus capreolus*) faces a wide diversity of environmental and climatic conditions, therefore several factors shape its life-history traits and cause significant variability in parameters of fitness. However, contrary to effects of different environmental factors and phenotypic traits, the effect of genetics on fitness and reproductive performance of roe deer has been understudied so far. We aimed to determine throughout Slovenia: i) spatial distribution of neutral and immunogenetic variation, ii) connection between neutral vs. adaptive potential and environmental conditions, iii) effect of genetic variation on body mass and reproductive ability of yearling roe deer does. We focused to yearling females due to: i) higher site fidelity than adults, therefore we minimized the influence of spatial behaviour, ii) much higher variability in reproductive performance comparing to adult does. Genetic analysis was performed on 15 neutral loci (microsatellites) and adaptive major histocompatibility complex (MHC; DRB exon 2) using next generation approach. Spatial clustering of neutral genetic diversity bears the differentiation of populations into two geographically associated clusters, and revealed an isolation by distance pattern. Our results show a positive relationship between mean microsatellite heterozygosity, standardized body mass and reproductive ability (potential litter size) of primiparous does. This suggests that genetic diversity has an important influence on fitness and increment rates in roe deer. Moreover, our data also confirm that gene flow plays a prominent role in shaping MHC polymorphism across large spatial scale, while the interplay between gene flow and selection is stronger in connected populations.

UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT

THE RATIOS OF STABLE ISOTOPES OF CARBON AND NITROGEN IN BONE COLLAGEN: VARIATIONS WITHIN INDIVIDUALS AND WITHIN POPULATIONS OF MODERN RED DEER (*Cervus elaphus*)

Maciej Sykut¹, Sławomira Pawełczyk², Bogumiła Jędrzejewska¹, Magdalena Niedziałkowska¹

¹Mammal Research Institute PAS

²Silesian University of Technology

The analyses of stable isotopes of carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) in bone collagen are used in paleoecological studies to reveal animals' diet and habitat use. However, such studies have some limitations. Firstly, due to paucity of fossil samples, it is assumed that all bones in the skeleton have the same ratio of stable isotopes. Secondly, as the sex and age of the studied individuals are often unknown, such differences among specimens are usually neglected in these kind of research. The aims of our study are to investigate the variability in stable carbon and nitrogen isotope ratios in bone collagen of modern red deer: 1) among different parts of their skeleton 2) among individuals within the same population. We studied individuals from 8 populations dwelling forest and mixed habitats in Poland and open areas of the Rum Isle in Scotland, UK. We measured $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ in: (1) three different parts (Coronoid Process, Mandibular Angle, Corpus) of 9 mandibles; (2) three different bones (mandibles, finger bones, metatarsal bones) in skeletons of 12 deer; (3) bones of 90 individuals with known age; and (4) bones of 83 males and 104 females.

The ratios of stable carbon and nitrogen isotopes exhibited high correlations within mandibles ($\delta^{13}\text{C}$: $r > 0.76$, $p = 0.01$, $\delta^{15}\text{N}$: $r > 0.96$, $p < 0.001$). High correlations were also observed in pairs of bones: mandibles – fingers ($\delta^{13}\text{C}$: $r = 0.76$, $p < 0.001$, $\delta^{15}\text{N}$: $r = 0.92$, $p < 0.001$) and fingers – metatarsals ($\delta^{13}\text{C}$: $r = 0.88$, $p < 0.001$, $\delta^{15}\text{N}$: $r = 0.95$, $p < 0.001$). We did not find any relationship between the age and sex of the studied individuals and the ratio of stable isotopes in their bones

UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT

ROADS, FORESTRY, AND WOLVES INTERACT TO DRIVE MOOSE BROWSING BEHAVIOR IN SCANDINAVIA

Anne Loosen¹, Olivier Devineau¹, Barbara Zimmermann¹, Joris Cromsigt², Sabine Pfeffer², Christina Skarpe¹, Karen Marie Mathisen¹

¹*Inland Norway University of Applied Sciences,*

²*Swedish University of Agricultural Sciences*

As ungulate densities increase across Europe and North America, plant-herbivore interactions are increasingly important from an ecological and economic perspective. These interactions are particularly significant where agriculture and forestry are important and intensive grazing and browsing by ungulates can result in economic losses. We studied plant-herbivore interactions in a moose dominant system where forestry is a primary economy, roads are extensive and intensive, and wolves are recolonizing. Wolves and humans use low-traffic, secondary roads for travel and hunting, yet roadsides provide high-quality and quantity browse. Foraging theory predicts that moose will respond to riskier landscapes by selecting habitats that reduce predation risk. As available food declines, animals will increase their acceptance to predation risk in search of food. We evaluated moose response to roads during winter in areas with and without established wolf packs, testing if wolves and roads add to the landscape of fear. Between 2008 and 2018, we measured browsing and counted pellet groups each spring in Norway and Sweden. We used generalized linear mixed models to evaluate drivers of browsing pressure and the probability of browsing. We found browsing probability decreased with increasing distance from primary and secondary roads. However, in young forest stands when the probability of wolf use was high, browsing probability increased with distance from secondary roads. We also found support for different models depending on the tree species, emphasizing the need for species-specific modeling for plant-herbivore interactions. We argue roads and wolves should be better incorporated into management systems aimed at mitigating the negative effects of ungulate browsing.

UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT

DIET OVERLAP AMONG RED DEER, ROE DEER AND MOOSE DURING WINTER IN FOREST ECOSYSTEMS, NE POLAND

Mirosław Ratkiewicz¹, Eric Coissac², Magdalena Świsłocka¹, Magdalena Czajkowska¹, Pierre Taberlet², Marta Czernik¹, Rafał Kowalczyk³

¹*Institute of Biology, University of Białystok, PL*

²*LECA, Université Grenoble Alpes, FR*

³*Mammal Research Institute PAS, Białowieża, PL*

Large mammalian herbivores have huge impact on ecosystems. High population densities of several sympatric deer species may strongly affect forest regeneration, organism communities and increase wildlife-forestry conflicts. This may also lead to interspecific competition for food. Using DNA metabarcoding approach and NGS technology we studied winter diets of three deer species: moose, red and roe deer in the Biebrza valley, NE Poland (Europe) and possible niche partitioning (or alternatively, niche overlap) among these Cervids. We found the lowest dietary richness for moose. This parameter was almost three times higher for roe and red deer and their diets overlapped to a large extent. The largest proportion of coniferous plants (young trees and shrubs) in winter diet was found for moose (79%) and smallest for red deer (55%). All three Cervids were selective and strongly preferred Scots' pine. The studied deer species were assigned as browsers since grasses were absent (moose) or found at a very low frequencies (roe and red deer) in their stools during winter. Our results are in line with previous studies that showed competition for food between red and roe deer is likely. We give some recommendations for forest management that may help to decrease wildlife-forest conflicts in areas of high deer densities.

UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT

ALIEN VS. NATIVE – INFLUENCE OF FALLOW DEER *Dama dama* INTRODUCTION ON ROE DEER *Capreolus capreolus* POPULATION

Jakub Gryz¹, Dagny Krauze-Gryz²

¹Foreset Research Institute,

²Warsaw University of Life Sciences, Faculty of Forestry

Fallow deer has spread through Poland and central Europe. The process is driven by introductions to hunting grounds in order to rise income from trophy hunting. Meanwhile, food niche overlap and other negative interaction between fallow deer and indigenous cervids were documented. Therefore, the aim of our study was to assess influence of introduced fallow deer on local roe deer population. The study was done in central Poland (Experimental Forest District of Warsaw University of Life Science). In one forest complex (1000 ha) between 2008-2011 22 fallow deer were introduced. Introduction was successful and population reached density of at least 6 individuals/km². We compared results of driving census done between 1998-2008 (before introduction) and between 2009-2018 (after introduction) in order to assess density dynamics of roe deer under pressure of fallow deer. After the introduction we also applied other methods of cervids monitoring: camera trapping, direct observation, pellet group counting. All procedures were also conducted in a reference area (similar forest complex located 12 km from the introduction site) where fallow deer were absent. After introduction of fallow deer, density and productivity of roe deer decreased, whereas in the reference area density did not change and productivity increased. Camera traps recorded several cases of antagonistic interaction between fallow and roe deer in the feeding places. We also analyzed other factors which could have negatively influenced density of roe deer, like hunting pressure and weather condition. From an economical point of view introduction wasn't beneficial, income from trophy hunting and venison sale did not reimburse costs of introduction and damages caused by fallow deer in forest and agriculture lands.

UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT

RUSA DEER, AN INVASIVE SPECIES : INTER & INTRA-POPULATION ECOLOGY, DIET AND DENTAL MICROWEAR

Emilie Berlioz¹, Gildas Merceron², Marc Colyn³

¹Laboratoire Paléontologie Evolution Paléoécosystèmes Paléoprimatologie PALEVOPRIM, UMR-CNRS 7262, Université de Poitiers

²Laboratoire Paléontologie Evolution Paléoécosystèmes Paléoprimatologie PALEVOPRIM

³retired from CNRS

From 12 individuals introduced in 1870 in New Caledonia, hundreds of thousands rusa deer (*Cervus timorensis rusa*; Groves and Grubb 2011) are now present in this biodiversity hotspot. If rusa deer's favorite diet seems to be herbaceous monocotyledons whenever available, the important feeding plasticity of this taxa allows it to consume a large range of less preferred vegetal resources, including species with high environmental value, when its favorite diet is not available. Rusa deer impact their habitat by overgrazing, impeding vegetal regeneration by eating every sprout, provoking older tree's death by consuming their bark. It results in a habitat opening and an increased erosion that in turn impacts the water distribution and availability. This invasive species therefore constitutes a main concern for agriculture and ecology. Dental Microwear Texture Analysis, the study of the microscopic wear caused by food during mastication, has proven to be efficient enough in deciphering subtle inter and intra-population variations in diet. This approach, initially developed for paleontological purposes, presents a major potential as a monitoring tool for ungulate management and conservation problematics. 10 habitats were identified based on vegetation, climate, degradation by rusa deer, and human impact. 2500 mandibles were sampled on a 1-year cycle to consider seasonal dietary variations. 600 feces samples and 200 rumen samples were collected to explore further the feeding ecology of the very same individuals. The purpose of this talk is to present our dental microwear preliminary results and to initiate interdisciplinary collaborations to better understand the feeding ecology of rusa deer, in order to propose managing strategies that would be adapted to the New Caledonian case.

UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT

COMPOSITION AND DIET FLUCTUATIONS OF A REINTRODUCED POPULATION OF THE ATLAS DEER *Cervus elaphus barbarus* (BENNETT, 1833) IN THE AKFADOU FOREST (ALGERIA)

N Khammes-Talbi¹, Nora Khammes-Elhomsi¹, Stéphane Aulagnier

¹University M.Mammeri Tizi-Ouzou Algeria

The Atlas deer was reintroduced in the Akfadou forest in 2005, after a feasibility study, and the establishment of infrastructure for reintroduction. The objective of our study is to study its annual diet to help better understand its food needs to better protect and conserve. The method used to study the diet is the microscopic fecal analysis method, which is the most appropriate for herbivorous species. The diet of Atlas deer has been studied for two years (2014 and 2015) to determine if there are seasonal variations. For our study, we collected 120 samples, 12,000 plant fragments identified for each season. The first part of the results obtained was the development of a reference catalogue for 50 species or genera from foliar organs taken from the site. The food spectrum of Atlas deer during the study period shows great plasticity, it is mainly composed of monocotyledons such as Gramineae and Cyperaceae, and broadleaf weeds, especially the Cistus. Deer have very little palatability for Pteridophytes, and their abundance is very low. However, the consumption of these plant species varies according to the seasons studied, which testifies to the opportunism of these ungulates. The detailed analysis of the food remains found in faeces of Atlas deer, in the Akfadou forest, reveals a versatility of its trophic diet.

UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT

IMPACT OF WILD BOAR ROOTING ON ECTOMYCORRHIZAL FUNGI IN BOREAL FORESTS OF SWEDEN

Lars Hillström¹, Antonio Carpio², Marta Garcia Moreno³, Mikael Lönn¹, Guillermo Bueno⁴

¹University of Gävle, Sweden

²University of Cordoba, Spain,

³Complutense University of Madrid, Spain

⁴University of Tartu, Estonia

The wild boar (*Sus scrofa*) has undergone a remarkable expansion in Europe during recent decades. The increase in the abundance of wild boar has led to conflicts such as traffic accidents, agriculture damage, conservation problems and health risks. Despite the environmental importance of the wild boar, its adaptation to new environments has been examined by few studies. The aim of the present study was to investigate the potential effects of the wild boar on abundance and diversity of fungi in a boreal forest ecosystem in Sweden. The study was conducted in 11 study plots (6 plot with wild boar and 5 plots with no wild boar). The plots were sampled between September and November of 2018. The samplings were carried out in transects where squares of 2 x 2 meters separated by 100 meters were established. In each plot with no wild boar 5 square sampling were performed ($n = 5 \times 5 = 25$ square samplings), and in plots with wild boar, 10 square samplings were established per plot (five in rooting areas and five in areas with no rooting), ($n = 6 \times 10 = 60$ square samplings) The richness and abundance of fungi was established at the square sampling level. With regard to the factors affecting ectomycorrhizal fungi abundance, the percentage of rooting (to plot and sampling level) showed a significant and positive correlation with fungi abundance. Factors such as humidity, and treatment (area with wild boar and rooting; area with wild boar but no rooting; and area without would boar) showed a significant effect on fungi abundance. There was a significant effect of openness, presence of wild boar and rooting on species diversity of fungi. Two genus, *Boletus* and *Lycoperdon*, was significantly associated with rooting. This study showed wild boars quantitative and quality effects on fungi.

UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT

HABITAT USE BY ASIAN ELEPHANTS: CONTEXT MATTERS

Dinesh Neupane¹, Youngsang Kwon², Thomas Risch¹, A. Christy Williams³, Ronald Johnson¹

¹*Arkansas State University*

²*University of Memphis*

³*WWF-Myanmar*

Asian elephants are isolated in fragmented habitat patches in and around Bardia National Park (BNP), Nepal. To describe habitat use patterns and ecogeographical variables (EGVs) that determine an elephant's niche in BNP, we used a General Niche-Environment System Factor Analysis (GNESFA) modeling framework. Novel to our study was the comparison of niche requirements between core (residential) and corridor (travel corridor) areas to elucidate site-specific preferences of Asian elephants in BNP. Our study illustrated that, regardless of study area, elephants' habitat use was positively influenced by presence of grasslands, mixed forest, and landscape heterogeneity, whereas use was restricted by the topographic variables of slope and elevation. Results also demonstrated different habitat preferences between elephants in the core and corridor, which may be attributed to differences in potential dangers posed in these areas; in the core, elephant habitat preference was mainly associated with food resources such as grassland or mixed forest, whereas in the corridor, where elephants are more likely to encounter human conflict, the anthropogenic factor of distance to human settlements contributed the most in predicting elephant presence. Correlations among significant factors from the three methods (FANTER, ENFA, and MADIFA) demonstrated the consistent and reliable results of these approaches. We suggest a detailed conservation plan for the small populations of elephants in BNP and surrounding areas, while considering the protection of travel routes from human activities in the corridor habitats, and lastly, maintaining grasslands and waterholes in core habitats.

UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT

DISTRIBUTION AND ABUNDANCE OF WILDLIFE IN EUROPE: TOWARDS HARMONIZATION AND DEVELOPMENT OF NEW STRATEGIES IN THE COLLECTION AND USE OF DATA IN WILDLIFE MANAGEMENT

Karolina Petrović¹, Joaquin Vicente Baños², Jose Antonio Blanco², Marco Apollonio³, Ramon Soriguer⁴, Francesca Brivio³, Ezio Ferroglio⁴, Patrick Jansen⁵, Oliver Keuling⁶, Carmen Ruiz Rodrigues², Massimo Scandura³, Graham Smith⁷, Nikica Šprem⁸, Nera Fabijanić⁸, Stefania Zanet⁴, Tomasz Borowik¹, Tomasz Podgórski¹

¹Mammal Research Institute Polish Academy of Sciences

²Institute for Game and Wildlife Research

³University of Sassari

⁴Spanish National Research Council,

⁴University of Turin

⁵Wageningen University & Research, ⁶University of Veterinary Medicine Hanover

⁷Animal and Plant Health Agency,

⁸University of Zagreb

Through the ENETWILD project, carried out by a consortium of leading European wildlife research, health and management institutions, the European Food and Safety Authority (EFSA) aims to improve European capacities to monitor wildlife populations, develop standards for collection and validation of data, model species spatial distribution and abundance, create and promote a common data repository used for the analyses of risks of spread of zoonotic diseases. Here, we present our activities regarding the development of standards for data collection and validation, available to researchers, wildlife managers and conservationists, that allows for using and sharing data at a European level. Next, we present preliminary results on wild boar distribution and abundance, which is used as a model species. To address a lack of data on distribution and abundance of many European terrestrial mammals, the MammalNet project was developed and will be carried out in parallel with ENETWILD project. This pilot project aims to assess the viability of using citizen science in the monitoring of terrestrial mammals, evaluate the possible limitations, advantages and added values, as well as promote the best practices that would increase the quality of collected data and the participation of citizens. The project will be carried out in 4 pilot countries (Poland, Germany, Croatia and Spain) where citizens will be encouraged to use mobile and web applications to collect wildlife observations and camera trap data. In the second phase of the project, it will be expanded to the rest of Europe. We believe that collecting data on wildlife distribution and abundance in a harmonized way and engaging citizens in a scientific process can greatly improve wildlife management and disease risk assessment.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

EFFECT OF INTENSIVE GRASSLANDS MANAGEMENT ON THE ABUNDANCE OF WEASELS

Karol Zub¹, Anna Andruszkiewicz²

¹Mammal Research Institute Polish Academy of Sciences

²Research Institute Polish Academy of Sciences

Weasel reach highest densities in the open grasslands because this type of habitat provides easily accessible prey and better protection against predators. To find out how modern farming influences population dynamics of these predators in north-east Poland we analyzed the effect of grasslands mowing on the vegetation height and rodent abundance in years 2016-2019, and the long-term data on the density of weasels. Our results show that intensive mowing negatively affects the height of vegetation and causes isolation of suitable habitat patches. The abundance of rodents increases within not mown areas, but decreases where vegetation become short. This type of management changes also the structure of the rodent community, promoting smaller species. At the same time, the density of weasel declines despite locally high availability of the prey, because the area of isolated patches is much smaller than the mean daily home range of this species. In a consequence, weasels are more vulnerable to the predation when moving between suitable patches of vegetation. We suggest that the modification of the management schemes, leading to less frequent mowing of grasslands and providing better connectivity between vegetation patches, will be most beneficial for the environment.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

PAWS WITHOUT CLAWS? ECOLOGICAL IMPACT AND CONSERVATION OF WOLVES IN EUROPE'S HUMAN-DOMINATED LANDSCAPES

Dries Kuijper¹, Marcin Churski¹, Jakub Bubnicki¹

¹Mammal Research Institute, Polish Academy of Sciences

In Europe we have the unique situation that large carnivore species show a recovery, potentially also re-establishing their ecosystem impacts. However, we know very little of carnivore-induced trophic cascades in European human-dominated landscapes. Humans can influence in many ways, and often diminish, the functional role of large carnivores. Our case studies in the Białowieża National park, Polish and Swedish managed forests, illustrate how these human effects can modify the impact of large carnivores. As humans are a dominant factor influencing ecosystems in Europe, we should be careful with simplistic views on carnivore impact without full recognition of possible indirect effects of humans on carnivore and prey behaviour. These human aspects can also not be ignored in wolf conservation, as the recolonization of wolves in European landscapes poses a conservation challenge to protect this species and manage conflicts. In a recent study we provide an objective, science-based discussion on possible management approaches using existing knowledge on large carnivore management from Europe and other parts of the globe. Each scenario, has its unique impact on wolf ecology and prospects of reducing wolf-human conflicts. Despite the large challenges in human-dominated landscapes, we argue that wolf management must focus on strengthening the separation between humans and wolves to prevent and reduce conflicts. Mutual avoidance provides the key to success, and is critical to avoid creating the conditions for reinstating wolf persecution as the default policy in Europe.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

WOLF AT YOUR DOOR: MOVEMENT OF ESTABLISHED AND DISPERSER WOLVES AND KILL SITES DISTRIBUTION IN RELATION TO HUMAN INFRASTRUCTURES

David Carricondo-Sanchez¹, Barbara Zimmermann¹, Petter Wabakken¹, Ane Eriksen¹, Milleret Cyril², Andrés Ordiz², Ana Sanz-Perez³, Håkan Sand⁴, Camilla Wikenros⁴

¹*Inland Norway University*

²*Norwegian University of Life Sciences*

³*Biodiversity and Animal Conservation Lab, Forest Sciences Center of Catalonia*

⁴*Swedish University of Agricultural Sciences*

Large carnivore populations have recently recovered in Europe. Recoveries are associated with range expansions that are bound to occur into human dominated land. This will increase the frequency of direct human-wildlife interactions, which often lead to conflicts that diminish the likelihood of coexistence with large predators. The case of the Scandinavian wolf is a clear example of this. The recovery and expansion of this population encountered a number of meeting points between wolves and people that generated conflict due to apparent proximity of wolves to houses, and competition with hunters for big game species. Nevertheless, many studies show that large carnivores generally avoid human disturbance. Here, we studied the movement decisions of wolves in relation to human infrastructures within their home ranges and during dispersal to show that, alike other large carnivore species, wolves generally avoid humans. However, specific circumstances like nighttime or winter season, may bring them closer to human infrastructures. Because habitat selection can be motivated by prey availability, we also studied the distribution of wolf kill sites within the home range and found that wolves moved and preyed following moose densities. In conclusion, Scandinavian wolves, as other large carnivores, show a high degree of behavioral plasticity and adaptability in relation to human infrastructures. They will consistently avoid these features, although they might ease this avoidance when the probability of interacting with humans is low.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

A STANDARDIZED METHOD FOR CONDUCTING AND ANALYSING EXPERIMENTAL HUMAN APPROACHES ON WOLVES

Ane Eriksen¹, Erik Versluijs¹, Boris Fuchs¹, Barbara Zimmermann¹, Petter Wabakken¹, Léa Bouet², Andrés Ordiz³, Kristoffer T. Nordli¹, David Carricondo-Sanchez¹, Peter Sunde⁴, Håkan Sand⁵, Lucrezia Gorini¹, Frank Michler⁶, Camilla Wikenros⁵, Benjamin Gillich⁶, Siegfried Rieger⁶

¹*Inland Norway University of Applied Sciences, Department of Forestry and Wildlife Management*

²*Université Jean Monnet Saint-Étienne*

³*Norwegian University of Life Sciences*

⁴*Aarhus University*

⁵*Swedish University of Agricultural Sciences*

⁶*Eberswalde University for Sustainable Development*

As wolves recolonize areas of Europe ranging from remote forests to areas of high anthropogenic impact, fear of wolves is a recurring source of conflict. Wolves can be perceived as dangerous and unpredictable, but knowledge about their behavior when encountering humans may mitigate fear and facilitate human-wolf coexistence. The shared challenge related to fear of wolves across their recolonized range calls for shared tools for evaluating their responses to humans. We have developed a protocol for evaluating the responses of GPS-collared wild wolves to approaching human observers, and tested it in Scandinavia and Germany. We present (1) a standardized field protocol for conducting experimental approaches on wolves using GPS collars that are remotely programmable to 1-minute positioning frequency, and controlling for factors such as observer type and habitat parameters; (2) a descriptive comparison of two statistical methods (upper control limit and changepoint analyses) for defining flight initiation distance; (3) a description of the use of changepoint analyses to define the wolf's resettling position after the disturbance; and (4) the first, promising analyses of accelerometry data for documenting fine-scale wolf movement and posture. Accelerometry may allow us to identify any initial reaction to the approaching human before the displacement that can be detected using GPS positions, and has the potential to provide information about wolf behavior at an unprecedented level of detail. A common, standardized protocol for experimental human approaches on wolves across Europe will provide knowledge applicable at a local, national and international level, as it allows to compare wolves' responses within and between populations and along a gradient of anthropogenic impact.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

THE EFFECTS OF WOLVES RETURNING TO FOREST ECOSYSTEMS

Adam Wójcicki¹, Zbigniew Borowski¹

¹Forest Research Institute

The wolf population in Poland has been growing for over twenty years, returning to the areas, from whose it disappeared or was exterminated. The functioning of large predators in ecosystems affects their preys directly by reducing their numbers and indirectly by forcing them to modify their behaviour. These effects may have an impact on the lower elements of the food chains (the trophic cascade phenomenon). We conducted our research in three types of ecosystems located in forests: (1) not colonised by wolves, (2) inhabited by wolves recently and (3) where the wolves have been present for decades. In order to verify the reactions of wolves' potential preys to the variable risk of predation, an experiment involving the exposure of a wolf odor and a control odor was carried out. We analysed the behaviour of deer and roe deer in these ecosystems with low and high risk of predation. Also, we analysed the impact of wolf on the spatial distribution and the intensity of browsing within the youngest stages of forest stands development. The behaviour of cervids at a high risk of predation differed, depending on the wolf presence in ecosystem. The strongest anti-predatory responses were observed in forests where the wolf's population has been functioning for a long time. In ecosystems, where the wolf did not occur or has been occurring recently, they were much weaker. Other factors (the hunting season, the individual species and its sex) also affected the anti-predatory behaviour. The presence of wolves in the ecosystem and the time since they colonised it had no effect on the feeding of cervids on the forest plantations and thicket stands and caused no differences in the spatial distribution and pressure of these herbivores on tree vegetation, as well as the rate of tree growth.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

CONSERVATION STRATEGIES FOR THE ARCTIC FOX

Anders Angerbjörn¹, Karin Norén¹, Johan Wallén¹

¹Stockholm University

The arctic fox is threatened to go extinct in Sweden, Norway and Finland. The threats are several with increasing density of red foxes, decreasing food abundance and/or low population size with a demographic trap. But there are several actions to halt the decline in arctic fox numbers and instead turn it into an increase. Supplemental food (1) can increase both number and size of litters. Red fox hunting (2) can increase the number of litters and survival of arctic foxes. Reintroduction of captive bred arctic foxes (3) have also been successful. The different actions have been employed during 15 – 25 years in different populations. Analyses of population growth rate of reproductive events show that all three actions can under some circumstances double a population over a four year period. However, all methods have also their shortcomings. Food supplementation works best together with red fox hunting. Red fox hunting alone is not efficient. Reintroduction works nicely together with supplemental food. But in some cases the reintroduction did not result in a population increase. The methods are also sensitive to intensity but also to the phase of the rodent cycle. We will further discuss the possibility to optimize the methods by combining them and to use them selectively over a rodent cycle.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

USING HABITAT SUITABILITY MODELLING TO INFORM PROPOSED REINTRODUCTIONS OF EUROPEAN WILDCAT *Felis silvestris* TO ENGLAND AND WALES

Jenny Macpherson¹, Sébastien Devillard², Sandrine Ruetten³, Michael Hudson⁴, Stephen Carter⁵

¹*Vincent Wildlife Trust,*

²*Université Claude Bernard Lyon*

³*Office National de la Chasse et de la Faune Sauvage*

⁴*Durrell Wildlife Conservation Trust*

⁵*Vincent Wildlife Trust*

Reintroductions are an increasingly important tool used by conservation managers to counteract biodiversity loss. However, reviews of their outcomes have often reported low rates of success. One reason frequently given for failure is low habitat suitability in the release area. Species distribution models can be used to predict the geographic distribution of suitable habitat and maximise the effectiveness of reintroduction programmes. Wildcats used to be found throughout mainland Britain, but loss of woodland habitat and historical predator control resulted in extinction in England and Wales, and hybridisation with feral cats in Scotland. In conjunction with ongoing work in Scotland, successful reintroductions of wildcat to suitable areas of England and/or Wales, could be a major proactive step towards improving the conservation status of the species in Britain. MaxEnt was used to predict areas with the highest habitat suitability for wildcat across England and Wales, where proposed reintroductions could be focussed.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

HOW DO EUROPEAN WILDCATS (*Felis silvestris silvestris*) MANAGE TO SETTLE IN A HEAVILY FRAGMENTED LANDSCAPE?

Mathias Herrmann

OEKO-LOG field research

In Germany the population of the European wildcat is recovering. But can wildcats recolonize a landscape dominated by human infrastructure and surrounded by roads and settlements? Based on earlier radio tracking studies, the habitat preferences of the European wildcat were analyzed. Klar et al. (2008) set up a habitat model based on this knowledge and predicted wildcat corridors. The predictions of the habitat and corridor model were applied in an area densely populated by humans. The predictions showed a forest patch suitable for wildcats and a corridor connecting this forest patch with the central population „Pfaelzerwald“. The corridor crossed belt of settlements and was only 200 m narrow. Using this corridor wildcats had to cross a fence surrounding the habitat patch, two major roads, one 6 line highway and a railroad. Main questions: would it be possible for wildcats to find this habitat patch surrounded by infrastructure? will wildcats be able to establish a local population there? will wildcats use the predicted corridor? Results: Wildcats managed to settle permanently and reproduce in the isolated habitat patch. Migrating from one habitat patch to the next they managed to cross different roads and railway lines. The animals migrated through the small forest patch as predicted by the model. The predictions of the model forecast the real situation for the wildcat well. Concluding from the results, we hypothesize that the investigated wildcat population could not survive by itself, because of the small size. In consequence, an exchange with the central population in the „Pfaelzerwald“ is necessary. The small forest gap in the linear settlement belt and the permeability of the traffic ways are essential for this exchange.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

DIET OF FOXES IN WARSAW – COMPARISON OF THE RESULTS FROM THREE DIFFERENT METHODS OF ASSESSMENT

Mateusz Jackowiak¹, Jakub Gryz², Dagny Krauze-Gryz¹

¹*Warsaw University of Life Sciences*

²*Forest Research Institute*

The research was conducted in the area of Warsaw in 2017-2019. Three different methods of red foxes' diet assessment were used – scat analysis, collecting of prey remains near the dens and camera-traps registration of preys brought to dens. Scats were collected throughout a year and their analysis followed the Goszczyński methodology (1974). Scats were soaked in water with detergent for 24 hours, sifted and dried in 60°C for 24 hours. Then, macro- and microscopic analysis was conducted. Two other methods were used only in breeding season when dens were used by foxes and cubs were present. Dens were regularly controlled during the breeding season. Prey remains detected near the dens were noted and removed to exclude recounting. To detect prey brought to dens camera-traps installed near the dens were used at the turn of February and March and deinstalled in August or September.

Until the end of June, 2019, 73 scats were collected, 92 prey remains were registered and 148 photos of foxes with prey were taken by camera-traps. The scat analysis is being continued, but preliminary results showed high amount of rodents and birds in foxes' diet in Warsaw. The results of two other methods were quite similar. The most abundant fox preys were birds in both methods (43%, N = 92 in prey remains collection and 34%, N = 148 in camera-traps data). Mammals had a smaller share (about 22-33%, according to method). Anthropogenic food in foxes' diet was not more frequent than one fifth of total (similar in both methods). There was a part of food which identification was impossible in camera-traps data. On the basis of camera-traps data, spatial variability of foxes' diet was also found, which is probably dependent on location and local availability of specified food resources.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

VARIATIONS IN THE INTERSPECIFIC RELATIONSHIPS OF SYMPATRIC CARNIVORES IN A FLUCTUATING PREY SCENARIO IN A BOREAL ECOSYSTEM

Rocio Cano-Martinez¹, David Carricondo-Sanchez¹, Olivier Devineau¹, Morten Odden¹

¹Inland Norway University of Applied Sciences

Cyclic fluctuations of prey impose multiannual resource variation for carnivore communities, and have profound effects in the functioning of these ecosystems. Since different predators within a community can share the same fluctuating prey, changes in prey availability may influence their interspecific interactions. In boreal ecosystems, prey resources fluctuate considerably in space and time and environment characteristics, such as snow condition or ecosystem productivity, greatly determine these dynamics. Furthermore, these ecosystems are among the most vulnerable to climate change and anthropogenic disturbances, and carnivore communities are dramatically changing in these biomes. The aim of this study is to assess how rodent cyclic fluctuations affect the interspecific interactions and habitat use of a guild of medium- and small-sized predators: red fox (*Vulpes vulpes*), pine marten (*Martes martes*) and weasels (*Mustela erminea* and *Mustela nivalis*). We analyzed 8 years of snow tracking data using structural equation modeling to assess hypothesized networks of causal relationships. Our results indicate that increases in rodent abundance seem to change the relationship between these competing predators, as well as their habitat selection. Pine marten and weasels seem to avoid red fox during years of rodent increase, which might reflect a higher degree of competition avoidance when food is abundant. Additionally, they tend to select agricultural lands when rodent abundance decreases. Red fox, as a generalist predator, seem to be less influenced by rodent increase, probably due to prey switching behavior. Overall, our study highlights the importance of considering sympatric competitors when managing carnivore populations, as well as the dynamics of their prey.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

COMPARISON OF GREY WOLVES AND RED FOXES DIET IN HABITATS OF DIFFERENT QUALITY

Zuzanna Wikar¹, Adrian Zwolicki¹, Maciej Szewczyk²

¹Department of Ecology and Zoology of Vertebrates, University of Gdańsk

²Institute of Genetics and Biotechnology, University of Warsaw

Grey wolves *C. lupus* as apex predators have impact on ecology of smaller predators, e.g. red foxes *V. vulpes*. Coexistence with wolves entails both with danger, because they often kill foxes, and availability of rich source of food – carrion. We compared sympatric canids' diet in Tuchola Forest (TF), one of the biggest forests in Poland (ca. 3000 km²) and Iława Lakeland (IL) in 2016-2018. We chose study areas basing on habitat suitability model for Polish wolves – area in TF was described as very good habitat and isolated, small forest (ca. 85 km²) in IL was area of low suitability. We collected and analysed 139 wolves' and 104 foxes' scats. Diet of studied canids on both areas was dominated by wild ungulates. In TF red deer *C. elaphus* and in IL wild boar *S. scrofa* were main prey. There were significant differences between areas in wolves' consumption of red deer, which was preferred in both forests, roe deer *C. capreolus*, which was avoided and wild boar, which was absent in diet of wolves from TF and was preferred by pack from IL. Livestock, mainly dogs *C. familiaris*, but also cattle *B. taurus*, was detected only in diet of wolves from IL. Use of wild ungulates didn't differ between wolves and foxes, their food niches' width also show it's main food group for both species. Niches of both canids in each study area overlapped stronger than niches of wolf packs from both forests. However, foxes' niches from TF and IL strongly overlapped. Our results show that wolves diet is shaped by availability of wild ungulates that results from size of the forest and it's fragmentation, which confirm results of earlier studies of wolves diet from areas with strong anthropogenic pressure. They also reveal that diet of apex predator strongly affects diet of foxes.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

FOSSORIALITY IN A RISKY LANDSCAPE: WOLVES DRIVE BADGER DENNING BEHAVIOUR IN BIAŁOWIEŻA PRIMEVAL FOREST

Tom Diserens¹, Marcin Churski¹, Jakub Bubnicki¹, Esmee Schutgens¹, Kira Rokx¹, Rafał Kowalczyk¹, Dries Kuijper¹

¹Mammal Research Institute, Polish Academy of Sciences

Many medium-sized carnivores (mesocarnivores) are fossorial and utilise burrows to reduce their risk of being killed or disturbed by a predator. But despite mounting evidence that risk can indirectly affect mesocarnivore behaviour, little attention has been given to how it affects their denning behaviour. The European badger is a fossorial species that uses burrows (setts) for daytime rest. The way badgers use setts varies greatly in response to a variety of factors such as food abundance, weather and presence of juveniles, but the role of risk has thus far been unexplored. In this study we used the badger as a model species to disentangle the effects of top-down (wolf and human predation risk) and bottom-up factors (food abundance) driving a fossorial species' denning behaviours in Białowieża Forest, an area where badgers live sympatrically with wolves and humans. Using camera traps we investigated how badger frequency of sett use, frequency of sett sharing with other mesocarnivore species (raccoon dog, fox) and emergence time from setts varies across a gradient of wolf space use (proxy for wolf risk) and distances to human settlements (human risk), while taking into account variation in earthworm abundance. We found that lower wolf risk and higher food abundance positively affected frequency of sett use, but the effect of wolf risk was much larger than that of food abundance. Frequency of sharing with other mesocarnivores was affected only by human risk, whereas emergence time was not affected by either risk factor. I will discuss how these results improve our understanding of the dynamic role that burrows play in mitigating predation risk in fossorial species and contribute to predicting the ecological effects of the on-going wolf recolonisation of European forests.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

MARTENS IN A CHANGING WORLD – BODY SIZE VARIATION OVER SPACE AND TIME

Anna Wereszczuk¹, Sim Broekhuizen², Alexander Csanády³, Tomislav Dumić⁴, Tim R. Hofmeester⁵, József Lanszki⁶, Aksel Bo Madsen⁷, Gerard Müskens⁸, Malamati A. Papakosta⁹, Iñigo Zuberogoitia¹⁰, Andrzej Zalewski¹

¹Mammal Research Institute, Polish Academy of Sciences, Białowieża, Poland

²Wageningen Environmental Research, Wageningen, the Netherlands

³University of Prešov, Department of Biology, Faculty of Humanities and Natural Sciences, Prešov, Slovakia

⁴Department of Wildlife Management and Nature Conservation, Karlovac University of Applied Sciences, Karlovac, Croatia

⁵Resource Ecology Group, Wageningen University, Wageningen, the Netherlands; Department of Wildlife, Fish, and Environmental Studies, Swedish University of Agricultural Sciences, Umeå, Sweden

⁶Carnivore Ecology Research Group, Kaposvár University, Kaposvár, Hungary

⁷Department of Bioscience - Kalø, Aarhus University, Aarhus, Denmark

⁸team Animal Ecology, Environmental Sciences Group, Wageningen University & Research, Wageningen, Netherlands

⁹School of Forestry and Natural Environment, Lab of Wildlife & Freshwater Fisheries, Aristotle University of Thessaloniki, Thessaloniki, Greece

¹⁰Estudios Medioambientales Icarus S.L., Bilbao, Spain

In the geographic range of a species, environmental conditions vary greatly and in order to adapt to this variation, animals change their ecology, behaviour and/or morphological traits. Based on Bergmann's rule, animals should adapt their body size to the accelerating climate change in the last few decades. However, do changes in climate conditions over time affect the body size variation in a similar way as climatic variation over the geographical range? The goal of this study was to analyse the magnitude of variation in body mass of pine marten (*Martes martes*) and stone marten (*Martes foina*) in both space and time. We have analysed the body mass of more than 3000 pine and stone martens from Europe, collected between 1960 and 2019. We found that the body mass of pine and stone martens has changed over the geographical scale, but with contrasting patterns between the species. The variation of stone marten body mass showed a nonlinear pattern, decreasing between 1960 and 1980 and increasing from 1980 to 2019. In both species, the magnitude of body mass variation over time was larger than in the geographical scale. These differences may be related to differences in physiological adaptations to climate conditions in both species, as pine martens evolved in the boreal forest, while stone martens evolved in a sub-tropical climate, as well as to different habitats occupied by them (forest by pine martens and anthropogenic area by stone martens). These results suggest that both species will show different population responses (density variation, range shift or expansion) to climate warming.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

DETECTING METHODS FOR AN OPPORTUNISTIC AND EXPANDING MESOCARNIVORE IN SW EUROPE: THE EGYPTIAN MONGOOSE (*Herpestes ichneumon*)

Esther Descalzo¹, Miguel Delibes-Mateos², Francisco Díaz-Ruiz³, José Jiménez¹, Pablo Ferreras¹

¹Instituto de Investigación en Recursos Cinegéticos IREC, CSIC-UCLM-JCCM, Ciudad Real, Spain

²Instituto de Estudios Sociales Avanzados IESA-CSIC. Córdoba, Spain

³Universidad de Málaga, Departamento de Biología Animal, Málaga, Spain

The Egyptian mongoose (*Herpestes ichneumon*) is the only Herpestidae species that occurs naturally in Europe. Traditionally, it occurred only in the SW Iberian Peninsula, from where it is expanding. However, its situation is unclear in central Spain, where hunters complain because of its alleged impact on small game species. To clarify the species distribution and assess its expansion, efficient detection methods are needed. We compared the performance of four detection methods: 1) sign surveys on transects on-foot, 2) baited camera-traps and 3) hair-traps, either baited or 4) unbaited. We replicated these methods in ten sampling units within four study areas. One-kilometre transect was surveyed in each sampling unit (i.e. 10 per study area), searching for mongoose faeces and footprints. We deployed a baited camera-trap, a double baited hair-trap and a single unbaited hair-trap in each transect. These detecting devices were weekly checked during a month, and walking transects were biweekly surveyed. All the methods detected the species in some of the study areas. An occupancy framework was used to estimate method-specific probabilities of detection (P). Baited hair-traps were the most efficient method (mean $P \pm SD$: 0.40 ± 0.07) followed by sign surveys on foot (0.30 ± 0.06). Camera-traps (0.26 ± 0.06) and unbaited hair-traps (0.22 ± 0.09) were the least efficient methods. Variability in detectability among study areas of sign surveys was high, whereas it was low for baited double hair-traps. Considering the cost, efficiency and variability of each method, we recommend a combination of baited hair-traps and sign surveys as the most efficient alternative to detect Egyptian mongooses in southern Europe.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

EVIDENCE OF URBANIZATION OF THE ARCTIC FOX NEAR REYKJAVÍK CAPITAL

Ester Rut Unnsteinsdóttir

The Icelandic Institute of Natural History

In an ongoing pilot study, an attempt is made to evaluate the response of a small generalist canid, the Arctic fox (*Vulpes lagopus*), to a rapid extension of the capital, Reykjavik. The study area is a 5x5 km plot, adjacent to the edge of the capital area. The western part of the study area (5x1 km) is along a highway and includes a recent residential area with 1.600 apartments, a school, premises with shopping centres (IKEA, Costco, etc.), golf course and scattered buildings at each side of a vegetated lava field, which converses into a recreational area where the natural habitat of the native Arctic fox used to be. The closest natural den sites are 3,5km away from the highway and it was predicted that the foxes would move even further away as the capital expanded. We used Spypoint cameras and later set out Tomahawk traps for capturing foxes (to fit with GPS collars) at successful camera stations. In February to December 2018, 6-7 individual foxes appeared on 114 photos in camera stations, all within 1,5km distance from the highway. Additionally, 2-4 different individuals were photographed at the golf course and IKEA. In total, we could identify 10-11 different individuals from photos, thereof 5-6 adults and 5 cubs. None of the foxes came into the traps but adult Icelandic foxes rarely enter baited traps. The project is still ongoing and this summer, two cubs have been spotted inside a trap that is located 1,5 km from the highway. They will hopefully be captured in the autumn when they are big enough to carry the collars. In contrast to our predictions that the foxes would avoid human activities, the first results suggest that the local foxes not only remained in their former area, but even moved their litters (or made new dens) closer to the expanding capital edge.

MAMMAL PALEOECOLOGY: IMPLICATIONS FOR CONSERVATION AND RESTORATION

MAMMAL PALEOECOLOGY: IMPLICATIONS FOR CONSERVATION AND RESTORATION

Hervé Bocherens¹, Rafał Kowalczyk²

¹University of Tübingen, Dept of Geosciences, Tübingen, Germany

²Mammal Research Institute, Polish Academy of Sciences, Białowieża, Poland

Extant mammal species have experienced dramatic changes in their abiotic and biotic environment during past millenia, due to climate change and increasing human impact. Many species have reduced distribution ranges and persist as relict populations, sometimes in suboptimal habitats. To establish a valid environmental baseline for efficient conservation and possibly re-introduction of new populations of such species through restoration strategies, it is essential to understand the past distribution and ecology of these species. Only investigations of fossil, sub-fossil and historical material can provide such information. Novel research methodologies, such as tooth wear analysis, stable isotopic tracking and paleogenetics, are yielding crucial results to design conservation and restoration strategies. Moreover, understanding why so many large mammal species disappeared in the recent past, while other - sometimes closely related species - persisted, could provide case studies of extinction mechanisms that might help design efficient conservation strategies for surviving species. This is particularly important due to global warming that will affect the majority of species in the near future. In this session, we aim to bring together paleoecologists and ecologists to develop guidelines and research networks to bring the power of paleoecology to conservation biology.

MAMMAL PALEOECOLOGY: IMPLICATIONS FOR CONSERVATION AND RESTORATION

ADAPT OR DIE—RESPONSE OF LARGE HERBIVORES TO ENVIRONMENTAL CHANGES IN EUROPE DURING THE HOLOCENE

Emilia Hofman-Kamińska¹, Hervé Bocherens², Dorothée G. Drucker², Ralph M. Fyfe³, Witold Gumiński⁴, Daniel Makowiecki⁵, Martina Pacher⁶, Giedrė Piličiauskienė⁷, Tomasz Samojlik¹, Jessie Woodbridge³, Rafał Kowalczyk¹

¹Mammal Research Institute PAS

²University of Tübingen

³University of Plymouth

⁴Warsaw University

⁵Nicolaus Copernicus University

⁶Universität Wien

⁷Vilnius University

Climate warming and human landscape transformation during the Holocene resulted in environmental changes for wild animals. To track the response of habitat use and foraging of large herbivores to natural and anthropogenic changes in environmental conditions during the Holocene, we investigated carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) stable isotope composition in bone collagen of moose (*Alces alces*), European bison (*Bison bonasus*) and aurochs (*Bos primigenius*) in Central and Eastern Europe. All three species showed significant changes in their $\delta^{13}\text{C}$ values reflecting a shift of foraging habitats from more open in the Early and pre-Neolithic Holocene to more forest during the Neolithic and Late Holocene. This shift was strongest in European bison, suggesting higher plasticity, more limited in moose, and the least in aurochs. Significant increases of $\delta^{15}\text{N}$ values in European bison and moose are evidence of a diet change towards more grazing, but may also reflect increased nitrogen in soils following deglaciation and global temperature increases. Among the factors explaining the observed isotope variations were time (age of samples), longitude and elevation in European bison, and time, longitude and forest cover in aurochs. None of the analysed factors explained isotope variations in moose. Our results demonstrate the strong influence of natural (forest expansion) and anthropogenic (deforestation and human pressure) changes on the foraging ecology of large herbivores, with forests playing a major role as a refugial habitat since the Neolithic, particularly for European bison and aurochs. We propose that high flexibility in foraging strategy was the key for survival of large herbivores in the changing environmental conditions of the Holocene.

MAMMAL PALEOECOLOGY: IMPLICATIONS FOR CONSERVATION AND RESTORATION

HOLOCENE EXTINCTION OF AUTOCHTHONOUS MAMMALS IN THE CARPATHIAN BASIN (CENTRAL EUROPE) AND ITS ECOLOGICAL CONSEQUENCES

Attila Németh¹, Annamária Bárány¹, Piroska Pazonyi², Enikő Magyar^{2,3}, József Pálffy^{2,3}

¹*Hungarian Natural History Museum*

²*MTA-MTM-ELTE Research Group for Paleontology*

³*Department of Environmental and Landscape Geography of the Eötvös Loránd University,*

Mammals are a key target group for conservation biology. Insights into the patterns and driving forces behind their past extinctions can help us to better understand the present situation, and to predict and mitigate future biodiversity loss. Here we summarise the Holocene extinction of mammals in the Pannonian or Carpathian Basin, a distinctive and biogeographically well-constrained, predominantly lowland region in Central Europe. Our comprehensive analysis combines data from different disciplines for a better understanding of the ecological consequences of species extirpation to entire ecosystems. About 10% of the mammalian fauna of the region went extinct during the Holocene. The temporal distribution of extinctions is non-random as most taxon range terminations are concentrated around two discrete events. The lack of synchronous and severe climate and vegetation changes and the coincidence with transitions in human history suggest a primary role of anthropogenic disturbance. These extirpations not only resulted in the disappearance of the characteristic species, but also caused the transformation and reorganization of entire ecosystems, which lost a whole range of ecological functions and their resilience was reduced compared to the previous natural system. These losses also have significant ramifications for conservation biology. Ongoing conservation efforts are aimed to preserve ecosystems, which are unbalanced, ecologically transformed and suffering from the consequences of missing keystone or ecologically important species. Awareness of the ecological legacy of Holocene extinctions opens new perspectives for conservation and help to develop more efficient strategies and action plans.

MAMMAL PALEOECOLOGY: IMPLICATIONS FOR CONSERVATION AND RESTORATION

CONCEPTUAL RECONSTRUCTION OF LATE PLEISTOCENE LARGE MAMMAL COMMUNITIES ON THE PALAEO-AGULHAS PLAIN REVEALS RESILIENCE TO CLIMATE CHANGE BUT VULNERABILITY TO MODERN HUMAN PREDATORS

Jan Venter¹, Christopher Brooke¹, Curtis Marean², Herve Fritz³, Charles Helm⁴

¹*Nelson Mandela University*

²*Arizona State University*

³*University of Lyon1*

⁴*Peace Region Palaeontology Research Centre*

Recent evidence indicates that the now submerged continental shelf, the Palaeo-Agulhas Plain, in southern Africa, formed a novel ecosystem during periods of low sea level during the late Pleistocene. This terrestrial landscape potentially provided nutrient-rich forage and habitats to a variety of large herbivores and associated predators. This is in stark contrast to the faunal assemblage found in the present-day Cape Floristic Region, which is dominated by landscapes with nutrient-poor soils and unpalatable plants. The archaeological record for the region provides some clues on species occurrence of the region. Here we reconstruct Late Pleistocene species communities for the Palaeo-Agulhas Plain and investigate potential gaps in the record using Hutchinson's weight ratio theory. We then compare the results to modern occurrences of mammals on the Cape South Coast and the Serengeti (a comparable migratory system in East Africa). Both sea-level and sampling effort (minimum number of individuals in archaeological records) influenced species numbers found during the last seven marine isotope stages. Large mammals showed an extraordinary resilience to extreme habitat loss caused by changing sea levels where, especially the large grazers, survived as refugee species during high sea levels and low habitat availability. However the combination of habitat loss and modern human weapons were the cause of severe extinction rates during the last 400 years.

MAMMAL PALEOECOLOGY: IMPLICATIONS FOR CONSERVATION AND RESTORATION

CONSERVATION PALEOECOLOGY OF SOUTHEAST ASIAN GORALS (*Naemorhedus*) AND SEROW (*Capricornis*) THROUGH STABLE ISOTOPIC TRACKING SINCE 400,000 YEARS

Kantapon Suraprasit¹, Rasmi Shoocongdej², Jean-Jacques Jaeger³, Yaowalak Chaimanee³, Hervé Bocherens¹

¹Department of Geosciences, Biogeology, University of Tübingen

²Department of Archaeology, Faculty of Archaeology, Silpakorn University

³PALEVOPRIM, UMR CNRS 7262 INEE, Université de Poitiers

In Southeast Asia, the subfamily Caprinae is represented by two threatened genera, *Naemorhedus* (goral) and *Capricornis* (serow), living today in mountainous areas and upland forests. Co-occurrences of both recognized genera with three species (*N. goral*, *N. griseus*, and *C. sumatraensis*) have been documented in Pleistocene fossil sites in Thailand. However, the co-existence patterns in relation to diet and habitat preferences of these three species are poorly known. We used stable carbon and oxygen isotope analyses of tooth enamel to reconstruct the diets and habitats of these three Pleistocene sympatric taxa, to test the species co-occurrence patterns through time, and to guide the future habitat restoration for their surviving populations. We analyzed 93 caprine samples from five sites in Thailand during the past 400,000 years (Middle Pleistocene to Early Holocene) as well as some modern specimens. Carbon isotope analysis revealed different ecological patterns between *Capricornis* and *Naemorhedus*. During the Pleistocene glacial-interglacial cycles, *C. sumatraensis* had a wide range of diets and habitats varying from pure C₃ to C₄ vegetation, while both *Naemorhedus* species from all Thai fossil sites fed on pure C₄ plants or a mixture of both types in an open habitat canopy such as a lowland grassland, different from where they are living today. This suggests that *C. sumatraensis* was a greater ecological generalist than *Naemorhedus*, in both diet and habitat. The habitat restriction of the extant representatives of these species in closed-canopy upland forest is likely due to warmer Holocene climate and to human impacts. Therefore, we suggest considering open habitat landscapes for sustaining the remaining populations of *N. goral* and *N. griseus*.

MAMMAL PALEOECOLOGY: IMPLICATIONS FOR CONSERVATION AND RESTORATION

THE NW IBERIAN BROWN BEAR DIET FROM UPPER PLEISTOCENE TO NOWADAYS: AN STUDY ON STABLE ISOTOPES

Ana García-Vázquez¹, Ana C. Pinto Llona², José Vicente López-Bao³, Fernando Ballesteros⁴, Aurora Grandal-d'Anglade¹

¹University Institute of Geology, University of A Coruña

²Museo Arqueológico Regional, Research Associate, Alcalá de Henares

³Unidad Mixta en Investigación de la Biodiversidad, Oviedo University

⁴Fundación Oso Pardo

The brown bear (*Ursus arctos*) is a common species in the Holocene fauna of the Iberian Peninsula that in historical times underwent a significant reduction in its distribution and population size by the increasing human pressure. In addition, although less abundant, is also found in Pleistocene deposits of the Cantabrian mountain range, sharing space and perhaps habitat with the most abundant cave bear (*Ursus spelaeus*). In order to better understand the ecology of this species, it is useful to know its diet and its relation to other large mammals in the past, and to determine its ecological niche evolution along time from before the last glacial maximum (LGM) to its current situation. We performed here stable isotope analysis ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) on bone collagen from ~40 fossil brown bears dating from Late Pleistocene to historic times, from the western range of the Cantabrian Mountains, and hair keratin and bone collagen of modern bear from the same geographical range. These data were compared with fossil and modern fauna from the same area. Modern Cantabrian brown bears include in their diet only 20% of animal matter. The diet of cave and brown bears in the Cantabrian Mountains was also based on vegetable matter, although their different isotopic signatures suggest different ecological niches: wooded lowlands for the cave bear and steep highlands with scarce tree cover for the brown bear. Holocene brown bears maintains isotopic signatures similar to the Pleistocene ones in spite of the climatic tempering, which seems to be related to an even greater displacement toward the uplands due to the growing anthropic pressure. Modern brown bears show the same trophic level, with a small increase in $\delta^{15}\text{N}$, reflecting an increase in anthropogenic pressure (livestock, manuring...).

MAMMAL PALEOECOLOGY: IMPLICATIONS FOR CONSERVATION AND RESTORATION

ECOLOGICAL NICHE OF RED DEER (*Cervus elaphus*) AND CHANGES IN ITS RANGE IN EUROPE AND THE URAL MOUNTAINS SINCE THE LATE PLEISTOCENE

Magdalena Niedziałkowska¹, Karolina Doan², Maciej Sykut¹, Marcin Górny¹, Krzysztof Stefaniak³, Natalia Piotrowska⁴, Bogumiła Jędrzejewska¹, Bogdan Ridush⁵, Sławomira Pawełczyk⁶, Paweł Mackiewicz⁷, Ana Stanković⁸

¹Mammal Research Institute Polish Academy of Sciences

²Museum and Institute of Zoology, Polish Academy of Sciences

³Department of Palaeozoology, University of Wrocław

⁴Radiocarbon Laboratory Institute of Physics – Center for Science and Education, Silesian University of Technology

⁵Department of Physical Geography, Geomorphology and Paleogeography, Yuriy Fedkovych Chernivtsi National University

⁶Radiocarbon Laboratory Institute of Physics – Center for Science and Education, Silesian University of Technology

⁷Department of Genomics, Faculty of Biotechnology, University of Wrocław

⁸Institute of Genetics and Biotechnology, University of Warsaw, Institute of Biochemistry and Biophysics Polish Academy of Sciences

The aims of our study was to reveal the changes in range and explore the role of climate and environmental conditions determining the distribution of red deer (*Cervus elaphus*) in Europe and the Urals over the last 50 ka years. We collected 984 records of the radiocarbon dated subfossils of the species (including 93 dates obtained in the frame of our own study) from 54 000 calibrated years BP (54 ka cal BP) until contemporary times. We compiled available climatic data and biome type for the localization and the corresponding time intervals of each of the deer samples. Since the Late Pleistocene, the range of red deer decreased, when the climate was getting colder and increased in warmer periods. However, due to different environmental conditions in western and eastern Europe as well as western Asia, these processes were asynchronous and differed between those regions. The range of red deer during the Last Glacial Maximum (LGM) was larger than previously thought and covered vast areas north and east of the well-known southern LGM refugia in Europe. The ecological niche of red deer was stable during the last 54 ka: the majority of red deer inhabited forests. The contribution of forest habitats in red deer localities significantly decreased during the last 4 ka, most likely due to deforestation of Europe caused by humans. Mean January temperature was the limiting factor for the species distribution. Over 90% of samples were found in areas, where mean January temperature exceeded -10°C. The temperate climatic zone has been optimal for the species since the Late Pleistocene. Under the conditions of enormous, large-scale changes in climate and available habitats, the species tracked the environmental set-up to which it has been well adapted. The project was financed by the National Science Centre (grant no UMO-2013/11/B/NZ8/00888).

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY

SUMMER AND WINTER DIETS OF *Neomys fodiens* AND *Sorex minutus* (SORICIDAE): CAN THE WEAKLY EXPRESSED DEHNEL'S PHENOMENON IN THESE SPECIES BE EXPLAINED BY HIGH AVAILABILITY OF THEIR PREY IN WINTER?

Leszek Rychlik¹, Klaudia Kępką¹, Paweł Kardynia¹

¹Department of Systematic Zoology, Institute of Environmental Biology, Faculty of Biology, Adam Mickiewicz University, Poznań

Dehnel's phenomenon (winter reduction of body size to decrease food requirements) is in *Neomys fodiens* and *Sorex minutus* [below denoted by NF and SM] less expressed than, e.g., in *S. araneus*. We tested the hypothesis that this lower expression is due to a greater availability of prey eaten by these species in winter. We compared between summer and winter the availability of the main types of invertebrates and the composition of NF and SM diets. Shrew diets were determined by the analysis of faecal samples collected from box traps during live trapping in the years 2007-2010. The availability of almost all invertebrates of epifauna decreased in winter, however, the abundance of Araneae, Coleoptera, Diptera larvae, Gastropoda and especially Diplopoda and Isopoda in litter increased. Also, the abundance of benthic invertebrates (especially Diptera larvae) was higher in winter. Although the diets of both species were less diverse in winter than in summer, they were similar (did not differ significantly) in both seasons. Terrestrial Coleoptera, Araneae and Diplopoda, and aquatic Isopoda, Amphipoda, and larvae of Trichoptera and Coleoptera were the most frequently eaten prey by NF in both seasons. SM hunted only on terrestrial prey and Araneae, Coleoptera, Isopoda, Acari, and Diplopoda were most frequently eaten in both seasons. In NF the frequency of Diptera larvae and Diplopoda as well as the share of aquatic prey increased in winter diet, reflecting the higher availability of these prey types in this season. The higher share of Araneae, Isopoda and Diplopoda in the winter diet of SM can be similarly explained. Thus, it cannot be excluded that the availability of prey eaten by NF and SM is so high in winter that they are not forced to a great reduction of their body size.

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY

ACOUSTIC SIGNALS ACCOMPANYING DIRECT CONTACT IN TWO RODENT SPECIES: THE BANK AND THE ROOT VOLES

Alek Rachwald¹, Andrzej Kołaczyński², Zbigniew Borowski¹

¹Forest Research Institute

²Warsaw University of Life Sciences

The aim was to study the signals emitted by two rodent species the bank (*M. glareolus*) and the root (*M. oeconomus*) voles in situations of interspecimen contact in controlled conditions. To achieve this goal, contacts were arranged in male-male, female-female and male-female pairs for each of the studied species. There was always only one pair of animals in the room, and a single exposure lasted 30 minutes. Animal responses were recorded using cameras with the Noldus Media Recorder software and recorded on a full-range acoustic recorder and analyzed with BatSound Pro software. In total, 46 bank and 59 root voles were tested in the study. We recorded a total of 4261 root vole signals and 4006 bank vole signals. We observed three types of interactions accompanied by acoustic activity: contact with aggression, contact without aggression and vocalization without direct contact. In the case of both studied species, the largest share of aggressive contacts concerned two males. (max. 40% of contacts male-male for root voles), while the lowest level of aggression was observed for a male-female pair (min. 0% of aggressive contacts male-female for bank voles). The number of emitted signals averaged: root vole 170.4 signals/30 min, bank vole 174.2 signals/30 min. As a result of the research, we have shown that both tested vole species regularly use acoustic signals in intra-specific communication. Acoustic contacts in all tested situations took place only in the audible band (the strongest signal component did not go beyond the acoustic band). In the case of the root vole, aggression signal was emitted at a frequency of 7.0 kHz (min-max: 1.1-13.4 kHz), while of the bank vole it was 6.3 kHz (min-max: 1-13,6 kHz). The ultrasonic components of the signals had much lower intensity.

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY

LOOKING AFTER ENERGY BUDGET: RANGING BEHAVIOUR AND HABITAT USE OF THE DESERT HEDGEHOG

Carly Pettett¹, Afra Al-Hajri², Hayat Al-Jabiry², David Macdonald³, Nobuyuki Yamaguchi²

¹WildCRU, Department of Zoology, Oxford University

²Department of Biological and Environmental Sciences, Qatar University

³WildCRU, Department of Zoology, Oxford University

We investigated seasonal changes in the ecology and behaviour of the desert hedgehog (*Paraechinus aethiopicus*) in Qatar, particularly in respect to differences in behaviour between hedgehogs living in arid environments and hedgehogs in temperate mesic environments. We radio-tracked 30 hedgehogs in Qatar over two years, and measured home range size, habitat preference, travel speed, activity and body mass. Whilst we found no difference in body mass between males and females, male home range size was over twice as large as that for females. Unlike hedgehogs in Europe, males maintained large home ranges during the non-breeding season. This behaviour may be sustained by the low cost of maintaining a large home range; males travelled less far per hour during the non-breeding season. Habitat use was non-random; arid areas with human influence, including rubbish dumping sites, was the most selected habitat type compared with its availability. Dense scrub and/or trees was the most selected habitat for nesting. This study gives us greater understanding as to how hedgehog taxa are adapted to their environment and therefore how they may be conserved, for example, the recent increase of "lower" level human activities, including irrigated farms and food waste, in harsh arid environments may have influenced the space use by Ethiopian hedgehogs.

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY

DOES ANIMAL PERSONALITY AFFECT MOVEMENT IN HABITAT CORRIDORS? EXPERIMENTS WITH COMMON VOLES (*Microtus arvalis*) USING DIFFERENT CORRIDOR WIDTHS

Gabriele Joanna Kowalski¹, Volker Grimm², Antje Herde³, Anja Guenther⁴, Jana A. Eccard⁵

¹*Animal Ecology, Institute of Biochemistry and Biology, University of Potsdam*

²*Department of Ecological Modelling, Helmholtz Centre for Environmental Research-UFZ and Plant Ecology and Nature Conservation, University of Potsdam*

³*Department of Animal Behaviour, Bielefeld University*

⁴*Department of Evolutionary Biology, Bielefeld University and Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Biology*

⁵*Animal Ecology, Institute of Biochemistry and Biology, University of Potsdam and Ecological Research Station Gülpe, University of Potsdam*

Corridors through fragmented landscapes are critical for the exchange of individuals and genes between populations in fragmented landscapes. The functionality of corridors may be influenced by habitat characteristics and animal personality. We investigated the mobility of translocated common voles in two corridor systems 60 m in length and differing in width (1 m and 3 m). Voles' personality was phenotyped in repeated open field and barrier tests. Observed behavioural traits were highly repeatable and described by a continuous personality score. Subsequently, animals were tracked via an automated very high frequency (VHF) telemetry radio tracking system to monitor their movement patterns in both corridor systems. Although personality did not explain movement patterns, corridor width determined the amount of time spent in the habitat corridor. Voles in the narrow corridor system entered the corridor faster and spent less time in the corridor than animals in the wide corridor. Thus, landscape features seem to affect movement patterns more strongly than personality. Meanwhile, site characteristics, such as corridor width, could prove to be highly important when designing corridors for conservation, with narrow corridors facilitating faster movement through landscapes than wider corridors.

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY

DO COMMON SHREWS *Sorex araneus* (SORICIDAE) OF NOVOSIBIRSK AND TOMSK CHROMOSOMAL RACES DIFFER IN BEHAVIOURAL SYNDROMES?

Leszek Rychlik¹, Boris Sheftel², Philipp Tumasian³

¹Department of Systematic Zoology, Institute of Environmental Biology, Faculty of Biology, Adam Mickiewicz University, Poznań

²A.N. Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences, Moscow, Russia

³Moscow Zoo, B. Grusinskaya 1, Moscow, Russia

We tested if common shrews of the Novosibirsk and Tomsk chromosomal races [below denoted by NOV and TOM] differ in terms of boldness, exploratory behaviour and aggressiveness. We used 14 NOV shrews (from left side of the Yenisei River near Mirnoye) and 13 TOM shrews (from left side) in an experiment comprised of 3 tests. In the boldness test, we measured the latency to leave a box by a shrew to an empty terrarium. In the exploration test (lasting 5 min), a shrew explored the empty terrarium and we noted its horizontal (crosses of lines dividing floor into 4 rectangles) and vertical locomotion (jumps). In the aggression test (15 s), the experimenter held a shrew by its tail in the centre of terrarium and counted the numbers of bites, squeaks and struggles. All tests were usually conducted 1 day after shrew capture (trial T1) and repeated 3 days later (T2). The data analyzed with linear mixed models showed that the races had not significant influence on latency, crosses and bites. However, latency time was moderately influenced by sex of shrews (females left the box quicker than males); number of crosses was influenced by body mass (heavy shrews moved less than light shrews) and by trial (shrews moved more in T1 than T2); number of bites was also influenced by trial (shrews bit more in T2 than T1). Within 6 analysed behaviours, there were more significant correlations between results obtained in T1 and T2 in TOM than NOV (4 vs 2). Among 35 correlations between different behaviours, there were significantly more meaningful correlations in TOM than NOV (12 vs 3). This suggests that behavioural syndromes were displayed by TOM rather than NOV shrews, but more animals of both races should be tested. Different ecological factors influencing shrew behaviour will be discussed.

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY

SYNCHRONIZATION OF RODENT REPRODUCTION AND TREE FRUCTIFICATION IN OAK COMMUNITIES

Victoria A. Vekhnik¹, Vladimir P. Vekhnik¹, Olga A. Rozentsvet², Elena S. Bogdanova²

¹*I.I. Sпрыgin Zhiguli State Nature Biosphere Reserve, Samara Oblast, Russia*

²*Institute of Ecology of the Volga River basin of RAS, Samara oblast, Russia*

Some species of mammals can reproduce in anticipation of future food abundance: in the case of anticipatory reproduction they give birth to juveniles before the actual yield due to environmental cues, in others, the anticipation is based on abiotic factors. Since 2003 we have studied the reproduction of the edible dormouse *Glis glis*, an example of an animal with anticipatory reproduction. In 2017–2019 we conducted comparative research of the reproduction of a background species, the yellow-necked mouse *Apodemus flavicollis*. In dormice, mating and pregnancy are observed every year. In the years of a shortage of acorns mass resorption occurs: the overwhelming majority of females resorb all embryos. In consequence juveniles usually are born only once every 2–3 years. In mice, the sexual activity of males has the main role in the regulation of reproduction. During the maturation of acorns the share of active males decreases as well as the share of females in oestrus. In poor mast years oestrous females prevail, and the sexual activity of males is negligible. Thus, mating of dormice begins long before and in mice at the beginning of the growth of acorns. In both cases, by the time the acorns are ripe, the juveniles become independent. Instead of any prediction, anticipatory reproduction consists of feeding on immature seeds during pregnancy and lactation, eliminating a delay between forage yield and rodent reproduction. A possible reason for this synchronization is the content of the diet. During the maturation of acorns, the proportion of triacylglycerols, the main constituents of body fat increases considerably. A decrease in the content of sterols can contribute to the lower reproductive activity of males. This study was funded by RFBR and Samara Oblast, project № 17-44-630288.

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY

CAN WE GET ALONG? THE ROLE OF COMPETITIVE INTERACTIONS AND FOREST MANAGEMENT IN SHAPING A GUILD OF TERRESTRIAL RODENTS

Stefania Gasperini¹, Alessio Mortelliti², Paola Bartolommei¹, Cristina Bencini¹, Andrea Bonacchi³, Carlo Cinque¹, Emiliano Manzo¹, Roberto Cozzolino¹

¹Fondazione Ethoikos

²Department of Wildlife, Fisheries, and Conservation Biology, University of Maine

³Fondazione Ethoikos/U.R. Ecologia comportamentale, Etologia e Gestione della fauna, Dipartimento di Scienze della Vita, Università degli Studi di Siena

By modifying natural habitats, humans are altering the mechanisms facilitating coexistence among species. Consequently, evaluating influences of anthropogenic activities on interspecific dynamics is a priority for field ecologists. In a fully replicated field experiment we explored the role of competition in shaping rodent communities inhabiting forest areas subject to different silvicultural practices. We surveyed populations of *Apodemus flavicollis*, *A. sylvaticus* and *Myodes glareolus* in the 12 woodland sites every other month for 3 years using a capture-mark-recapture protocol. We modelled the response of vital rates parameters (scaled mass index, survival and population density) to competitors' density and to resource variables (acorn biomass, fruit biomass and percentage of shrub cover). No significant negative effects of inter-specific competition on population density were found for all species. Survival and body mass of *A. flavicollis* were negatively influenced by the density of *M. glareolus* and *A. sylvaticus*. Conversely, the density of *A. flavicollis* had negative effects on the survival of the other two species. Trophic resources more strongly affected the vital rates of the species. Specifically, density of *A. flavicollis* was negatively influenced by high fruit production, whereas its survival and body mass were positively affected by shrub cover. Fruit resources had a strong positive effect on *A. sylvaticus*. Finally, *M. glareolus* density was positively influenced by high acorn biomass. Our findings show that trophic resources rather than interspecific competition are the major force shaping the studied communities, suggesting that habitat segregation and niche partitioning among species might facilitate the species' coexistence in managed forests.

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY

EFFECTS OF A SIMULATED SEASONAL DIETARY SHIFT ON THE WOOD MOUSE GUT MICROBIOTA; FROM THE LAB TO THE WILD

Kirsty Marsh¹, Aura Raulo², Sarah Knowles²

¹Royal Veterinary College

²Oxford University

Over the last few decades, the gut microbiota (the community of microbes residing in the gastrointestinal tract) of mammalian hosts has emerged as an important influence on host health and disease. Many studies of humans and lab animals have shown that diet is a strong determinant of the composition and function of the gut microbiota. More recently, studies of wild hosts have emerged demonstrating the natural temporal variability of the gut microbiota and have pointed towards seasonal dietary variation as the main driver, however few studies have tested this hypothesis. For instance, the gut microbiota of wood mice (*Apodemus sylvaticus*) has been shown to undergo marked seasonal restructuring between summer and autumn, thought to be driven by shifts between insect- and seed-based diets. We pair a controlled diet shift experiment in captive wood mice with data from a wild population, to test the role of dietary shifts in driving seasonal restructuring of the microbiota. Using multivariate analyses, bacterial taxa responding most strongly to the experimental diets were identified and the hypothetical seed:insect ratio of wild samples was predicted by comparing the community structure to that of the experimental samples. We show that changes in the relative abundance of diet-associated bacteria and the predicted seed:insect ratio significantly coincides with the major seasonal restructuring of the wild wood mouse gut microbiota from July to October. These findings support the hypothesis that natural fluctuations in gut community structure are driven by seasonal changes in food availability of the host. Understanding the ecology of host-associated communities in a natural setting will enable a better understanding of the importance of these communities for host health.

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY

TROPHIC NICHE PARTITIONING AND DIETARY COMPETITION IN SMALL RODENTS, MEASURED USING STABLE ISOTOPES

Piotr Chibowski¹, Marcin Brzeziński¹, Małgorzata Suska-Malawska¹

¹Faculty of Biology, University of Warsaw

We captured small rodents in four types of forest environments: wet alder forest, coniferous forest and two types of deciduous forests: with and without artificially planted pine during spring and autumn of two consecutive years. We caught 510 individuals and measured the carbon and nitrogen isotopic composition in the hair of three dominating species: bank vole (152 individuals), yellow-necked mouse (290) and field mouse (33). Stable isotopes were also measured in main food sources of those species: ground herbs, seeds, invertebrates and other. We found no differences in diet composition between males and females and between juvenile and adult individuals within a species. In several sites and all species, we found a visible decrease in trophic niche size between autumn 2017 and 2018, despite slightly higher rodent numbers in the latter year. The second autumn was also the year with smaller niche overlap between yellow-necked mice and bank voles. In general, yellow-necked mice had wider isotopic niches. Based on the isotopic composition of food sources we assume this is due to a relative high proportion of invertebrates in their diet. Field mice were caught mainly in alder forest and had very diverse isotopic signatures suggesting, that those were migrating individuals from different environments. There is an increase in $\delta^{13}\text{C}$ values of herbs between autumn and spring of about 2 ‰ in all study sites, which has not been found in rodent hair. Some differences in isotopic niche, based on raw data, faded and some appeared after applying accurate values of trophic discrimination, which we measured during a dietary experiment on bank voles and yellow-necked mice.

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY

THINK BEFORE YOU SPEAK! USING THERMAL IMAGING FOR DETECTING INTENTION AND PREPARATION TO VOCALIZE

Vlad Demartsev¹, Glenn Tattersall², Ariana Strandburg-Peshkin¹, Marta Manser³

¹University of Konstanz

²Brock University

³University of Zurich

Acoustic signals play a role in numerous aspects of animals' lives and are extensively studied across multiple taxa on structural, combinatorial and functional levels. However, the signal production phase is the terminal stage of a signalling event. Preceding the audible vocalization, there is stimulus processing, decision making and preparation for sound production. These often non-detectable stages are integral to the dynamics of signalling, as any of them might result in a vocalization not being produced. Monitoring the stages preceding vocal production will allow us to answer questions related to signal planning and the dynamics of signalling motivation. One way to assess the intention to vocalize is by looking at the preparation of articulators. In human conversations, the next speaker identity is predicted by changes in breathing, with participants motivated to speak next taking deeper breaths. Additionally deeper inhales were associated with longer sub-sequential speaking, indicating early planning of a conversational turn. We examine if similar phenomena exist in vocal interactions of wild meerkats (*Suricata suricatta*). For working with free-ranging animals we are developing a noninvasive procedure, using thermal imaging for breathing depth and rate detection, as expiration and inspiration are associated with surface temperature changes in the animals' nasal region. Synchronization of breathing curves with audio recordings can expose stereotypic breathing patterns, preceding vocalization events. Detection of preparation for calling might indicate to what extent animals plan the timing and duration of their vocal bouts and potentially show if external stimuli can negatively affect calling motivation, suppressing the planned vocalization.

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY

ACTIVITY PATTERNS AND THERMOREGULATION IN MALE PARTI-COLOURED BATS *Vespertilio murinus*

Zuzanna Hałat¹, Marcin Zegarek¹, Ireneusz Ruczyński¹

¹Mammal Research Institute, Polish Academy of Sciences, Białowieża, Poland

Flight is an expensive mode of locomotion, therefore maintaining positive energy balance can be challenging for small insectivorous bats, especially during a period of insect scarcity or increased energy expenditures. In males higher energy intake is required during spermatogenesis and growth of the testes. Bats can increase foraging effort in order to consume more energy or reduce metabolic rate to decrease the energy expenditure. Our aim was to find out what are the foraging and thermoregulatory strategies when males stay in summer aggregations and after they leave. We conducted our study in the village of Białowieża in 2017–2018. We captured bats using harp traps and radio-tracked them with the temperature sensing transmitters. We obtained data from 65 bat-days and conducted emergence counts from the known roosts during 56 evenings. Our results indicate that males were foraging longer when insect abundance was higher and when they were solitary. Higher heterothermy index was observed when insect abundance was lower and in the beginning of June. Nights with higher prey availability provided bats with possibility of higher caloric intake and allowed to balance the cost of flight, so they did not need to enter torpor the day after. Increased efficiency of foraging with roost mates allowed for shorter foraging periods. Bats used less torpor in July, what could be caused by higher ambient temperature. Higher number of bats was observed in roosts, when insect abundance was lower, what can indicate that social warming also plays the role in maintaining positive energy balance. This work was funded by the Polish National Science Centre on the basis of decision number DEC-2013/10/E/NZ8/00725.

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY

THE IMPORTANCE OF MULTI-SPECIES BAT ROOSTS: HOST-PARASITE RELATIONSHIPS BETWEEN BATS AND BAT FLIES OF SOUTH-EASTERN EUROPE

Áron Péter¹, Levente Barti², István Csósz², Alexandra Corduneanu³, Mihály Földvári⁴, Gábor Földvári⁵, Sándor Hornok⁶, Andrei D. Mihalca³, Attila D. Sándor³

¹University of Agricultural Sciences and Veterinary Medicine of Cluj-Napoca, Faculty of Veterinary Medicine, Department of Parasitology and Parasitic Diseases

²Romanian Bat Protection Association, Central Branch, Odorheiu-Secuiesc

³University of Agricultural Sciences and Veterinary Medicine of Cluj-Napoca, Faculty of Veterinary Medicine, Department of Parasitology and Parasitic Diseases

⁴Natural History Museum, University of Oslo, Oslo

⁵Department of Parasitology and Zoology, University of Veterinary Medicine, Budapest; Evolutionary Systems Research Group, Centre for Ecological Research, Hungarian Academy of Sciences, Tihany, Hungary

⁶Department of Parasitology and Zoology, University of Veterinary Medicine, Budapest

Bat flies are strongly connected to their hosts and often they are the most abundant parasites on bats. They show a strong specialization in the parasitic life style to exploit the bats with their morphological or behavioral adaptations. The European species are described as having high host specificity, often exploiting just one or a few related species as hosts. Bat flies have been confirmed to be vectors for Bartonella or Hemosporidia species. From epidemiological point of view, it is important to evaluate the vector potential of bat fly species. Our aim in this study was to characterize the bat fly species by their level of specificity and assess information on this host-parasite relationship. We collected more than 2200 bat flies (9 species) from the South-East European region and studied their seasonality and host specificity. A total of 2801 individual bats (13 out of 28 species had flies, prevalence 36%) were screened. We found four fly species to be highly host specific, with the other four species having more than one main host. We conclude that the level of infestation shows an increasing trend from spring to autumn and the level of specificity of most bat fly species is lower in autumn. In contrast, occurrences of bat flies on secondary hosts was higher in spring, due to lack of multi-species host assemblages in roosts. The level of infestation, season and the local host species composition all have effect on the level of host specificity of bat flies.

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY

ADAPTIVE DIFFERENCES IN HOST SELECTION AND SEASONALITY OF BAT-SPECIALIST TICKS IN EUROPE

Attila D. Sándor¹, Alexandra Corduneanu¹, Áron Péter¹, Andrei Daniel Mihalca¹, Levente Barti², István Csósz², Krisztina Szőke³, Sándor Hornok³

¹University of Agricultural Sciences and Veterinary Medicine of Cluj-Napoca, Romania

²Myotis Bat Conservation Group, Miercurea Ciuc, Romania

³Department of Parasitology and Zoology, University of Veterinary Medicine, Budapest, Hungary

To exploit most effectively their host resources, parasites are in constant race to counterbalance and overcome their host's defense mechanisms. They use a number of adaptive strategies to increase their reproductive success and transmission, like host specificity and seasonality in occurrences (synchronizing their reproduction to the hosts' life cycle, etc.). European bat species are host for three specialist hard- and two soft ticks. Here we report details on host range and seasonality of infestation of these ticks on wild caught bats in South-east Europe. We collected ticks from bats (30 species) living in underground shelters (caves and mines) from Romania and Bulgaria. Using tick-host relationships we tested several hypotheses on host-parasite evolutionary adaptations regulating host-specificity, seasonality and sympatric speciation. We observed significant differences between host specificity and the seasonality of abundance between the morphologically different bat specialist ticks (*I. simplex* and *I. vespertilionis*) likely caused by their host specificity and their respective host seeking behavior. The two highly generalist, but morphologically similar tick species (*I. ariadnae* and *I. vespertilionis*) showed temporal differences in occurrence and activity, thus exploiting significantly different host communities while occurring in geographical sympatry. We conclude that bat-specialist ticks show a wide range of adaptations to their hosts, with differences in specificity, seasonality of occurrence, the prevalence and intensity of infestation and all these contribute to a successful division of temporal niches of ticks sharing morphologically similar hosts occurring in geographic sympatry.

PALEOGENETICS

MIDDLE PLEISTOCENE GENOME CALIBRATES THE EVOLUTIONARY HISTORY OF CAVE BEARS

Axel Barlow, Johanna L. A. Paijmans, Federica Alberti, Boris Gasparian, Guy Bar-Oz, Ron Pinhasi, Elena Belyaeva, Irina Foronova, Martina Pacher, Love Dalén, Gennady Baryshnikov, Michael Hofreiter

Palaeogenomics provides an opportunity to directly study the genetic processes underpinning key events in mammalian evolution. However, outside of permafrost, the current time-depth for palaeogenome retrieval is the Late Pleistocene, representing only a small fraction of the total evolutionary histories of many mammalian clades. We present a ~1x palaeogenome from a 367,000 year old Middle Pleistocene cave bear from Kudaro 1 cave in the Caucasus Mountains. Analysis of Middle and Late Pleistocene cave bear genomes reveal multiple instances of mito-nuclear discordance, suggesting that their mitochondrial relationships have been shaped to a large extent by incomplete lineage sorting and/or maternal gene flow. Using the temporal separation of the Kudaro 1 genome from its Late Pleistocene relatives, we directly estimate the ursine bear genome substitution rate and apply this to our revised nuclear phylogeny. This reveals a key period in Holarctic bear evolution around 1 million years ago associated with the divergence of the major cave bear lineages, the divergence of brown bears and polar bears, and, shortly after, the end of gene flow between cave bears and brown bears. This period coincides with the Middle Pleistocene Transition when glacial cycles shifted from a ~40 to a ~100 thousand year periodicity with extended glacial periods and more abrupt and intense interglacials. Most importantly, with an age encompassing an estimated 23% of the total evolutionary history of cave bears, the Kudaro 1 genome extends the time-depth for palaeogenome sequencing of non-permafrost mammals well into the Middle Pleistocene.

PALEOGENETICS

DIVERSE RESPONSES OF COMMON VOLE (*Microtus arvalis*) POPULATIONS TO LATE GLACIAL AND EARLY HOLOCENE CLIMATE CHANGES – EVIDENCE FROM ANCIENT DNA

Mateusz Baca, Danijela Popović, Katarzyna Baca, Anna Lemanik, Karolina Doan, Ivan Horáček, Juan Manuel López-García, Sandra Bañuls-Cardona, Piroska Pazonyi, Emmanuel Desclaux, Evelyne Crégut-Bonnoure, Claudio Berto, Jadranka Mauch Lenardić, Barbara Miękina, Xabier Murelaga, Gloria Cuenca-Bescós, Magdalena Krajcarz, Zoran Marković, Alexandru Petculescu, Jarosław Wilczyński, Monika Vlasta Knul, John R. Stewart, Adam Nadachowski

The abrupt climate changes during the Late Glacial and the Pleistocene to Holocene transition deeply transformed the terrestrial ecosystems and was the cause of major faunal reorganisations. Here we used ancient DNA to investigate the impact of those changes on common vole (*Microtus arvalis*) populations in Europe. Common vole is a temperate rodent species widespread in Europe. Genetic diversity of its contemporary populations and fossil record suggests that it may have survived cold episodes, like Last Glacial Maximum, not only in traditional Mediterranean glacial refugia, but also at higher latitudes in so-called cryptic northern refugia. However, the impact of Late Glacial climate changes on the evolutionary history of the common vole remains unclear. To address this issue, we analysed mtDNA cytochrome b sequences from more than a hundred common vole specimens from 30 paleontological and archaeological sites scattered across Europe. Our data suggests that populations from the European mid- and high latitudes suffered a local population extinctions and retractions as a result of end-glacial and Early Holocene climate changes. The recolonization of earlier abandoned areas took place in Middle to Late Holocene. In contrast at low latitudes in Northern Spain we observed a continuity of vole population. This indicates different responses of common vole populations to end-glacial climate and environmental changes across Europe and corroborate the hypothesis that abrupt changes, like those associated with YD and the Pleistocene to Holocene transition had significant impact on populations at mid and high latitudes of Europe.

PALEOGENETICS

HIGHLY DIVERGENT POPULATION OF NARROW-HEADED VOLE FROM THE LATE PLEISTOCENE EUROPE

Mateusz Baca¹, Danijela Popović¹, Anna Lemanik², Katarzyna Baca¹, Ivan Horáček³, Adam Nadachowski²

¹Centre of New Technologies, University of Warsaw

²Institute of Systematics and Evolution of Animals, Polish Academy of Sciences

³Department of Zoology, Charles University

During the Late Pleistocene, narrow-headed voles (*Lasiopodomys gregalis*) inhabited Eurasia's vast territories, frequently becoming the dominant small mammal species among steppe-tundra communities. We investigated the relationship between this species' European and Asiatic populations by sequencing the mtDNA genomes of two extant specimens from Russia and 10 individuals from five Central European sites, dated to the post-LGM period. Phylogenetic analyses based on a large portion of mtDNA genomes highly supported the positioning of *L. gregalis* within Arvicolinae. Intraspecific phylogeny revealed a deep divergence of European narrow-headed voles from Asiatic ones and their sister position against the modern *L. gregalis* and *L. raddei*. The divergence was estimated to a minimum 230 thousand years ago. This suggests, contrary to current biogeographic hypotheses, that during the interstadial periods narrow-headed vole did not retreat to the east but survived the unfavourable conditions within the refugial areas in Europe. Based on this result, we propose the establishment of a species status for the Late Pleistocene European narrow-headed vole. This study was supported by Polish National Science Centre grants no. 2015/19/D/NZ8/03878 to M.B and 2017/25/B/NZ8/02005 to A.N.

PALEOGENETICS

NEOLITHIC REVOLUTION TRIGGERED DEMOGRAPHIC EXPANSION OF AN AFRICAN OPPORTUNISTIC CARNIVORE

Rita Rocha¹, Ahmed Eddine², Noureddine Mostefai², Yamna Karsene³, Koen De Smet⁴, José Carlos Brito¹, Dick Klees⁴, Casten Nowak⁵, Bernardino Cocchiararo⁵, Susana Lopes¹, Peter Van Der Leer⁴, Raquel Godinho¹

¹*CIBIO/InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto*

²*Laboratory of water conservatory management soil and forest, Faculty of Sciences of nature and life, University of Tlemcen*

³*Laboratory of livestock and wildlife, Arid land Institute of Medenine*

⁴*Society of North African Big Carnivores Stichting*

⁵*Senckenberg Research Institute and Natural History Museum Frankfurt*

The diffusion of Neolithic technology together with the Holocene Climatic Optimum fostered the spread of human settlements and pastoral activities in North Africa, resulting in profound and enduring consequences for the dynamics of species, communities and landscapes. A variety of opportunities particularly related to food availability, makes human-dominated areas an attractive habitat for opportunistic carnivores. It is thus expected that the Neolithic human population growth had a positive impact on opportunistic wild carnivores that show a propensity for living in cultural landscapes. We investigate the demographic history of the Northwestern African wolf population to understand if demographic trends of this generalist and opportunistic carnivore reflect the increase in availability of food and other human-related opportunities that have emerged after the arrival of the Neolithic economy in North Africa. Using both nuclear and mitochondrial molecular markers, we found consistent evidence supporting our hypothesis that the Northwestern African wolf population experienced a meaningful expansion concurring with a period of rapid population expansion of cattle and other domesticates linked to the advent of agricultural practices during the Neolithic revolution. Although signatures of human-driven demographic processes are well reported in the literature, there is little evidence of historical favourable co-existence of post-Neolithic humans and wild mammals in Africa. We provide evidence of population expansion of an opportunistic species during the Neolithic human revolution, which is possibly related to the increase of human-related resources, such as food availability. Surprisingly, this idea has been little explored.

MAMMALS IN ANTHROPOGENIC LANDSCAPE

CARNIVORES IN ANTHROPOGENIC LANDSCAPES

Duško Ćirović

Faculty of Biology, University of Belgrade

During the last century and at the beginning of this century humans induced rapid environmental changes. In order to provide enough resources they transformed landscapes with natural ecosystems into human-dominated landscapes where people strongly influenced biological processes through urban ecosystems. Inside this new created human-dominated matrix, natural habitats are present only in the form of more-or-less isolated patches and linear structures, mostly along rivers. These serious structural changes in land cover had a particularly strong influence on carnivore species due to their high trophic position in the ecosystems. These changes affect the key aspects of their ecology. Depending of species plasticity and adaptability the ranges, population numbers and densities of some carnivores increased, but on the other hands others decreased. Inside the newly created human-dominated landscapes, generalists have advantages in comparison to specialists as they are capable to use numerous easily-available anthropogenic resources, and in the course of time these carnivore species developed resilience to human disturbance within the altered landscapes. Opportunistic feeding strategies allow them to use rodents from croplands, animal leftovers at local landfills and trash cans, and pets' food as main food sources. These changes in their feeding ecology allow some carnivore species to provide important ecosystem services within the human-dominated landscapes. Potential ecological disservices have been recognized, mostly in form of health risks for human population and domestic animals. Spatial changes also affect genetic structure of carnivore populations, with potential implication on their evolution and habitat use, as well as behavior of carnivore species within the human-dominated landscapes.

MAMMALS IN ANTHROPOGENIC LANDSCAPE

RESISTANCE MODELLING INFERS PHYSICAL AND BEHAVIOURAL GENE FLOW BARRIERS TO THE RED FOX (*Vulpes vulpes*) ACROSS THE BERLIN METROPOLITAN AREA

Alain Frantz¹, Sophia Kimmig²

¹Musée National d'Histoire Naturelle, Luxembourg

²Leibniz Institute for Zoo and Wildlife Research, Berlin

Urbanization affects key aspects of wildlife ecology. Dispersal in urban species may, for example, be impacted by geographical barriers but also by a species' inherent behavioural variability. There are, however, no functional connectivity analyses resting on continuous individual-based sampling across a rural-urban continuum that would allow a thorough assessment of the relative importance of physical and behavioural dispersal barriers. We used 16 microsatellite loci to genotype 374 red foxes from the city of Berlin and surrounding rural regions in order to study genetic structure and dispersal behaviour of a mobile carnivore across the urban-rural landscape. We assessed the functional connectivity of our study area applying an individual-based landscape genetic optimization procedure. Three commonly used genetic distance measures yielded different model selection results, with only the results of an eigenvector-based multivariate analysis reasonably explaining genetic differentiation patterns. Genetic clustering methods and landscape resistance modelling supported the presence of an urban population with limited dispersal across the city border. Artificial structures (railways, motorways) served as main dispersal corridors within the cityscape, yet urban foxes avoided densely built-up areas. We show that despite their ubiquitous presence in urban areas, their mobility and behavioural plasticity, foxes were affected in their dispersal by anthropogenic presence. A distinction of man-made structures and sites of actual human activity, rather than natural versus artificial structures, is thus essential to understand urban fox dispersal and perhaps that of other urban wildlife to predict how behaviour can shape population genetic structure beyond physical impacts.

MAMMALS IN ANTHROPOGENIC LANDSCAPE

RED FOX POPULATION DYNAMICS IN HABITATS OF DIFFERENT ANTHROPOPRESSION LEVELS

Dagny Krauze-Gryz¹, Jakub Gryz², Karolina Jasińska¹, Mateusz Jackowiak¹

¹Warsaw University of Life Sciences, Faculty of Forestry

²Foreset Research Institute

Red fox (*Vulpes vulpes*) has a very wide range and being highly adaptive can live in different habitats, including highly transformed areas like city centres and industrial areas. Its population dynamic depend on prey availability but is also driven by disease outbreaks. In Poland rabies used to be the factor that limited red fox population. Nowadays, thanks to general program of anti-rabies vaccination, the disease occurs in the population only occasionally. In our study we compared changes in population density in three areas in Poland, which were subject to various levels of anthropogenic changes. Those were: Białowieża Primeval Forest (vast forest complex, high level of naturalness, presence of big predators), Rogów Forest District (field and forest mosaic, small forest complexes, no big predators), and Warsaw (the biggest city in Poland, ca. 2 million inhabitants). In all three areas snow tracking on transects was used to assess population density. We compared our data with this available for the last decades. We found out that in all three areas, population of red fox increased significantly. It was highest in field and forest mosaic. With no big predators to limit the population it reach the level of 1.8 ind./100 ha in winter. Nevertheless, when compared to densities recorded in the 1980s, the highest increase was seen in Warsaw. Here, in the past red foxes were rarely recorded while nowadays they occur in the whole city. Highest densities were recorded in natural areas of Warsaw (i.e. forests and rural areas) but no in typical urban habitats. This suggest that this population will develop in the nearest future. Overall, we showed that population increase was higher in areas subject to anthropogenic transformation.

MAMMALS IN ANTHROPOGENIC LANDSCAPE

HOW DOES ANTHROPOGENIC NOISE IMPACT THE BEHAVIOUR OF A KEYSTONE SPECIES?

Graeme Shannon¹, Lisa Angeloni², Kevin Crooks², Megan McKenna³, Kurt Fristrup³, George Wittemyer²

¹Bangor University

²Colorado State University

³National Park Service

Research on the impacts of anthropogenic noise has grown rapidly over the past two decades – documenting a diverse range of biological responses from shifts in individual behaviour to structural change in ecological communities. However, there have been only a limited number of studies examining the impacts of noise on free-ranging terrestrial mammals, with research predominantly focusing on songbirds, marine mammals and fish. Using playback experiments and a gradient of urban noise across our study sites, we investigated the effects of anthropogenic noise on the foraging, and anti-predator behaviour of a keystone species in North American prairie systems, the prairie dog (*Cynomys ludovicianus*). By conducting multiple experiments, we also aimed to explore the specific mechanism(s) driving the observed behavioural responses. Exposure to road noise significantly lowered aboveground activity, reduced foraging and increased vigilance. However, unlike a number of marine species, prairie dogs were not distracted by road noise and detected an approaching human “predator” at greater distances and took flight more rapidly during noisy periods than quieter control periods. Furthermore, prairie dogs did not adjust the acoustic characteristics of their alarm calls in noisy environments – a commonly documented response in urban birds. Anthropogenic noise has the potential to drive a range of behavioural and physiological responses across taxa, but elucidating the specific mechanisms driving these responses can be challenging. Our research now sheds light on how prairie dogs appears to respond to noise predominantly as a source of increased risk, rather than as a distraction or through acoustical masking as shown in other commonly studied species.

MAMMALS IN ANTHROPOGENIC LANDSCAPE

EVALUATION OF HUMAN INFLUENCE ON THE ACTIVITY OF MEDIUM – LARGE MAMMALS IN MYANMAR FORESTS

Giacomo Cremonesi¹, Francesco Bisi¹, Lorenzo Gaffi², Alessandra Gagliardi², Lucas Armand Wauters¹, Damiano Giovanni Preatoni¹, Adriano Martinoli¹

¹Environment Analysis and Management Unit, Guido Tosi Research Group, Department of Theoretical and Applied Sciences, University of Insubria

²Istituto OIKOS Italia

Human presence can influence wildlife, and in particular mammal communities, driving animals to change their behaviour to avoid, or reduce, direct contact with humans by minimizing spatio/temporal overlap and increasing niche segregation. With the increase of human activity, Myanmar forests represent a strongly altered habitat, indeed in the last decades a very high deforestation rate has been reported as well as illegal hunting. In our study we used data from camera traps positioned in two different regions of Myanmar: Rakhine, near the Rakhine Yoma Elephant Range Wildlife Reserve, and Sagaing, inside the Htamathi Wildlife Sanctuary. Within the two study areas, 8 survey sites were selected (4 per each area) and a camera trapping scheme was set up with 30 camera traps for each site, activated for a minimum of 45 days during the dry season. Each site was then classified as “high” or “low” level of anthropic disturbance, based on human signatures camera trap capture rates. We tested for possible temporal segregation between wildlife and humans to obtain evidences that animals changed their activity patterns in relation to human presence. Secondly, we investigated the temporal overlap between mammals and humans along the entire camera trap study period. In contrast with our initial hypothesis, that human presence affects animal behaviour, we found that the mammal species monitored during this study seem not to change their daily activity patterns: activity pattern actually do not differ between high and low disturbance areas, and neither wildlife showed avoidance of human presence in time. Probably most of the species in the area already developed a high resilience to human disturbance due to habituation both to human presence and to the altered environment.

MAMMALS IN ANTHROPOGENIC LANDSCAPE

LINKING BIODIVERSITY TO ECOSYSTEM SERVICES: THE SMALL MAMMAL COMMUNITY OF NE PORTUGAL AGROECOSYSTEMS

Joana Paupério¹, João Queirós¹, João Alexandre Cabral², Hélia Vale-Gonçalves¹, António Mira³, Sara M Santos³, Sandra Aresta¹, Paulo Célio Alves⁴, Ricardo Pita³

¹*InBIO/CIBIO-UP, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto*

²*CITAB, Centro de Investigação e Tecnologias Agroambientais e Biológicas, Universidade de Trás-os-Montes e Alto Douro UTAD*

³*Unidade de Biologia da Conservação. Departamento de Biologia, Universidade de Évora*

⁴*Departamento de Biologia, Faculdade de Ciências da Universidade do Porto, Porto, Portugal*

The spread and intensification of agriculture are recognised as important global threats to biodiversity, and thus to the maintenance of ecosystem functions and services. Biological pest management is one of the main ecosystem services often supported by traditional agroecosystems holding high levels of biodiversity. However, there is still limited understanding on how biodiversity levels actually relate with biological control, particularly in the case of small mammal species embedded in diverse communities facing agricultural intensification. Here we present part of the results of an ongoing research project (AGRIVOLE) that aims to unveil the response of small mammal communities to agroecosystem structure and agricultural practices, and to evaluate how such responses may affect either the potential for pest outbreaks or the persistence of species of conservation concern. Based on over 1000 barn owl pellets collected in 35 sites spatially distributed across NE Portugal, and detailed land-cover maps within 1.5 Km buffers centred in each collection site, we analyse the spatial pattern of small mammals' community and its relation to landscape variables describing agroecosystem structure and agriculture intensification. Specifically, we use generalized linear models to test the general hypothesis that lower diversities and higher abundance of potential pests should be associated to more intensive agricultural landscapes. Overall, we expect that our results will provide useful first insights on links between small mammal diversity, and their role in agroecosystems under agricultural intensification, thereby contributing to foster sustainable agricultural management linking pest control to biodiversity conservation.

MAMMALS IN ANTHROPOGENIC LANDSCAPE

BEHAVIOURAL ADJUSTMENTS OF NON-COMMENSAL RODENTS TO URBAN ENVIRONMENTS

Valeria Mazza¹, Melanie Dammhahn¹, Annika Schirmer¹, Claudia Götttsche¹, Jana A. Eccard¹

¹*University of Potsdam*

A fundamental question of current ecological research concerns the drives and limits of species responses to human-induced rapid environmental change (HIREC). Behavioural responses are a key component because behaviour links individual responses to population and community changes. Consistent behavioural differences between conspecifics (animal personality) may be important determinants or constraints of animals' adaptation to urban habitats. Research in the past few years discovered many behavioural adaptations to urban environments. However, this research is heavily biased towards species with high dispersal abilities. Very little is known about the determinants and constraints of successful adaptation to urban environments of species more limited in dispersal. Here, we focused on ground-dwelling rodents, which are often found in urban areas, partly as synanthropic. We tested whether urban and rural populations of small mammals differ in mean trait expression, flexibility and repeatability of behaviours associated to risk-taking and exploration of novel environments. Using a standardized behavioural test in the field, we quantified exploration and boldness of rodents from nine sub-populations, presenting different levels of urbanisation and anthropogenic disturbance. The level of urbanisation positively correlated with boldness, exploration and behavioural flexibility, with urban dwellers being bolder, more explorative and more flexible in some traits than rural conspecifics. Thus, individuals seem to distribute in a non-random way in response to human disturbance based on their behavioural characteristics. Personality might therefore play a key role in the successful coping with the challenges of HIREC.

MAMMALS IN ANTHROPOGENIC LANDSCAPE

DO NATURAL MARGINS OF ARABLE FIELDS SUPPORT SMALL MAMMAL POPULATIONS?

Grete Tõnisalu¹, Ülo Väli¹

¹*Estonian University of Life Sciences*

Biodiversity conservation strategies in agricultural landscape often recommend keeping margins of arable fields in natural conditions. However, effect of such management method has been estimated only in limited number of taxa and quantitative analysis on the optimal width of such „green margins“ are seldom conducted. We analysed the potential effect of such management method on small mammals because they have an important role in ecosystem as herbivores by transferring biomass from plants to predators. They occupy various habitats from deep forests to open landscape. Also, they show various degree of specialism from generalists to specialists of various habitat types. We measured abundance of three rodent species at ecotones between forests and three types of open agricultural biotopes (cereal fields, rapeseed and grassland fields). The maximum density of rodents was found at the forest/grassland ecotone. The positive edge effect did not exceed ten meters. There were highest densities of the Yellow-necked mouse *Apodemus flavicollis* and Striped field mouse *A. agrarius* next to ecotones and *A. agrarius* was also found in open habitats. Yellow necked mouse preferred forests and edge habitats over open habitats. Also the highest density of Bank voles *Myodes glareolus* was recorded next to grasslands, but the abundance of this species increased towards forest interior and they prefer old(er) forests. Summarizing, our results support maintaining narrow grasslands at margins of crop fields. Such management practice would strengthen natural communities at ecotones, but also in adjacent open land and forests.

MAMMALS IN ANTHROPOGENIC LANDSCAPE

COMMUNITY ASSEMBLY RULES OF INSECTIVOROUS BAT SPECIES IN MAN-MADE PLANTATIONS IN ISRAEL

Claudia Allegrini¹, Carmi Korine¹, Boris Krasnov¹

¹Mitrani Department of Desert Ecology, Swiss Institute of Dryland, Environmental and Energy Research, Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev

Pine plantations are characterized by simply-structured coniferous monocultures and are considered as habitats where species richness of birds and bats is low. Our main goals were: 1) to assess species richness and composition of bat communities, and 2) to identify factors driving community assembly in bats in pine plantations, Israel, as it may be crucial for their assessment and conservation. Specifically, we expected a role of environmental filtering shaping these communities. Acoustic sampling was carried out in 35 forest sites of Israel and echolocation calls were analyzed for species identification. Through the ESLTP analysis, an extension of the RLQ approach, occurrences of species were used to find relationships between environmental characteristics and functional traits of species, considering phylogenetic context and spatial distribution of pine plantations. 22 out of the 32 insectivorous bat species found in Israel, use pine plantations as foraging sites. 20 of them are categorized as endangered species. Communities show both phylogenetic and trait clustering, confirming the role of environmental filtering as a mechanism of community assembly in these forests. The ESLTP analysis showed that climatological and environmental characteristics of forests, such as temperature, precipitation, elevation and latitude shape communities of bats in pine plantations in Israel. These results can be used to predict responses of bat species to environmental changes and to disturbances, such as fire, that may occur in natural forests and pine plantations.

GENERAL SESSION

THE ECONOMIC COST OF INVASIVE MAMMALS

Franck Courchamp¹, Christophe Diagne¹, Anne-Charlotte Vaissiere¹, Juliette Baron¹

¹CNRS - Université Paris Sud, France

Biological invasions are a major driver of biodiversity loss and ecosystem dysfunction and have a tremendous societal impact. Among the countless invasive species, mammals have notoriously had some of the largest impacts. However, quantifying these impacts is a major obstacle to convince decision makers of the importance of this major component of global change. Awareness and acknowledgement may have to go through the quantification of impacts with monetary values, as it is often more convincing to decision makers and policymakers than more indirect values such as biodiversity loss. Here, we provide the most comprehensive and robust global-scale data compilation of the monetary costs associated with invasive mammals. We developed an original, standardised methodology to collect information from both peer-reviewed and unpublished literature, while minimizing both publication bias and omission. From a pool of 11,000 publications, we found that the minimum economic costs associated directly and indirectly (including control and research costs) with invasive mammals are in the order of billions of dollars annually worldwide, with Europe incurring the largest costs. We discuss (i) the reasons why these costs are likely to be grossly underestimated and (ii) the mismatch between the important economic cost of IAS and the disproportionately lower concern of management authorities and the general public. By providing the first rigorous global summary of accessible monetized costs of invasive alien mammals, we provide an essential basis for national and international policies in the management of invasive species.

GENERAL SESSION

PARASITOLOGICAL INVESTIGATIONS OF RACCOONS FROM SEVERAL LOCATIONS IN GERMANY AND LUXEMBURG

Natalia Osten-Sacken

Veterinary Center UMK Toruń

Raccoons (*Procyon lotor*) were introduced to several European and Asian countries during the last century. This alien species is particularly abundant and wide spread in Germany and other neighboring countries. Because of their omnivorous life style, raccoons might be exposed to infection with many kinds of parasites. Several studies in many countries proven also frequent infection by *Baylisascaris procyonis*, the specific parasite of this animal. The raising contact with humans and pets, because of growing raccoon population in town and cities, as well handling and gutting as a game species might increase the infection risk for humans. Our study was done in the years 2014-2016 on 111 carcasses from several locations in Germany and Luxembourg, during which several organs, blood samples, feces and digestive tracts were collected. We found by Luxemburgish animals no evidence for *Baylisascaris procyonis* in opposite to German raccoons among which almost a half was infected. The further investigation showed existence of eggs, cysts and reproductive stages of different parasites like *Taenidae* spp., *Mesocostoides* sp., *Capillaridae* spp., *Ancylostoma* sp., *Dipylidium caninum*, *Coccidia* and *Toxoplasma gondii*. The statistical analysis showed no significant differences in the presence or count of different kinds of parasites depend of weight but some differences between sexes could be proved. There were also some variances in occurrence and count of certain parasite species by comparing the results from directly dissections and further analysis of other taken samples.

GENERAL SESSION

KNOW YOUR ENEMY: A MOLECULAR APPROACH IDENTIFIES MULTIPLE KEY FACTORS DRIVING A SMALL MAMMAL INVASION-EXTINCTION EVENT ON AN ISLAND

Samuel Browett¹, Rachael Antwis¹, Naiara Sales¹, Thomas Curran², Denise O'Meara², Kevin Bown¹, Joseph Jackson¹, Jon Yearsley³, Ian Montgomery⁴, Jeremy Searle⁵, Allan McDevitt¹

¹University of Salford

²Waterford Institute of Technology

³University College Dublin

⁴Queens University Belfast

⁵Cornell University

Invasive mammals are still a huge concern for conserving native biota globally. Ireland's smallest resident mammal, the pygmy shrew (*Sorex minutus*), is rapidly being out-competed and replaced by the invasive greater white-toothed shrew (*Crocidura russula*). This invasive shrew was discovered in 2007 and has been spreading rapidly across the island at a rate of ~5km per year. Considering these two species co-inhabit other regions of Europe, this raises the question of why they cannot coexist in Ireland. This study applies DNA metabarcoding to shrew gut contents to investigate two linked factors in this invasion-extinction event; i) resource use and ii) gut microbial community structure. This was applied to over 300 shrews of both species sampled across radial transects in Ireland, two seasons, and a natural 'control' site in France where both species occur together in high abundance. Identifying the invertebrate prey taxa using the COI genetic region indicates a changing dietary preference of the invasive shrew along the invasive route. While pygmy shrews show a broad range diet, Irish populations remain unable to sufficiently adapt their diet in response to this new competitor. By targeting different genetic regions, the bacterial (16S region) and fungal (ITS region) communities of the shrews were characterised using DNA metabarcoding. During this invasion there is evidence of structural changes in the microbial communities in both species, which may reflect changing condition of fitness during invasion and/or stresses induced by restricted resource availability. This multi-faceted approach on a well-studied invasive system has demonstrated the importance of identifying multiple factors occurring simultaneously in invasion-extinction events in mammals.

GENERAL SESSION

MULTISPECIES RESERVOIR OF SPIROMETRA ERINACEI EUROPAEI (CESTODA: DIPHYLLOBOTHRIDAE) IN WILD MAMMALIAN HOSTS IN NE POLAND

Eliza Kondzior¹, Małgorzata Tokarska², Rafał Kowalczyk², Andrzej Zalewski², Iwona Ruczyńska², Ewelina Hapunik², Marta Kołodziej-Sobocińska²

¹*Institute of Biology, University of Białystok; Mammal Research Institute, Polish Academy of Sciences*

²*Mammal Research Institute, Polish Academy of Sciences*

Spirometra erinacei europaei is the tapeworm which reproduces mainly in felids and canids. The first intermediate host is a copepod, in which proceroid larvae develop and the second intermediate host may be amphibians and reptiles. The paratenic hosts are birds or mammals (including human), in which plerocercoids (spargana) once more settle in the tissues. Spargana cause sparganosis – severe food- and water-borne disease. European records are incidental. In Poland the presence of *S. erinacei europaei* has recently been confirmed genetically in badger, wild boar, lynx and grass snake; however, the first reports from Białowieża Primeval Forest (BPF) date back to the 1940s. We studied spread of the parasite in wild mammalian hosts in NE Poland. A total of 529 dead mammals including: raccoon dog, badger, pine marten, stone marten, red fox, American mink, European polecat, lynx, and river otter were collected and necropsied. We found *S. erinacei europaei* larvae in 165 (31.2%) of studied mammals. To identify the parasite species 18S rRNA gene fragment were analyzed. The highest diversity of infected species was in BPF. The mean infection intensity in all studied species was 14.3 larvae per one animal (range 1-276) with the highest infection intensity in badgers from BPF – 82.7. Our study revealed that in Europe many mammal species are *S. erinacei europaei* reservoirs. The frequency and level of infection differed between locations. The highest prevalence in BPF indicates beneficial environmental conditions for this parasite. Further research is required to confirm which environmental and biological factors have the most significant impact on the level of infection in European mammals. The study was financed by the National Science Centre project no. 2016/21/B/NZ8/02429.

GENERAL SESSION

COMBINING QUESTIONNAIRE SURVEY AND BIOGEOGRAPHIC MODELS TO UPDATE AND FORECAST THE DISTRIBUTION OF THE ONLY MONGOOSE SPECIES IN EUROPE

Esther Descalzo¹, Francisco Díaz-Ruiz², José Jiménez¹, María Martínez-Jauregui³, Mario Soliño³, Ana Luz Márquez², Miguel Ángel Farfán², Raimundo Real², Miguel Delibes-Mateos⁴, Pablo Ferreras¹

¹Instituto de Investigación en Recursos Cinegéticos IREC, CSIC-UCLM-JCCM, Ciudad Real

²Universidad de Málaga, Departamento de Biología Animal, Málaga

³Instituto Nacional de Investigación Agraria INIA, Centro de Investigación Forestal CIFOR, Madrid

⁴Instituto de Estudios Sociales Avanzados IESA-CSIC. Córdoba

The study of carnivore distribution is challenging, because these species are often hardly detectable. One of these species is the Egyptian mongoose (*Herpestes ichneumon*), the only mongoose currently present in Europe. Since historical times it occurred in south-western Iberia, from where it has spread to the North and East over the past decades. In this study, our main goals were: 1) updating the current distribution area of the species in central Spain (Castilla-La Mancha region), one of the most recent expansion areas, and 2) identifying suitable areas for the mongoose in order to forecast its potential future expansion. Data on mongoose occurrences during 2010-2018 were obtained through an online questionnaire survey with environmental rangers of the regional government of Castilla-La Mancha. We received responses of 309 rangers out of the 467 total number of rangers in the study area (66.2%); >90% of the study area was surveyed. We used logistic regression and the favourability function and a set of environmental variables to model the species current potential distribution and to forecast its potential future distribution. Our results reveal that the Egyptian mongoose is currently present in almost the whole western sector of the region, where the environmental favourability is medium-high. Our findings also suggest that the mongoose expansion could continue to the southeast of the study area, which presents environmental favourable conditions for the species. Our approach, based on the combination of questionnaire survey and biogeographic models, could be also applied to assess the current and expected future distributions of other carnivore species, which could help improve their management and conservation.

GENERAL SESSION

SPATIAL VARIABLES ASSOCIATED WITH THE GEOGRAPHICAL RANGE SHIFT OF EUROPEAN HAMSTER (*Cricetus cricetus*) IN POLAND

Aleksandra Zarzycka¹, Katarzyna Bińkowska¹, Marcin Brzeziński¹

¹Faculty of Biology, University of Warsaw

European hamster (*Cricetus cricetus*) is considered to be one of the most endangered mammalian species in Europe. Since the second half of the 20th century, we can observe a constant decrease both in geographical range and population densities. In Poland, this species has disappeared from over 75% of previously occupied locations within the last 50 years. Intensification of agriculture and climate change are considered the most important factors of this decline. However, it is not fully understood to which extent particular factors are affecting this species. To answer this question we used methods of spatial statistics, which allow for the identification of hidden patterns and dependencies. In the first phase of the analysis, we used historical occurrence data to compare distributions of hamsters in Poland in the 1970s and the beginning of the 21st century. We chose several environmental and anthropogenic spatial variables and conducted Environmental Niche Factor Analysis on the scale of the whole country. The variable with the strongest influence on the shift in geographical range was soil type. We hypothesize that due to the worsening environmental conditions caused by both anthropogenic pressure and climatic changes, the survival of this fossorial species is only possible in areas with high availability of soils with optimal properties. We have tested this hypothesis by conducting burrow inventory on the area of over 230 ha agricultural fields in Lesser Poland Voivodeship. Collected hamster occurrence data have been used in a second habitat suitability analysis on a smaller spatial scale. Among geographical variables most relevant to hamster distribution we identified the distance to areas with preferred soil types and to the forest, as well as aspect and slope angle.

GENERAL SESSION

THE BEAVER FACILITATES SPECIES RICHNESS AND ABUNDANCE OF TERRESTRIAL AND SEMI-AQUATIC MAMMALS

Janne Sundell¹, Wenfei Liao², Ophélie Huet³, Erminia Scarpulla⁴, Petri Nummi⁵

¹Lammi Biological Station, University of Helsinki

²Faculty of Biological and Environmental Sciences, University of Helsinki

³Department of Animal Biology and Genetics, Master Behavioural Ecology, Evolution and Biodiversity, University of Tours, Faculty of Sciences and Technologies

⁴Department of Biological, Geological and Environmental Sciences, University of Bologna

⁵Department of Forestry, University of Helsinki

Wetlands and their species have been in drastic decline during the past century. From a biodiversity perspective, the return of beavers to their riparian habitats could compensate this development. We studied the facilitation of a mammalian community by the ecosystem engineering of the American beaver (*Castor canadensis*) in a boreal setting. Using two methods, i.e. camera trapping and snow track survey, we found that both mammalian species richness and activity were significantly higher in beaver patches than in the controls. Of individual species, the moose (*Alces alces*) used beaver patches more during both the ice-free season and winter. The Eurasian otter (*Lutra lutra*), the pine marten (*Martes martes*) and the least weasel (*Mustela nivalis*) made more use of beaver sites during the winter. Our study highlights the role of ecosystem engineers in promoting species richness and abundance, especially in areas of relatively low productivity. Promoting facilitative ecosystem engineers is feasible in habitat conservation or restoration. Beaver engineering may be especially valuable in landscapes artificially deficient in wetlands.

GENERAL SESSION

MAMMAL MAPPING IN RUSSIA

Andrey Lisovsky¹, Valery Stakheev², Alexander Saveljev³, Boris Sheftel⁴, Oleg Ermakov⁵, Dmitri Smirnov⁵, Sergey Titov⁵

¹*Zoological Museum of Moscow University*

²*Federal Research Center The Southern Scientific Centre of the RAS*

³*Russian Research Institute of Game Management and Fur Farming*

⁴*A.N. Severtsov Institute of Ecology and Evolution, Russian Academia of Science*

⁵*Penza State University*

Despite of long tradition of faunal studies in Russia, the united summary review was never published or processed as a database. Recently such database „Mammals of Russia” was created. The database unites records from professional zoologists as well as amateurs and photographers. All submitted records go through validation by specialists, members of Russian Theriological Society. Special block of internet site accumulates publications on Russian fauna that are available for search using common bibliographic parameters as well as species names and geography. Another block maintains the actual list of fauna, taking recent taxonomic studies into account. At the current state, more than 30 000 validated records cover Russian territory, mainly its European part. Collected data will be used as a part of the Atlas of European Mammals that will be created soon in the frame of EMMA2 project. Now the database holds records on 91% of European Russia species. Maps of geographical distribution of studies of different groups of species allow planning current faunistic researches. Mobile application serves the field data collecting. The study was supported by the Russian Science Foundation (18-14-00093).

GENERAL SESSION

NETWORKING AT SEA: UNRAVELING MIXED-SPECIES CETACEAN SIGHTINGS

Mridula Srinivasan

NOAA Fisheries

The prevalence of mixed-species or heterospecific animal groups is an interesting facet of animal ecology. However, distinguishing co-occurring animals from interacting mixed-species groups is especially difficult for cetaceans observed momentarily at sea. Despite this inherent limitation, longitudinal data of cetacean mixed-species sightings can yield valuable insights on the patterns and characteristics of these ephemeral events. Using a >20-year dataset of mixed-species cetacean sightings collected from ship-board line-transect surveys in the eastern Tropical Pacific and California Current, this study evaluates whether observed mixed-species sightings are due to chance based on Markov Chain Monte Carlo randomization tests, and then measures the tendency of some species to appear in mixed-species groups and to co-occur persistently with select species. Thereafter, using social network analysis tools, mixed-species sightings in the two study areas are analyzed to identify prominent species based on the number and quality of relationships with multiple species, which could potentially control information flow regarding resources or other biological information. Additionally, the social networks in the two areas are compared. Finally, based on species characteristics, prey and habitat preferences, additional hypothetical frameworks are presented to expound the processes underlying the formation of mixed-species groups.

GENERAL SESSION

PREDATORS AND MEGAHERBIVORES HAVE CONTRASTING IMPACTS ON NITROGEN AND PHOSPHORUS STOICHIOMETRY IN AN AFRICAN SAVANNA

Elizabeth le Roux¹, Laura S. van Veenhuisen², Graham I.H. Kerley¹, Joris P.G.M. Cromsigt³

¹*Nelson Mandela University*

²*Utrecht University*

³*Swedish University of Agricultural Science*

Pleistocene megafaunal extinctions were skewed towards larger body sizes, leaving present-day mammal communities smaller in body-size compared to that of the past. We are only beginning to appreciate how earth system processes have been, and are still being, influenced by the absence of the largest species. One very compelling field of inquiry is how the loss of large species, and particularly the loss of the species least vulnerable to predation, has altered consumer-driven biogeochemical cycling and lateral nutrient transport. In this study we add to this effort by asking whether the size of an herbivore could influence ecosystem stoichiometry. We show that herbivores that vary in size have different faecal N:P ratios with less phosphorus relative to nitrogen in species of larger body size i.e. faecal N:P ratios increase with body size. In addition, we show that smaller species, that are generally more vulnerable to predators, distribute their relatively low N:P ratio faeces predominantly to safer areas. On the other hand, megaherbivores distribute their relatively high N:P ratio faeces more evenly across the predation risk gradient. We demonstrate that such allometric differences in faecal distribution and faecal stoichiometry, in turn influence grass and soil N:P ratio. Thus megaherbivores and predators, through their influence on prey species, have opposite effects on ecosystem N:P stoichiometry.

POSTER PRESENTATIONS

POSTER PRESENTATIONS

SQUIRRELS

P1 SEARCH FOR BORNAVIRUS AND OTHER VIRUSES IN SQUIRRELS

Vanessa Schulze¹, Nicola Ferrari², Claudia Romeo², Peter W. W. Lurz³, Michael A. Steele⁴, Shealyn Marino⁵, Kore Schlottau⁶, Martin Beer⁶, Rainer G. Ulrich¹, Bernhard Ehlers⁷

¹Institute of Novel and Emerging Infectious Diseases, Friedrich-Loeffler-Institut, Greifswald - Insel Riems, Germany

²Dipartimento di Medicina Veterinaria, Università degli Studi di Milano, Milan, Italy

³Royal Dick School of Veterinary Studies and Roslin Institute, University of Edinburgh, Edinburgh, United Kingdom

⁴Department of Biology, Wilkes University, Wilkes-Barre, Pennsylvania, USA

⁵Department of Biology, Wilkes University, Wilkes-Barre, Pennsylvania, USA

⁶Institute of Diagnostic Virology, Friedrich-Loeffler-Institut, Greifswald-Insel Riems, Germany

⁷Division 12 'Measles, Mumps, Rubella and Viruses Affecting Immunocompromised Patients', Robert Koch Institute, Berlin, Germany

The recent discovery of a zoonotic bornavirus (Variegated squirrel bornavirus 1, VSBV-1) to be the causative agent of four lethal encephalitis cases in humans was accompanied by its detection in Variegated squirrel (*Sciurus variegatoides*), Red-tailed squirrel (*Sciurus granatensis*), Prevost's squirrel (*Callosciurus prevostii*), Finlayson's squirrel (*Callosciurus finlaysonii*) and Swinhoe's striped squirrel (*Tamias swinhoei*) at private holdings and zoos. As there is not much known about pathogens in squirrels, we continue the VSBV-1 screening in squirrels and evaluate these samples for additional pathogens. For this purpose, we collected samples from eight squirrel species of the family Sciuridae: Eurasian red squirrel (*Sciurus vulgaris*), Eastern grey squirrel (*Sciurus carolinensis*), Variegated squirrel, Pallas' squirrel (*Callosciurus erythraeus*), Prevost's squirrel, Richardson's ground squirrel (*Urocyon richardsonii*), American red squirrel (*Tamiasciurus hudsonicus*) and Eastern chipmunk (*Tamias striatus*). These animals originate from their natural distribution range in America and Canada, from introduced populations in Italy and the United Kingdom and from different holdings in Germany. The investigations were done with Panbornavirus RT-qPCR and VSBV1-specific RT-qPCR for detection of bornaviruses and several conventional PCRs for detection of other viruses. The VSBV-1 screening of 214 of the tested squirrels gave negative results, while 24 were previously tested positive for VSBV-1 (already reported in Schlottau et al. Variegated squirrel bornavirus 1 in squirrels, Germany and the Netherlands. Emerg Infect Dis. 2017; 23: 477–81). In contrast to this in seven of the eight tested squirrel species novel viruses could be detected that are currently further characterized.

SQUIRRELS

P2 THE IDENTIFICATION OF RE-INVASION PATHWAYS FOLLOWING ERADICATION OF THE GREY SQUIRREL (*Sciurus carolinensis*) USING GENETIC AND GENOMIC DATA

Rebecca Synnott¹, Allan McDevitt², Samuel Browett², Naiara Sales², Craig Shuttleworth³, David Everest⁴, Catherine O'Reilly⁵, Denise O'Meara⁵

¹Molecular Ecology Research Group, Eco-Innovation Research Centre, School of Science and Computing, Waterford Institute of Technology, Cork Road, Waterford, Ireland

²University of Salford, School of Science, Engineering and Environment, UK

³Bangor University, School of Natural Sciences, Anglesey, UK

⁴Animal and Plant Health agency, Department for Environment, Food & Rural Affairs, UK

⁵Molecular Ecology Research Group, Eco-Innovation Research Centre, School of Science and Computing, Waterford Institute of Technology, Cork Road, Waterford, Ireland

Invasive species can cause major ecological and economic impacts. The management and control of these invaders is a challenge to stakeholders due to economic, ecological and social constraints. In the British Isles, the invasive North American grey squirrel (*Sciurus carolinensis*) has been shown to contribute to the decline of the red squirrel (*S. vulgaris*) through resource competition and the spread of disease. The grey squirrel has been subjected to extensive control efforts in the UK which can temporarily reduce the population, but if control is not sustained, the population can recover. In the case of the Isle of Anglesey, an island connected to mainland Wales via man-made bridges, complete eradication of the grey squirrel occurred in 2013. However, in 2015, several individuals had returned, possibly from the surrounding areas through natural dispersal or intentional release. Previous studies in Anglesey have shown that prolonged control efforts in partially isolated environments can lead to a loss of genetic diversity, an effect that might accelerate population decline and the success of an eradication programme. The aim of this study is to identify re-invasion pathways into Anglesey from surrounding areas following control efforts. This will be achieved using genomic and genetic approaches including SNPs (using ddRAD), microsatellites and mtDNA on hundreds of animals sampled between 2011 and 2019. Comparisons will be made across genetic markers to determine the methods that provide the best resolution for the identification of the source of re-invasion across fine spatial and temporal scales. The results will inform ongoing adaptive management efforts to allow the recovery of red squirrels in Anglesey, and the continued management of grey squirrels.

SQUIRRELS

P3 BRIDGING THE GAP BETWEEN CONSERVATION GENETICS AND RED SQUIRREL (*Sciurus vulgaris*) CONSERVATION MANAGEMENT

Rebecca Synnott¹, Colin Lawton², Catherine O'Reilly¹, David. G. Tosh³, Denise O'Meara¹

¹Molecular Ecology Research Group, Eco-Innovation Research Centre, School of Science and Computing, Waterford Institute of Technology, Cork Road, Waterford, Ireland

²Animal Ecology and Conservation Group, School of Natural Sciences, Ryan Institute, National University of Ireland, Galway, Ireland

³Ulster Museum, National Museums Northern Ireland, Belfast BT9 5AB, UK

The red squirrel (*Sciurus vulgaris*) suffered population declines in Britain and Ireland due to habitat removal and fragmentation, historical trade and movement of the species, and competition from the invasive North American grey squirrel (*Sciurus carolinensis*). In recent years, the red squirrel has demonstrated a natural recovery in Ireland, possibly coinciding with the recovery of a native carnivore, the pine marten (*Martes martes*), and a subsequent decline of the grey squirrel. It is likely that further population reinforcement projects of the red squirrel will occur throughout Britain and Ireland as stakeholders attempt to restore and conserve ecosystems. The aim of this project is to demonstrate how conservation genetics can be used to support and inform practical management decisions for the long-term survival and management of red squirrel populations. The study will demonstrate how genetic tools can be used to support reinforcement projects to avoid risks such as inbreeding, outbreeding and disease susceptibility while demonstrating sensitivity to the conservation of the genetic heritage of the species. The application of the techniques will be demonstrated through the genetic assessment of a translocation project in the West of Ireland, current conservation and reinforcement projects in Northern Ireland and historical red squirrel samples.

SQUIRRELS

P4 DEVELOPMENT AND CHARACTERIZATION OF NEW POLYMORPHIC MICROSATELLITE MARKERS FOR EURASIAN GROUND SQUIRREL, THE YELLOW GROUND SQUIRREL, *Spermophilus fulvus*

Olga Batova¹, Sergey Titov², Nina Vasilieva¹, Liudmila Savinetskaya¹, Andrey Tchabovsky¹

¹A.N. Severtsov Institute of Ecology and Evolution RAS, Moscow, Russia

²Penza State University, Penza, Russia

Ground squirrels are ecosystem engineers and keystone species in many open landscapes of Eurasia, America, and Africa. They are model objects for population studies, behavioural ecology, life-history theory, and conservation biology, the research areas where microsatellite analysis is widely applied and fruitful. So far, microsatellite markers have been developed for only few Palearctic ground squirrels. We tested and characterized 14 markers previously developed for other ground squirrels and 10 new loci with tri- and tetranucleotide repeats in the yellow ground squirrel, *Spermophilus fulvus*, a species widely distributed in Eurasia. We found polymorphism in 10 loci, 5 of them were highly polymorphic (5-7 alleles). These markers will benefit studies of the population genetic structure, paternity, mating system, reproductive success, and interspecific hybridization in *S. fulvus* and other Eurasian ground squirrels. Supported by RFBR (19-04-00577).

SQUIRRELS

P5 FAST EXPLORERS: THE FIRST EXPERIENCE OF GPS TRACKING IN YELLOW GROUND SQUIRRELS

Nina Vasilieva¹, Liudmila Savinetskaya¹, Nikita Vasiliev²

¹*A.N. Severtsov Institute of Ecology and Evolution RAS, Moscow, Russia*

²*Moscow State University, Moscow, Russia*

Space use pattern is a key component of animal behavior and ecology. Recent progress in tracking technologies has allowed such studies even in secretive small-sized species. However, specific life-history traits of fossorial and semi-fossorial mammals (i.e., underground lifestyle) prevent the use of standard tracking devices. Yellow ground squirrels (*Spermophilus fulvus*) are poorly-studied big (up to 2 kg) diurnal desert rodents that use deep burrows. We developed a methodology of GPS-tracking for *S. fulvus* and studied space use and circadian activity patterns in 2 adult males in April during the mating period, and in 3 males and 2 females during the last week prior to hibernation in the wild (Saratovskaya oblast', Russia). Small (12 g) GPS loggers with photosensitive sensors were glued on the skin on the squirrel's back. In spring, both males spent all day (8:00-18:00) aboveground, and travelled daily up to 3.5 km with speed up to 13 km/h, which is very long as compared with the average female home range diameter (30-50 m). This supports our hypothesis that males use competitive mate searching strategy. Nevertheless, they always spent nights in their hibernating burrows. Before hibernation, the squirrels demonstrated high individual variation in space use: one male did not move from the burrow further than 20 m; the other male traveled daily to the same feeding place in 400 m from his burrow; the third male as well as one female travelled in different directions and used several burrows. The second female hibernated in 2 days after trapping. Aboveground activity in summer was not continuous and was shorter than in spring. All individuals hibernated at 16-28 June. The high mobility of some individuals prior to hibernation is unexpected and demand future investigations.

CONSERVATION AND POPULATION GENETICS

P6 REVEALING THE DIET OF THE LESSER HORSESHOE BAT (*Rhinolophus hipposideros*) IN IRELAND VIA DNA METABARCODING

Thomas Curran¹, Samuel Browett², Denise O'Meara¹, David O'Neill¹, Catherine O'Reilly¹, Andrew Harrington¹, Allan McDevitt²

¹Molecular Ecology Research Group/Eco-Innovation Research Centre, School of Science and Computing, Waterford Institute of Technology, Cork Road, Waterford, Ireland

²Ecosystems and Environment Research Centre, School of Environmental and Life Science, University of Salford, Salford, UK

R. hipposideros has the most restricted range of any resident bat species in Ireland, with the next closest population occurring on the west coast of Britain resulting in the isolation of the Irish population from all other European populations. In Ireland, *R. hipposideros* is protected by Irish and European law (Wildlife Act 1976; EU Habitats Directive). Understanding the diet of *R. hipposideros* is important for making informed conservation management decisions, and to understand the role it plays in the provision of ecosystem services. Traditional morphological approaches to dietary analysis of bat faeces can result in the over-representation of hard bodied versus soft bodied insects but DNA metabarcoding approaches employing next generation sequencing (NGS) facilitate the simultaneous and unambiguous identification of multiple taxa/species from a single DNA extract. In this study, we used DNA that was extracted from faecal samples collected at *R. hipposideros* roosts which had been species and sex-typed using real-time PCR and individuals identified via genotyping. Using DNA metabarcoding, the dominant prey groups revealed in the diet were Diptera and Lepidoptera, with Hymenoptera, Coleoptera, Neuroptera and Trichoptera also identified. Female bats had greater amounts of Lepidoptera in their diet in comparison to males, suggesting sex-specific hunting strategies. Pest species such as mosquitoes (*Culiseta spp.*, *Culex pipiens*) and midges (*Culicoides punctatus*) implicated in the spread of disease were detected, highlighting the role of *R. hipposideros* in the provision of ecosystem services relevant to human and animal health. The combination of these molecular techniques can be used to understand the individual and gender-specific prey preferences of *R. hipposideros*.

CONSERVATION AND POPULATION GENETICS

P7 SEQUENCING DE NOVO Y CHROMOSOME REFERENCE GENOME OF THE DOG

Maris Hindrikson¹, Raquel Godinho¹, Pedro Silva¹

¹CIBIO-InBIO, University of Porto

Y chromosome fulfills a number of important functions that have been understudied outside of model organisms. The reason for this is difficulties in the assembly of Y chromosome, due to the haploid and highly repetitive nature of this chromosome. This has impeded the development of genetic markers used to study male-specific dispersal and population genetics in mammals, and to evaluate sex bias during hybridization in natural populations. More generally, the lack of Y chromosome sequences prevents our complete understanding of vertebrate genome function and evolution.

Despite the whole genome been constructed and annotated for the female dog (CanFam3.1), the dog Y chromosome reference genome does not exist. However, reference Y chromosome sequence for dog would be of most importance and prove most valuable in the future in various research areas connected to canids. The main methods used in sequencing de novo dog Y chromosome reference genome, such as chromosome flow-sorting, whole-genome sequencing (using Oxford Nanopore sequencing platform) technology and post-sequencing bioinformatic analysis, are discussed in poster.

CONSERVATION AND POPULATION GENETICS

P8 POTENTIAL ROLE OF A Y CHROMOSOME IN POSTHITIS DISEASE ETIOLOGY IN THE EUROPEAN BISON MALES

Sazia Kunva¹, Małgorzata Tokarska¹

¹Mammal Research Institute, Polish Academy of Science

The European bison was salvaged from extinction approximately 100 years ago. All the founders of contemporary population of the Lowland line (living in Białowieża Forest) were descendants of just 7 individuals. Posthitis is an incurable inflammation of the penis and prepuce that affects 6-8% of Lowland bison males every year, with no respect to their age. In the last 30 years many attempts were undertaken to explain the etiology of the disease, but none of them succeeded. For many years an instinctive explanation, though never verified, was monomorphy of Y chromosome of the Lowland line. The main aim of this study is to identify species specific SNPs (Single nucleotide polymorphism markers) associated with the development of posthitis disease in European bison. One of the most impactful methods to identify disease susceptibility genes for complex traits in humans and animals is Genome-wide association studies (GWAS). We are using GWAS to trace the candidate genes and their variants associated with the posthitis occurrence in the Lowland bison. The species specific SNP markers are being identified and they will be used in all genome-wide-association assays in the project. The same material will be utilized for validation of the Y chromosome's role in the posthitis etiology. As a reference chromosome for autosome analyses, we are using *Bos taurus* genome as European bison genome is available only in scaffold form. Y chromosome genome is not present in *Bos taurus* genome. So we are applying to align our data with human Y chromosome. Such endeavor will allow the extensive analyses of sex chromosome role, enabling verification of the hypothesis of the Y chromosome as a key factor in the disease etiology. The studies are financed by NCN grant: 2016/23/B/NZ9/03411.

CONSERVATION AND POPULATION GENETICS

P9 NONINVASIVE MONITORING OF A CRITICALLY ENDANGERED NEOTROPICAL PRIMATE

Mariane Kaizer¹, Naiara Sales¹, Thiago Alvim, Fabiano Melo, Karen Strier, Jean Boubli, Robert Young, Allan McDevitt¹

¹*University of Salford*

Primate populations are threatened globally, and noninvasive monitoring tools are becoming crucial to determine effective conservation actions. Using an integrative approach combining arboreal camera trapping and genetic tools we conducted a population assessment of the critically endangered northern muriqui (*Brachyteles hypoxanthus*) in the Atlantic Forest of Brazil. In Caparaó National Park, canopy camera traps were deployed and faecal samples were obtained to monitor a neglected population of this endemic species. Here, we demonstrated the efficiency of canopy camera traps for detecting and monitoring non-habituated groups in remote areas. This method provided important information, regarding population size and demographic composition, demonstrating its applicability for arboreal primate surveys. Complementary, genetic analyses using the mtDNA (HVRI region) and microsatellites demonstrated high genetic diversity in this endangered primate in the Park and highlighted the importance of this population for safeguarding the genetic variability of the species across its entire range due to the presence of many unique haplotypes. This multidisciplinary approach contributed towards our understanding of the demographic composition, genetic diversity and structure of this high priority population and will provide guidance for future population management and should lead to more effective conservation actions.

CONSERVATION AND POPULATION GENETICS

P10 AUTOMATIC MICROSATELLITE GENOTYPING FROM NONINVASIVE GENETIC SAMPLING IN WOLVES

Isabel Salado¹, Alberto Fernández-Gil¹, Carles Vilà¹, Jennifer Leonard¹

¹Doñana Biological Station Spanish National Research Council

Ecological and genetic studies of large mammals often need to deal with their elusiveness. Noninvasive genetic sampling has overcome this difficulty by using other DNA sources, such as feces or hairs, which allow obtaining powerful data without disturbing the individuals. Because microsatellites are molecular markers usually short in length, they can be extracted from these low quantity and quality DNA samples. Also, because of their high polymorphism just a few markers are enough for reliably individual identification, kinship determination or population genetics. However, the high error rates and the need of multiple replicates make the genotyping process expensive and time consuming. Thanks to the reduction of costs for next-generation sequencing approaches and the recent development of specific softwares, automatic genotyping is now possible. These bioinformatic tools infer the genotypes directly from sequences through different algorithms, increasing the throughput of the data. However, does each of these softwares result equally in a correct genotype? Or there is one more reliable than others? Which requirements they need to work properly? Are they user-friendly? These questions are relevant to facilitate the generalized implementation of high throughput approaches in genetic noninvasive studies. In our study, we compare the results of different automatic genotyping softwares using sequences from several microsatellite loci extracted from feces of Iberian wolves.

CONSERVATION AND POPULATION GENETICS

P11 LANDSCAPE GENETICS OF URBAN ENVIRONMENT, EXEMPLIFIED BY *Apodemus* MODEL

Tomasz Gortat¹, Robert Rutkowski², Alicja Gryczyńska¹, Robert Meronka¹, Miłostawa Sokół¹, Michał Kozakiewicz¹

¹Faculty of Biology, Biological and Chemical Research Centre

²Museum and Institute of Zoology Polish Academy of Sciences

In theory, urban environment should induce fragmentation of wild species, given that groups of individuals inhabiting patches of suitable habitat are more or less isolated. Indeed, many studies have underlined that genetic differentiation is more marked among local populations within urban areas, as opposed to those present in the natural environment. The genetic structure is therefore more pronounced, while particular species' genetic differentiation among local urban populations loses the isolation-by-distance pattern usually observed in a natural population. Landscape genetics investigates interaction between landscape features and microevolutionary processes, such as gene flow genetic drift and selection. Analytical approaches of this emerging field allow to explicitly and quantitatively test for landscape-genetic relationship. We used these methods to detect barriers and define corridors within urban landscape, affecting population genetic structure of two rodent species. We analyzed populations of *Apodemus agrarius* and *Apodemus flavicollis* inhabiting 17 locations situated at different distances from the city centre (Warsaw, Poland) and exposed to various degrees of human pressure. Both species have different urban history. The first of them has been present in Warsaw for over 100 years. In contrast, *Apodemus flavicollis* occurs in the city no more than 25 years. All individuals were genotyped using microsatellite markers. Both, individual and population approach were used for testing hypothesis about gene flow in heterogeneous landscape of urban environment. We assumed that the different time of presence of *Apodemus agrarius* and *Apodemus flavicollis* in the city will be confirmed by the difference in the flow of genes between local populations of these species.

CONSERVATION AND POPULATION GENETICS

P12 IDENTIFICATION OF MANAGEMENT UNITS FOR WOLVES IN POLAND USING POPULATION GENETIC DATA

Maciej Szewczyk¹, Sabina Nowak², Natalia Niedźwiecka², Michał Figura², Patrycja Tomczak², Przemysław Stachyra³, Tomasz Zwijacz-Kozica⁴, Kinga M. Stępniaik⁵, Robert W. Mysłajek⁵

¹Institute of Genetics and Biotechnology, Faculty of Biology, University of Warsaw

²Association for Nature „Wolf”

³Roztocze National Park

⁴Tatra National Park

⁵Institute of Genetics and Biotechnology, Faculty of Biology, University of Warsaw

One of the most important steps in conservation planning for populations of wild-living species is the recognition of their intraspecific diversity followed by delineation of adequate management units (MUs). Identification of MUs is primarily justified by the amount of genetic divergence at which populations become demographically independent, but MUs identified for wolves *Canis lupus* in Europe were based mainly on data on species distribution, geographic features, habitat quality, dispersal abilities and different management conditions. We examined wolf genetic structure in Poland based on 2110 samples collected from 2011 to 2018, using 13 polymorphic microsatellite loci and 230 bp fragment mitochondrial control region. We confirmed separation of Carpathian, Baltic and Central European wolf populations in Poland. We also suggested to consider an additional MU located in the south-eastern Poland, which we found to be genetically different from all other subpopulations. This is in concordance with earlier findings, which described a discrete subpopulation situated latitudinally between Carpathian and Baltic regions and extending eastward, beyond the Polish state border. Thus, we propose an update of MUs for wolves in Central Europe, taking under consideration all former studies together with results of our analysis. We are aware, that the exact borders between MUs should be treated with caution due to the exchange of individuals, which is the most intense at their edges. Nonetheless, we believe that our suggestion will be useful for future population-level management of wolves in Central Europe and will fuel wider international co-operation for conservation of this carnivore.

PHYLOGEOGRAPHY AND BIOGEOGRAPHY

P13 DETECTION OF HYBRIDIZATION IN EUROPEAN HEDGEHOGS

Kristýna Eliášová¹, Ignacio Lucas², Miroslava Loudová³, José Grau⁴, Pavel Hulva³, Barbora Černá Bolfíková⁵

¹*Department of zoology, Faculty of Science, Charles University, Prague*

²*Institut Cavanilles de Biodiversitat i Biologia Evolutiva, Valencia*

³*Department of zoology, Faculty of Science, Charles University, Prague*

⁴*Museum für Naturkunde Berlin, Berlin*

⁵*Department of Animal Science and Food Processing, Czech University of Life Sciences, Prague*

Hybridization and introgression played important role in the history of various species. It was reported that ancient hybridization could have accelerated the evolution of adaptive traits. On the other hand however, it is believed that hybridization speeds up the development of reproductive isolation between diverging species. Here we used RAD-Seq to study secondary contact zone in Central Europe of two hedgehog species, *Erinaceus europaeus* and *E. roumanicus*. Two individuals among 45 studied were identified as admixed with ~25 and ~5 % of introgressed genome. In recently non-admixed individuals, we detected a signal of historical introgression ranging from 1 - 3 % of the genome, indicating more frequent hybridization in the past. Genomic sites with signal of recent introgression were also enriched in signatures of historical introgression, implying that alien alleles in hedgehog genome are maintained by negative selection. We found evidence that gene flow is asymmetric, from *E. europaeus* into *E. roumanicus*. We hypothesize that historical introgression is pre-Glacial and was an important factor during the speciation process. Interactions between species were later shaped by repeated contractions of their area of distribution, followed by re-establishments of contact zones during multiple glacial periods. Our analysis provides a new insight into the contact zone dynamic, interspecific interactions and population structure of two common hedgehog species and helps to explain evolutionary forces shaping them. The project is supported by GA UK 538218.

PHYLOGEOGRAPHY AND BIOGEOGRAPHY

P14 GEOGRAPHICAL VARIATION OF SKULLS OF THE NORTHERN AND COMMON TREE SHREW COMPLEX

Hideki Endo¹, Truong Son Nguyen², Dinh Duy Nguyen², Tatsuo Oshida³, Masaharu Motokawa⁴

¹The University Museum, The University of Tokyo

²Department of Vertebrate Zoology, Institute of Ecology and Biological Resources, and Graduate University of Science and Technology, Vietnam Academy of Science and Technology

³Laboratory of Wildlife Ecology, Obihiro University of Agriculture and Veterinary Medicine

⁴The Kyoto University Museum, Kyoto University

Geographical variation was examined morphologically in the northern tree shrew (*Tupaia belangeri*) and common tree shrew (*Tupaia glis*) in some Indochinese and Malayan regions. We used totally 231 skull specimens of the two species stored in natural history museums. Osteometrical examination and principal component analysis elucidated the morphological differences among various populations. The northern and common tree shrews were distinguishable in the scattergrams of the principal component analysis. We confirmed the sympatric distribution of the two species around the Isthmus of Kra, southern part of Thailand. The northern tree shrew from various localities of Indochinese Peninsula appeared similar in skull size and shape. In the populations of the northern tree shrew, however, the Kanchanaburi population in western Thailand was significantly smaller than the other population in skull size, and constituted the morphologically separable group in our study. The population of the northern area of Vietnam could be distinguished from the other populations of Indochinese regions. Although the Isthmus of Kra has been considered as an important zoogeographical barrier, it does not act as a complete barrier between the two species of *Tupaia*. In addition to the Isthmus of Kra, we suggest that the western Thailand and northern Vietnam may have zoogeographical barrier that would separate the morphological characteristics in the northern tree shrew.

PHYLOGEOGRAPHY AND BIOGEOGRAPHY

P15 NEW DATA ON THE NORTHEASTERN BORDER OF THE DISTRIBUTION OF THE YELLOW-NECKED MOUSE (*Apodemus flavicollis*) IN THE MIDDLE URALS

Tatyana Fadeeva¹, Leonid Lvovskiy², Vladimir Isakov²

¹Perm Federal Research Center, Ural Branch Russian Academy of Sciences, Mining Institute

²Center for Hygiene and Epidemiology in Perm Territory

Few specimens of the yellow-necked mice (*Apodemus flavicollis*) were recorded in the catch of small mammals in 2016 and 2018 in the territory of Perm Territory (Middle Pre-Ural). Six specimens of mice were caught in Chernushinskiy district (mixed forest, south-west of Trun: 56 ° 26,36.11 „N 56 ° 17' 12.51" E) and one specimen – in Permskiy district (mixed forest, west of Molokovo: 57 ° 56,25.68 „N 56 ° 36' 28.83" E). The habitat of the yellow-necked mouse in Permskiy district (the most northeastern point of the detection at present) suggests the expansion of the area of this specie. *A. flavicollis* was found on the territories of the southern part (Kuedinskiy and Chaikovskiy districts) of Perm Territory earlier (Demidov, Demidova, 1990), as well as in the southwestern part (Krasnoufimskiy district) of Sverdlovsk region (Izvarin et al., 2013). Fossil remains of yellow-necked mice in this region were found only on the north of Perm Territory in sediments of the early Late Pleistocene in the Makhnevskaya ledyanaya cave (59 ° 26 '57.66" N 57 ° 41 '16.91" E). Bone remains of species of the genus *Apodemus* weren't found in sediments of the middle – end of the Late Pleistocene in this territory. Average values of the lengths of the upper and lower dentitions and the lengths of the first upper and lower molars (in mm) for fossil (L M1-M3 – 4.36 ± 0.04, L m1-m3 – 4.44 ± 0.03, L M1 – 2.14 ± 0.02, L m1 – 1.97 ± 0.03) and recent (L M1-M3 – 4.57 ± 0.06, L m1-m3 – 4.54 ± 0.05, L M1 – 2.23 ± 0.01, L m1 – 2.02 ± 0.03) yellow-necked mice from the study area exceed those values in samples from most of the populations of Central and East Europe. This study was funded by RFBR, project number 18-04-00982 and RFBR and Perm Region, project number 19-44-590001.

PHYLOGEOGRAPHY AND BIOGEOGRAPHY

P16 CHALLENGING THE MODEL OF THE IBERIAN PENINSULA AS A REFUGIUM FOR THE BROWN BEAR (*Ursus arctos* L.) IN THE LAST GLACIAL MAXIMUM

Ana García-Vázquez¹, Gloria González-Fortes², Ana C. Pinto Llona³, Aurora Grandal-d'Anglade¹

¹University Institute of Geology, University of A Coruña

²Department of Biology and Evolution, University of Ferrara

³Museo Arqueológico Regional, Research Associate, Alcalá de Henares

During Pleistocene glacial phases, the Iberian Peninsula was postulated as one of the refugia for temperate species that followed a model of contraction-expansion forced by climatic oscillations. The European brown bear (*Ursus arctos* L.) phylogeography was used to illustrate this model due to the relationship between modern Iberian and Southern Scandinavian populations. After an exhaustive compilation of available genetic and radiometric data from Western European brown bears, and adding new sequences of current bears from the Iberian Peninsula, we try to reconstruct their postglacial dynamics. For the model of the Iberia as a refugium to be fulfilled, the Iberian Pleistocene brown bears, would have to be the direct ancestors of the rest of the Atlantic post-glacial bears. Genetics and chronology show the contrary. After a gap in the record that coincides with the LGM, radiometric dating shows a sudden abundance of N Iberia bears that we interpret as a late recolonization of the Peninsula. In Britain the same pattern of sudden abundance is observed coinciding with the deglaciation, about 15000 yBP. In Iberia, this expansion occurred after the Younger Dryas. So, the first area of Atlantic Europe to be recolonized after the ice retreatment was the British Isles. Brown bears entered Iberian Peninsula delayed (around 10000 yBP), and finally Southern Scandinavia was the last place to be colonized (9500-7500 yBP) when a land bridge were suitable. We propose the existence of a cryptic refugium in continental Atlantic Europe, from where the bears would expand as the ice receded. The delay in the recolonization of Iberia could be due to the orographic characteristics of the Pyrenean-Cantabrian region and to the abundant presence of humans in the natural entrance to the Peninsula.

PHYLOGEOGRAPHY AND BIOGEOGRAPHY

P17 WHERE DOES THE ROOT VOLE FROM EASTERN POLAND COME FROM? GENETIC EVIDENCE FOR A CRIPTIC HIGH-LATITUDE REFUGIUM IN POLAND

Elżbieta Jancewicz¹, Ewa Falkowska², Mirosław Ratkiewicz³

¹Department of Forest Zoology and Wildlife Management, Faculty of Forestry, Warsaw University of Life Sciences – SGGW

²University of Warsaw, Faculty of Geology

³University of Białystok, Institute of Biology

Abundant fossil and molecular records confirm the survival of numerous plant, invertebrate and vertebrate species in high-latitude refugia of various continents during the last glaciation. In the Central Europe in an area of Poland (the Kraków-Częstochowa Upland and the Holy Cross Mountain), Pleistocene sediments dated to the last glacial maximum (LGM) also comprise remains of several rodent species typical of various environments, e.g. the humid- and cold-tolerant root vole *Microtus oeconomus* (Rodentia, Cricetidae). We analysed the genetic structure of 33 populations of the root vole located at different distances from the contemporary southern boundary of the species' range in eastern Poland. 908 bp of cytochrome b sequences and 12 microsatellite loci were analysed from 439 and 549 root voles respectively. 21 mtDNA cytb haplotypes belonging to the Central European (CE) phylogroup were found. Within the CE phylogroup of *M. oeconomus*, we identified with high bootstrap support a newly separated group of *M. oeconomus* CE-PL S that evolved from CE. This group is located in the southern and central part of eastern Poland and most likely diverged from phylogroup CE in a small, cryptic refugium situated in southern Poland, in the Kraków-Częstochowa Upland and/or the Holy Cross Mountains. These results were also confirmed by the analysis of microsatellite DNA.

PHYLOGEOGRAPHY AND BIOGEOGRAPHY

P18 THE HISTORY OF THE LANDSCAPE AFFECTS THE GENETIC STRUCTURE OF HYGROPHILOUS SPECIES: THE CASE STUDY OF THE ROOT VOLE FROM EASTERN POLAND

Ewa Falkowska¹, Elżbieta Jancewicz²

¹University of Warsaw, Faculty of Geology, Warsaw, Poland

²Department of Forest Zoology and Wildlife Management, Faculty of Forestry, Warsaw University of Life Sciences – SGGW, Warsaw, Poland

The modern habitat system is the result of historical changes in environments, and the disappearance or development of suitable habitats, favouring (or not) the occurrence of species with specific requirements. The aim of the study was to find a relationship between genetic variability of the hygrophilous species and the geological history of the post-glacial landscape. The research was carried out on the root vole *Microtus oeconomus* (Arvicolinae, Rodentia) in eastern part of Poland. This region has a zonal character as a result of subsequent Pleistocene glaciations: Sanian 1 (MIS 16), Sanian 2 (MIS 12), Odranian (MIS 6) and Vistulian (MIS 2-5b). It was assumed that (1) different history of glaciation at different latitudes translates into different number and different character (e.g. connectivity) of favorable habitats and also various time of colonization by species in post-glacial landscape zones, (2) different number of favorable habitats and a different level of their connectivity/isolation means a various course of in situ evolution; (3) different connectivity of favorable habitats, their different attractiveness and different availability translate into various directions and intensity of modern species migration. Based on analysis of 12 microsatellite loci and the 908 bp of cytochrome b sequences (mtDNA) collected from 549 vole individuals at 33 locations, the genetic structure of *M. oeconomus* in the landscape zones of eastern Poland was determined. Longitudinal variability of the relief in the area of eastern Poland (resulting from different limits of Pleistocene glaciations) and the related specific configuration of hydrogenic habitats are reflected in the genetic differentiation of the root vole.

PHYLOGEOGRAPHY AND BIOGEOGRAPHY

P19 DIFFERENT INTERACTIONS AT DIFFERENT AREAS ALONG THE CONTACT ZONE OF ROBERTSONIAN CHROMOSOMAL RACES OF *Mus musculus domesticus* (RODENTIA: MURIDAE) WITH MONOBRACHIAL HOMOLOGY

Nikolitsa Loukatou¹, Akylina Skoura, Konstantina Chorba, George Mitsainas¹

¹Section of Animal Biology, Dept. of Biology, University of Patras, Greece

The chromosomal study of the western house mouse *Mus musculus domesticus*, is very appealing, due to the appearance of Robertsonian (Rb) fusions: Non-homologous acrocentric chromosomes that fuse at the centromeric region, forming biarmed-Rb chromosomes and causing the reduction of the diploid chromosome number ($2n = 22-40$). In nature, many Rb races of the house mouse (i.e. Rb populations, homozygous for their Rb fusions) exist. Rb races characterized by common descent form Rb systems, three of which are known from Greece. This work summarizes the results of several studies at the Rb system of Peloponnese, along a unique area of potential contact between the Rb races GRKA with $2n = 28$ and GROL with $2n = 24$. Although sharing five Rb chromosomes, these Rb races are characterized by monobrachial homology, since the former is moreover homozygous for Rb(3.6) and the latter for Rb(1.3) and Rb(4.6). Their potential hybrids would form a pentavalent (1_1.3_3.6_6.4_4) during meiosis, with possible deleterious effects in fertility. Our studies have shown that along the studied contact zone, GROL and GRKA do remain very close to each other. Interestingly, though, at its western side, another Rb race with $2n = 30$, GRP1, comes between GROL and GRKA, forming hybrids with both Rb races and preventing their direct contact. The same happens at the eastern side of the contact zone, this time, however, the role of the intermediary played by the acrocentric population ($2n = 40$). At a central area of the contact zone, though, we did come across F_1 hybrids of GROL and GRKA ($2n = 26$), along with other complex hybrids, which denotes that they do manage to hybridize after all. This rather unexpected result demands the further elaborate study of this contact zone at the Rb system of Peloponnese.

PHYLOGEOGRAPHY AND BIOGEOGRAPHY

P20 INTRA- AND INTERSPECIFIC PHYLOGENY OF GENUS *Cervus* BASED ON COMPLETE MITOCHONDRIAL GENOMES

Maciej Matosiuk¹, Magdalena Świsłocka¹, Frank E. Zachos², Magdalena Czajkowska³, Anetta Borkowska³, Ghaiet M. Hajji⁴, Zbigniew Borowski⁵, Alexander P. Saveljev⁶, Ivan V. Seryodkin⁷, Tarlan Farahvash⁸, Hamidreza Rezaei⁹, Rasoul Vaez Torshizi¹⁰, Stefano Mattioli¹¹, Mirosław Ratkiewicz¹

¹Institute of Biology, University of Białystok

²Natural History Museum Vienna

³Institute of Biology, University of Białystok

⁴Zoological Institute, Christian-Albrechts-Universität

⁵Department of Forest Ecology, Forest Research Institute

⁶Russian Research Institute of Game Management and Fur Farming

⁷Pacific Geographical Institute FEB RAS; Far Eastern Federal University

⁸Islamic Azad University

⁹Gorgan University of Agricultural Sciences and Natural Resources

¹⁰Tarbiat Modares University

¹¹University of Siena

Genus *Cervus* has undergone through successful adaptative radiation during Pleistocene due to its enormous plasticity and its present distribution is most widespread among Cervids. Numerous studies have been carried out to untangle its phylogeny and evolutionary history. In this study we have sequenced 13 new mitochondrial genomes of red deer (*C. elaphus*) and wapiti (*C. canadensis*) and compared them with mitogenomes of Tarim red deer (*C. hanglu*), wapiti and sika deer (*C. nippon*) subspecies in order to: 1) resolve intraspecific mtDNA phylogeny of *C. elaphus*; and 2) investigate molecular evolution of mitochondrial genome in genus *Cervus*. Our analyses gave high support for a distinction of all five present-day *C. elaphus* haplogroups by the means of nucleotide and mitochondrial protein evolution. Interspecific comparisons also revealed high differentiation ranging from 3.5% to 7.0% in mtDNA protein-coding genes. Interestingly, the level of divergence between inland and island subspecies of *C. nippon* is close the level represented by species pairs in genus *Cervus* (3.0%). Our analysis indicates incongruence between mitochondrial and nuclear phylogeny of genus *Cervus*, and thus this issue should be investigated further to fully resolve the evolutionary history of this genus.

PHYLOGEOGRAPHY AND BIOGEOGRAPHY

P21 PHYLOGENETIC SIGNAL OF SMALL MTDNA AMPLICONS TO STUDY THE MAZAMA AMERICANA COMPLEX THROUGH NONINVASIVE GENETIC SAMPLING

Pedro Henrique Peres¹, Eluzai Sandoval¹, Márcio Oliveira¹, José Maurício Duarte¹

¹Deer Research and Conservation Center - São Paulo State University

The red brocket deer (*Mazama americana*) is recognized as a complex of cryptic species with striking karyotype variation and paraphyletic lineages. Biological material evaluated to date is limited, given the low number of samples, low accuracy of its geographical origin and spatial gaps. The difficulty to access forest neotropical deer samples has been successfully overcome through non-invasive genetic sampling and the use of scat-detection dogs. The design of appropriate genetic markers is essential for degraded samples analysis. We aimed to select small regions of mitochondrial DNA and analyze their phylogenetic signal to study the *M. americana* complex. We selected twenty individuals to compose a reference matrix containing the main cytotypes of the species and another fifteen animals representing 8 species of Odocoileini tribe. We partially sequenced Cyt B, Dloop, and ND5 genes to form a 2628 bp reference matrix. From this matrix, we designed specific primers to amplify five small regions (<300 bp) resulting in a 1398 bp matrix. We compared the polymorphism and the phylogenetic signal in trees generated by Bayesian Inference of both matrices and tested the amplification success of designed primers in fecal samples. The small matrix had equivalent polymorphism relative to the reference matrix and the phylogenetic hypotheses were mostly congruent and well supported in both matrices, recovering the cytotypes in monophyletic groups. Amplification success was over 90% in the overall set. The designed markers have the potential to provide an extensive and geographic assigned genetic sampling that will bring information about distribution and isolation of the species populations in South America, contributing for their taxonomic review and conservation status assessment.

CLIMATE CHANGE AND POPULATION DYNAMICS

P22 NON-FOREST PATCHES INSIDE A CONTINUOUS FOREST: SMALL MAMMALS IN THE MID-FOREST CLEARINGS OF THE BIAŁOWIEŻA PRIMEVAL FOREST

Elżbieta Jancewicz

*Department of Forest Zoology and Wildlife Management, Faculty of Forestry, Warsaw University of Life Sciences – SGGW
Warsaw, Poland*

The analysis was performed on clearings that were created over 100 years ago; they are located along the former narrow-gauge forest railway track and presently sustained in an open state due to more or less regular mowing. The clearings form a system of small patches of deforested environmental 'islands', variably connected by compartment borders and communication routes. The surface area of these patches is rather small, and their spatial distribution may reflect fragmented landscapes of different scale and character. The aim of the presented study was (i) to check the importance of small-sized non-forested patches for the number and species diversity of small forest and non-forest mammals and (ii) to investigate which features of these patches (physical and environmental) are most conducive to their use by this group of vertebrates. Over a period of more than ten years (2007-2018), for six years in spring, summer and autumn, the mammals were captured using life-traps (CMR catch-mark-release method). Based on the collected data, the richness of species, species diversity and relative abundance of small mammals in various non-forest patches inside a compact forest were determined. The presence of 13 species with different ecological characteristics has been recorded: 9 species of rodents (Rodentia) and 4 species of shrews Soricidae (Soricomorpha), including bicoloured white-toothed shrew *Crocidura leucodon*. The small mammals assemblage was dominated by common vole *Microtus arvalis*; equally abundant was yellow-necked mouse *Apodemus flavicollis*. It was concluded that different species of small mammals use mid-forest clearings in various ways.

CLIMATE CHANGE AND POPULATION DYNAMICS

P23 POPULATION VIABILITY ANALYSIS OF THE ITALIAN OTTER POPULATION

Anna Loy, Sara Diamente¹, Mirko Di Febbraro¹

¹*University of Molise*

Being a top predator of the high vulnerable freshwater ecosystems, the Eurasian otter suffered a severe decline in the last century. Despite enforcement of regulations and habitat restorations favored its recent recovery in many European countries, the Italian population is still Endangered in the national red list, being confined in less than 50 rivers of south-central Italy. To ensure that the population is self-sustaining over the long term we run a Population Viability Analysis (PVA) to forecast population health and extinction risk in 100 years. Special efforts were devoted to data collection and analysis to estimate current population size, carrying capacity, incidence of road kills on mortality rates, and impacts of catastrophes. For the latter we evaluated the frequencies of extreme droughts and floodings in the study area, having a detrimental effect respectively on resources availability and cub survival. To account for discrepancies in data and estimates, we built five groups of three scenarios, each group considering different values for initial population size, carrying capacity, number of catastrophes, percentage of reproductive females, and road kill mortality rates. Each scenario was run using Vortex with 1.000 iterations. Only in six over 15 scenarios Extinction Probability (EP) was 0 after 100 years, and the population reached and remained stable at carrying capacity. In nine scenarios EP varied from 14 to 100%, with road kills, percentage of reproductive females and catastrophes as the main responsible factor. Results evidenced that estimates of initial population size may greatly affect the final output, and underlined the need of mitigation measures to limit road collision risk and the impact of climate changes.

CLIMATE CHANGE AND POPULATION DYNAMICS

P24 ESTIMATING CABRERA VOLE ABUNDANCE BASED ON PRESENCE SIGN COUNTS: AN EVALUATION USING GENETIC NON-INVASIVE SAMPLING

Dinora Peralta¹, Teresa Vaz Freire², Tiago Mendes¹, Clara Ferreira³, Sara M Santos⁴, Paulo Célio Alves⁵, António Mira¹, Pedro Beja⁶, Joana Paupério⁶, Ricardo Pita¹

¹*Unidade de Biologia da Conservação, Departamento de Biologia, Universidade de Évora, Évora, Portugal*

²*Departamento de Biologia Animal, Faculdade de Ciências, Universidade de Lisboa, Lisboa,*

³*Animal Ecology - University of Potsdam, Potsdam, Germany*

⁴*ICAAM, Instituto de Ciências Agrárias e Ambientais Mediterrânicas, Universidade de Évora, Évora, Portugal*

⁵*Departamento de Biologia, Faculdade de Ciências da Universidade do Porto, Porto, Portugal*

⁶*InBIO/CIBIO -UP, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Vairão, Portugal*

Understanding the factors that affect the spatial and temporal variation of species population size provides baseline guidance for adequate conservation management, both for the protection of endangered species, and the control of pest outbreaks. Despite the great efforts and developments, knowledge of the size of wild populations remains a main challenge in ecology studies, particularly for elusive species of conservation concern. Capture–recapture (CR) methods remain the ‘golden standard’ for estimating species population size, but these are often hard to implement for rare and elusive species that are difficult to capture using standard methods (e.g. life-trapping, camera-trapping). In addition, CR methods are largely impractical and cost-prohibitive to conduct over large spatial scales, hampering proper evaluation of species population status and trends. Therefore, population size indexes (PSI) based on presence sign surveys have been often used as alternative measures for population monitoring. However, before being used in wildlife management decisions, PSI need to be validated against known standards. Here we assess the utility of presence signs counts as PSI for the Cabrera vole, a near-threatened, elusive small mammal, endemic to the Iberian Peninsula. We generated 18 PSI based on presence sign counts under varying sampling efforts and used GLMM to relate those PSI to the population size estimates based on CR data obtained from genetic non-invasive sampling. Overall, our results suggest that PSIs based on latrine counts conducted over relatively short-time sampling efforts may provide a useful, cost-effective alternative for monitoring Cabrera vole populations over large spatial scales, which should be crucial to inform conservation management of the species.

CLIMATE CHANGE AND POPULATION DYNAMICS

P25 FACTORS REGULATING ACTIVITY AND DAILY TORPOR IN *Crocidura suaveolens* (SORICIDAE) UNDER CHANGING TEMPERATE CLIMATE – RESEARCH PROJECT AND FIRST RESULTS

Kamila Grossmann¹, Leszek Rychlik¹

¹Department of Systematic Zoology, Institute of Environmental Biology, Faculty of Biology, Adam Mickiewicz University, Poznań

With the climate changes, many plant and animal species have recently shifted their geographic ranges. Among small mammals, such shifts are observed in some shrews (e.g. *Crocidura russula* and *C. suaveolens*) - species that are able to enter daily torpor and extended considerably their geographic ranges to the north and east. Did torpor help them in this process? The basic function of torpor is to prevent energy loss during periods of food shortage and hindered foraging. However, among other postulated, but poorly investigated, functions of torpor are: facilitating the colonization of new areas, facilitating the coexistence of competing species, reduction of predation risk. The objective of this project is to investigate in *C. suaveolens*, living at the edge of its geographic range, how abiotic (season, ambient temperature, photoperiod) and biotic factors (food availability, competition pressure, predation risk, social thermoregulation by huddling) influence its activity and use of daily torpor. A series of laboratory experiments with video-registration and manipulations of the mentioned factors are planned for 3 consecutive winters and 3 summers. Torpor is detected based on the decrease of body temperature using thermo-dataloggers mounted into the floor of nests. The first experiments (performed under summer temperatures and photoperiod changed back to winter regime) suggest that: (1) *C. suaveolens* rarely enters torpor under high temperatures, (2) long nights decreased total time of activity but did not influence torpor, (3) huddling reduced duration of activity. The results will extend our knowledge about the life strategies and survival mechanisms in small mammals, which can be used in forecasting further changes in geographical ranges and managing their populations.

UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT

P26 MONITORING OF IMPACT OF EUROPEAN BISON ON HABITATS – A PRELIMINARY RESULTS

Daniel Klich¹, Axel Schwerk², Bartłomiej Popczyk¹, Wanda Olech¹

¹Faculty of Animal Sciences, Department of Genetics and Animal Breeding, Warsaw University of Life Sciences – SGGW

²Faculty of Horticulture, Biotechnology and Landscape Architecture, Laboratory of Evaluation and Assessment of Natural Resources, Warsaw University of Life Sciences – SGGW

Conservation of European bison in situ brings in practice transformation of habitats under the influence of this herbivore and conservation measures. We present a preliminary results of an assessment of European bison influence on plant and carabid fauna in two enclosures (Kobiór Forest District, and Niepołomice Forest District), and monitoring assumptions of a new free living population of European bison (Augustów Forest District). European bison can significantly influence of plant communities and carabid fauna assemblages, but only in higher grazing intensity. The monitoring of plants and carabid fauna in Augustów Forest District is basing on the frequency of presence of the European bison herd in the targeted meadows within the forest complex. We also present first results of effects of watering places construction inside Augustów forest complex on amphibians and bats. A higher diversity of amphibians and bats was observed in reservoirs, that were created for European bison in comparison to natural ones. Artificial reservoirs presented appropriate conditions for amphibians for living and reproduction, also for great crested newt, which was encountered (a species protected under European law) which was found in two of five reservoirs.

UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT

P27 THE PROJECTS REALIZED FOR WISENT PROTECTION IN POLAND

Wanda Olech¹, Zuzanna Nowak-Życzyńska¹, Wojciech Bielecki², Daniel Klich¹, Krystyna Cielniak¹

¹Faculty of Animal Sciences, Department of Genetics and Animal Breeding, Warsaw University of Life Sciences – SGGW

²Faculty of Veterinary Medicine, Department of Pathology and Veterinary Diagnostics, Warsaw University of Life Sciences – SGGW

Wisent (*Bison bonasus*) is the first species from the Mammalia cluster, for whose national strategy has been approved, although the implementation of the planned activities is not easy and complete. The aim of wisent protection in Poland is to increase the range and size of the population by improving living conditions and creating new herds both free roaming and in captivity. To achieve this goal, funding is needed, and because there is no coverage of active protection costs from the state budget, efforts to obtain funds from various sources are needed. Thanks to the activity of breeders with the support of scientific centers, for over 10 years we have been able to obtain funds to finance the goals of the wisent protection strategy. We would like to present results of our activities and plans for future. The wisent population in Poland increased, new herds were reintroduced and new enclosures were established. The continuous monitoring of health status has been implemented. The results of research in various fields are very important for the future of the species. Actually we carry out two projects, one financed by Forest Fund and second cofinanced by EU money in frame of the Operational Program Infrastructure and Environment. These projects cover almost whole Polish population of wisent and involve 25 units of State Forests and Białowieża National Park.

UNGULATE ECOLOGY, CONSERVATION AND MANAGEMENT

P28 MANAGING BEHAVIOR, NOT NUMBERS– INVESTIGATING DRIVERS BEHIND UNGULATE IMPACT ON FORESTRY AND AGRICULTURE

Anna Widén

Wildlife, Fish and Environmental Studies

In Sweden numbers and distribution of ungulates increases, and during the last decades ungulate communities have changed from single or two species (moose and/or roe deer) to include species such as red deer, fallow deer, and wild boar. These species inhabit landscapes that are modified by humans, thus increasing human-wildlife conflicts, and we face a growing challenge of managing these animals. Ungulate management usually focuses on regulating population size by hunting, but this is often inefficient in terms of reducing their impact. Hunting effectiveness is often defined as numbers of killed animals per hunting effort, but there is a lack of knowledge if decreasing the number of animals reduces the damage correspondingly. One aspect that is usually not taken into account is how animal behavior might be affected by other management actions than hunting. There is therefore an urgent need for more knowledge of what drives ungulate behavior and distribution. To achieve this we will investigate how factors such as food availability, risk perception, thermal acceptance and landscape composition influences ungulate damage patterns. We will develop and test new management strategies with the aim of changing the distribution of wildlife, rather than just reduce numbers. In an area of 25x25 km in southern Sweden, we will conduct large scale landscape experiments including exclosures, manipulation of food and manipulation of risk. This area hosts all 5 ungulate species present in Sweden and are experiencing the most extreme ungulate densities in our country, with increasing human-wildlife conflict. Hopefully this study will result in new management methods that reduces ungulate impact.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

P29 THE BEST WAY TO IDENTIFY THE AFRICAN PAINTED DOGS: FIRST TRIAL OF COMPUTER-AIDED IDENTIFICATION

Kanako Ake¹, Tadatoshi Ogura², Gregory Rasmussen³, Yayoi Kaneko¹

¹*Tokyo University of Agriculture and Technology*

²*Kitasato University*

³*Painted Dog Research Trust, University of Zimbabwe*

In order to obtain accurate ecological information to conserve the endangered painted dog, individual identification from their tri-coloured pelage is essential. This is done in the field manually however it requires expert eyes, and is time-consuming, hence an accurate and efficient method is essential. Whilst computer-aided identification has been used in other species, to date it has not been attempted in painted dogs. To determine the feasibility of computer-aided identification, 15 painted dogs in Yokohama Zoo, Japan were photographed from October 17-20, 2017. Images were cropped in three ways; whole-body with background (BB), whole-body without background (BW) and a crop of the trunk (BT). Results were compared using three software (Hotspotter, Wild-ID, I³S), against human identification. 20 non-trained examinees visually identified 297 photos, which were the same images for software. In Hotspotter the different crops produced significantly different results BB = 86.5%, BW = 95.6%, BT = 90.6% (Cochran's Q test, BB:BT, BB:BW; $p < 0.05$). Three software was therefore compared using BW with the following accuracy rates: Hotspotter 95.6%, Wild-ID 52.5%, I³S 46.1%, with Hotspotter being significantly different (Cochran's Q test, $p < 0.05$). With visual identification, the mean accuracy rate was only 61.2%. These results highlight that visual identification may not be of value for untrained eyes, and whilst ultimately an expert eye will be needed to scrutinize the software identification, the software identification can be a valuable time-saving tool to expedite the identifications needed for this species. Whilst cropping of the background facilitates better software identification, though valuable it does add a time-consuming layer of work that perhaps could be automated.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

P30 HABITAT USE OF THE ENDANGERED SCANDINAVIAN ARCTIC FOXES

Rasmus Erlandsson¹, Anders Angerbjörn¹, Helen Rebane¹

¹Stockholm University

For territorial animals, territory quality (food availability and predation pressure) can have a large effect on survival, breeding success and in the long run, fitness. Habitat characteristics, such as vegetation types, topography and distance to unsuitable habitats changes the time available for an individual involved in foraging, juvenile care and territory maintenance. Such differences would be therefore be expected to generate different movement patterns and territory use. High definition small size tracking collars have recently made it possible to study animals with relatively small body size, in remote areas. The arctic fox (*Vulpes lagopus*) is well known for its ability of long-range dispersal over the arctic sea ice, and recently, individuals in Canada and Svalbard have been observed to move several 1000 km in a relatively short time. In contrast, the Scandinavian arctic fox population is isolated to mountain tundra areas in Sweden and Norway and despite their physical ability to move over long distances, they are typically restricted to their local mountain area all year long. During summer, adults invest considerable time in raising juveniles and are easily observed on den sites, but detailed information on habitat use has not been recorded. And habitat use and movement patterns outside the breeding season is at large unknown. Here we present the first high quality data on movement patterns and habitat use recorded from the endangered Scandinavian arctic fox population, and how it is related to territory characteristics.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

P31 EFFECT OF INBREEDING ON CUBS' BODY MASS IN EURASIAN LYNX (*Lynx lynx*)

Mariya Erofeeva¹, Sergey Naidenko¹

¹A.N. Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences

The development of industry and agriculture, the continuous growth of human population on Earth have dramatically increased anthropogenic pressure on natural ecosystems and wildlife. One of the most well-known problems is the fragmentation of natural habitats, and decrease of genetic diversity in these populations and increased probability of reproduction with genetically closely-related individuals (inbreeding). However, in felids the effect of inbreeding was studied rarely and data are scarce. We decided to study the effect of inbreeding on offspring quality in captivity in the Eurasian lynx. The aim of this study was to estimate body mass of cubs from the parents with a different inbreeding coefficient. This study was conducted in A.N. Severtsov Institute of Ecology and Evolution (the biological station Tchernogolovka), Russia in 1998-2016. During the whole period of the study all animals were kept in the same enclosures and had the same diet. We used body mass data for 22 litters (58 cubs). Correlation analysis of the body mass of cubs that were mothered by the parents with different inbreeding coefficients showed a significant negative correlation between these two parameters. Cubs' body mass in the first few days of their life correlated negatively with the inbreeding coefficient of their parents ($r = -0.8$; $t = 6.02$; $p = 0.001$). Average cubs' body mass at third-fourth days after birth varied from 355.4 ± 26.6 g (cubs of the parents with the inbreeding coefficient (0.37-0.46)) to 607.2 ± 34.75 g (cubs of unrelated parents). These differences in body mass disappeared to two months of age of cubs after the diet changes. This study showed that inbreeding have obvious effect on felids development. This study was supported by the Russian Science Foundation (18-14-00200).

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

P32 EURASIAN LYNX *LYNX LYNX* IN WESTERN POLAND – CURRENT STATUS AND PROSPECTS OF POPULATION DEVELOPMENT

Iga Kwiatkowska¹, Robert W. Mysłajek¹

¹University of Warsaw, Faculty of Biology, Institute of Genetics and Biotechnology,

Before becoming strictly protected in Poland in 1995, Eurasian lynx *Lynx lynx* occurred mainly in Carpathian Mountains and eastern part of the country. Thus it was expected, that due the protection it will recolonize western Poland, where vast forests with abundant roe deer populations are available. We have reviewed records of the lynx presence in western Poland (2000–2018), taking under consideration only records fulfilling the criteria of SCALP (Status and Conservation of the Alpine Lynx Population). We revealed, that after over two decades of species protection, the range of permanent occurrence of the lynx has not substantially extended westwards. Single individuals disperse through the entire country, but west to the Vistula river lynx reproduction is still restricted to Kampinos National Park and adjacent forests, where reintroduction of the species was conducted 1990s. We conclude, that dispersal of the lynx in central and western Poland is hampered by discontinuity of ecological corridors due to urbanization and development of transport infrastructure, while their settlement is hindered by the simplification of the structures of local forest, which are mostly highly managed Scots pine *Pinus sylvestris* monocultures.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

P33 RECOVERY OF THE EURASIAN OTTER (*Lutra lutra*) IN CENTRAL AND SOUTHERN ITALY: A NEW HOPE

Simone Giovacchini¹, Antonio Antonucci², Giuseppina De Castro³, Giovanna Di Domenico⁴, Mirko Di Marzio⁴, Maurizio Marrese⁵, [Anna Loy](#)¹

¹University of Molise

²Majella National Park,

³Associazione Teriologica Italiana ONLUS,

⁴Raggruppamento Carabinieri Biodiversità - Reparto Biodiversità Pescara

⁵Centro Studi Naturalistici ONLUS

The Eurasian otter is one of the most endangered mammals in Italy which range is restricted to the south central regions of the peninsula. Following implementation of EU regulations and freshwater habitats protection, the species is now recovering after decades of local extinctions. Here we present the results of opportunistic surveys run from 2015 to 2019 at 407 sites along the boundaries of the extent of occurrence (EOO) of the species. Results allowed to detect the return in the National Park of Abruzzo, Lazio and Molise (upper part of Sangro river) and a likely northward expansion (Pescara river basin). The widespread occurrence found in the Volturno-Calore hydrographic network led to the rejoining of two former distinct subpopulations. Recovering is proceeding faster along the Tyrrhenian compared to the Adriatic side, and otters are likely to colonize the Liri-Garigliano river basin in the short term, whereas recovery in northern river basins of Apulia is more problematic. As dispersal and colonization of new river basins is more likely to occur along coastal areas, future conservation actions should primarily focus on connectivity at the boundaries of the current EOO, through restoration and preservation of downstream portions of riverine habitat and mitigation of road kill risk in these highly disturbed and human populated areas.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

P34 THE MOSTELA: AN ADJUSTED CAMERA-TRAPPING DEVICE, A PROMISING MONITORING TOOL TO STUDY COMMON WEASEL (*Mustela nivalis vulgaris*)

Jeroen Mos¹, Tim Hofmeester¹

¹Dutch Small Mustelid Foundation

In many countries, the population status of weasel (*Mustela nivalis*) and stoat (*Mustela erminea*) is uncertain due to the difficulty of monitoring these species. In our study area near Dieren, the Netherlands, we tested the efficiency of a recently developed camera-trapping device, the Mostela, as a new monitoring technique for small mustelids. During March – October 2017 and February – October 2018 we placed Mostelas in linear landscape features and other microhabitats thought to be frequented by weasels. We tested for yearly and seasonal differences in trapping rate and detectability using an occupancy-modelling framework. We found:

- 1) a higher trapping success and naïve occupancy in 2017 than 2018;
- 2) a clear difference in detection probability between seasons;
- 3) the highest detection probability in summer 2017 and autumn 2018.
- 4) that in summer and autumn a Mostela placed in the field for 2 weeks gives a 95-98% probability of detecting a weasel if the species is present in the micro habitat;
- 5) that the Mostela technique generates useful ecological data on activity patterns and recognition of individual weasels.

Concluding, the Mostela shows great promise as a monitoring tool to study the occurrence and ecology of common weasels. Further development of individual recognition from images would enable using the Mostela for density estimates applying spatially-explicit capture recapture.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

P35 A GENETIC LOOK AT SCENT MARKING BEHAVIOUR IN WOLVES *Canis lupus*

Kinga Magdalena Stępnia¹, Maciej Szewczyk¹, Natalia Niedźwiecka², Robert W. Mysłajek¹

¹*Institute of Genetics and Biotechnology, Faculty of Biology University of Warsaw*

²*Association for Nature "Wolf"*

In wolves *Canis lupus* scent marking plays an important role in territory defence. In Europe studies on patterns of scent marking in wolves have mostly been conducted in mountains or primeval forests, while managed forest of the Northern European Plains have been neglected. We aimed to assess patterns of wolf territory marking with scats and urine in managed lowland forests in north-eastern Poland, using tracking and genetic analysis based on autosomal microsatellite loci. We found that all members of the wolf family groups leave scats and urine on roads. However, wolves the most intensively marked crossroads and its vicinity, especially on roads accessible only for four-wheel cars. We delivered further evidences, that crossroads of forest roads play crucial role in the wolf scent marking. Results of our study may be useful for the inventory of the wolf population based on collection of indirect signs of their presence or non-invasive genetic samples.

PREDATOR ECOLOGY, CONSERVATION AND MANAGEMENT

P36 MORPHOLOGICAL AND HISTOLOGICAL STUDY OF THE BEAR VOMERONASAL ORGAN

Jumpei Tomiyasu¹, Daisuke Kondoh², Hideyuki Sakamoto³, Naoya Matsumoto³, Shingo Haneda⁴, Motozumi Matsui⁴

¹*Department of Reproductive Immunology and Pathology, Institute of Animal Reproduction and Food Research, Olsztyn, Poland*

²*Laboratory of Veterinary Anatomy, Obihiro University of Agriculture and Veterinary Medicine*

³*Noboribetsu Bear Park, Noboribetsu, Japan*

⁴*Laboratory of Theriogenology, Obihiro University of Agriculture and Veterinary Medicine*

In non-territorial solitary animals, such as bears, indirect communication through chemical signaling is speculated to be effective to convey information. Behavioral studies have reported that male bears exhibit flehmen behavior which is considered as the transmission of chemical signals to vomeronasal organ (VNO), probably to detect the female estrus. The VNO is the peripheral receptor organ of the vomeronasal system and is closely associated with changes in reproductive behavior in mammals. However, little is known about morphological and histological properties of the VNO in bears. In the present study, to clarify the role of VNO in brown bears (*Ursus arctos*), histological, histochemical and ultrastructural analyses were conducted. The VNO of bears was located at the rostral half of the nasal region, and it opened into the mouth like the VNO of most carnivores. Receptor cells in the VNO of the bear possessed both cilia and microvilli like those of dogs. The secretory cells of ursine VNO were composed of vomeronasal gland cells, multicellular intraepithelial gland cells and goblet cells, and the histochemical and ultrastructural analyses showed that secretory granules in these cells had various properties. Furthermore, the multicellular intraepithelial gland cells were densely located in the invagination of the vomeronasal lumen at the middle region. To our knowledge, intraepithelial gland cells and the invagination in the VNO are unique features of brown bears. The VNO in the brown bear, especially the secretory system, is morphologically well-developed, suggesting that this organ is essential for information transmission in bears.

MAMMAL PALEOECOLOGY: IMPLICATIONS FOR CONSERVATION AND RESTORATION

P37 SMALL MAMMALS FROM EARLY NEOLITHIC SITES IN THE CENTRAL ZAGROS

Jeremy Herman¹, Mel Morlin², Robin Bendrey²

¹National Museums Scotland

²University of Edinburgh

The Early Neolithic settlements at Bestansur and Shimshara are situated in the western foothills of the Zagros mountain range, close to the Iraqi Kurdistan border with Iran. The buildings at Bestansur are almost 10,000 years old and this globally important site provides some of the earliest evidence for the transition to a sedentary human lifestyle. About 650 cranial and postcranial skeletal fragments from small mammals, collected from 2012 to 2014 during the Central Zagros Archaeological Project excavations at these sites, were examined and compared with museum reference material. Remains of house mice *Mus sp.* were by far the most frequent, consistent with the origin of their commensal habit in these first human settlements of the Near East. Some of the remains are indicative of intrusive burrowing, probably associated with a later period of human occupation, so further taphonomic analysis will be required to secure the Neolithic origin of specific remains. Other rodents from more than 10 genera have also been identified, including voles of the genus *Microtus*, as well as two species of hedgehog. The fauna is consistent with a dry and scrubby landscape, albeit with limited woodland and sources of water, and provides an indication of the habitat in which agriculture first developed here. Further work on faunal remains from these and other related sites may help us to understand better the ecological changes that have accompanied the agricultural transformation of the landscape over the last 10 millennia.

MAMMAL PALEOECOLOGY: IMPLICATIONS FOR CONSERVATION AND RESTORATION

P38 THE IMPACT OF MAJOR WARMING AT CA. 14.7 KA CAL BP ON ENVIRONMENT AT LOCAL SCALE (ORAWA-NOWY TARG BASIN, WESTERN CARPATHIANS, POLAND) ON THE BASIS OF THE SUCCESSION OF VERTEBRATE COMMUNITIES

Anna Lemanik¹, Mateusz Baca², Krzysztof Wertz¹, Paweł Socha³, Danijela Popović⁴, Teresa Tomek¹, Grzegorz Lipecki¹, Barbara Miękina¹, Aleksandra Żeromska⁵, Andrea Pereswiet-Soltan⁶, Zbigniew Szyndlar¹, Paweł Mackiewicz⁵, Adam Nadachowski¹

¹*Institute of Systematics and Evolution of Animals, Polish Academy of Sciences*

²*Laboratory of Palaeogenetics and Conservation Genetics, Centre of New Technologies, University of Warsaw,*

³*Department of Paleozoology, Institute of Environmental Biology, Wrocław University*

⁴*Laboratory of Palaeogenetics and Conservation Genetics, Centre of New Technologies, University of Warsaw; Institute of Biochemistry and Biophysics, Polish Academy of Sciences,*

⁵*Department of Bioinformatics and Genomics, Faculty of Biotechnology, Wrocław University*

⁶*Department of Paleozoology, Institute of Environmental Biology, Wrocław University*

There is a widespread belief that the abrupt warming ca. 14.7 ka cal BP had a profound impact on environment. However, the direct correlation between the global climatic event and changes in local environments is not obvious. Therefore, we examined faunal succession in intra-mountain basin of Western Carpathians to assess the potential influence of the climatic change between GS-2a and GI-1e on the local environment. We investigated three vertebrate assemblages (total NISP = 18,745; MNI = 7,515; 138 taxa) from Obłazowa Cave (western entrance) and the Rock overhang in Cisowa Rock, radiocarbon dated to the period before and after the global warming, between ca. 17.0 and 14.0 ka cal BP. Our data revealed that the major abrupt warming that occurred ca. 14.7 ka cal BP had little impact on the environment, which can suggest a resilience of local ecosystems to the global climate change in the Central Europe. The increase in fauna population sizes and species diversity in local biotopes was gradual and began long before the temperature increase. This is supported by the analysis of ancient DNA of *Microtus arvalis*, which showed a gradual increase in the effective population size since 19.0 ka cal BP. The results of palaeoclimatic reconstruction pointed to similar climatic conditions throughout the studied period. The differences in the annual mean temperatures in the area did not exceed 0.5°C.

MAMMAL PALEOECOLOGY: IMPLICATIONS FOR CONSERVATION AND RESTORATION

P39 PHYLOGEOGRAPHY, GENETIC DIVERSITY AND HABITAT USE OF MOOSE (*Alces alces*) IN EURASIA IN LATE PLEISTOCENE AND HOLOCENE - INTRODUCTION TO AN ON-GOING PROJECT

Magdalena Niedziałkowska¹, Danijela Popović², Mateusz Baca², Krzysztof Stefaniak³, Maciej Sykut¹, Piotr Chibowski², Małgorzata Suska-Malawska², Paweł Mackiewicz³

¹*Mammal Reserach Institute PAS*

²*University of Warsaw*

³*Wrocław University*

The genetic diversity of moose (*Alces alces*) was probably higher and the Eurasian population of the species was more homogenous in the past than it is observed in the contemporary times. We hypothesize that the range of moose, their effective population size and genetic diversity have been changing in time with climatic oscillations, namely decreasing in warmer periods. The moose survived the LGM in larger area than it was previously thought and responded differently than other species of Eurasian large mammals to climate changes. In the Holocene the range of moose shrunk significantly and the Eurasian population disappeared from some of its LGM refugial areas but probably survived in large continuous range in the eastern part of Europe and in some areas in Asia. In addition to climate oscillations also humans had significant impact on the distribution and genetic diversity of moose. In our project we plan to recognize the genetic diversity, to reveal habitat use and to identify the changes in the range of the species in Eurasia in the time period of the last 50 000 years using various interdisciplinary methods. In the final step, the changes in the range, occupied habitats, effective population size and the genetic diversity of moose will be compared with the climatic oscillations and the changes in ranges of different vegetation types since the Late Pleistocene. The study will be performed using novel research method such as analyses of the whole mtDNA genomes, stable isotope (¹³C,¹⁵N) analyses of bone collagen, AMS radiocarbon dating and spatial analyses using Geographic Information Systems (GIS). In our studies we will use both the contemporary samples as well as the fossil materials collected from different zoological collections in Eurasia. The project is financed by the National Science Centre (grant no. UMO-2018/29/B/NZ8/01173).

MAMMAL PALEOECOLOGY: IMPLICATIONS FOR CONSERVATION AND RESTORATION

P40 DIFFERENTIATION OF PLEISTOCENE AND RECENT *Saiga* IN TIME AND SPACE BASED ON MORPHOMETRIC STUDY OF CRANIAL REMAINS

Urszula Ratajczak¹, Krzysztof Stefaniak¹, Aleksandra Żeromska², Przemysław Gagat², Paweł Mackiewicz²

¹Department of Paleozoology, Institute of Environmental Biology, Faculty of Biological Sciences, University of Wrocław

²Department of Bioinformatics and Genomics, Faculty of Biotechnology, University of Wrocław

One of important components of Pleistocene steppe and steppe-tundra faunal complex was the saiga antelope (genus *Saiga*), which is now critically endangered and inhabits only several isolated regions in Central Asia. In the Pleistocene, however, saiga was widely spread from Europe, across Asia up to North America. This vast distribution both in space and time caused that several morphological forms were described. Most often two forms are recognized, borealis, which became extinct at the beginning of the Holocene, and tatarica, which has survived to the present. Since the diversity of this genus is not fully understood, we conducted extensive morphometric analyses of cranial material of saiga covering the whole region of its distribution, from the Pleistocene to the recent. The study showed that the borealis form was larger in several length skull dimensions and occipital region than tatarica, which in turn showed larger diameters of horncore base. Moreover, we found a significant decrease in many skull measurements of saiga since the Middle Pleistocene till modern times, which was probably associated with increasing humidity and climate warming as well as shrinkage of open steppe habitats favourable for this nomadic species. The observed significant differences between Pleistocene and recent forms as well as between various geographical subgroups indicate that the saiga population was subjected to temporal and spatial differentiation. However, the temporal factor was more important in variation of saiga skull than the geographical distribution.

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY**P41 DO OUR NEIGHBORS MAKE US STRONGER?****Galina Alekseeva¹, Polina Klyuchnikova¹, Sergey Naidenko¹***¹A.N. Severtsov Institute of Ecology and Evolution*

Group living implies a higher level of competition for resources, higher rates of pathogens transmission and multiple infections (Lochmiller, Deerenberg, 2000; Nunn et al., 2003). Accordingly, individuals at low- and high-density populations may have differences in immune function (Downs et al., 2015). Domestic cat lives both solitary and in large social groups (Pontier, Natoli, 1996; Say et al., 2002). We aimed to compare some indexes of innate immunity in domestic cats living at different population density. The study was conducted in the steppe region (Zabaikalsky Krai, Russia) in November 2018. We weighed cats and collected their blood samples in Kulusutay village (63 animals/km²; n = 24, 16 males and 8 females) and surrounding herdsmen stations (0.25 animals/km²; n = 23, 13 males and 10 females). We counted the total WBC number and the number of different types of leukocytes for all animals. Body mass of cats from the village was less than ones from herdsmen stations ($F_{(1,43)} = 4.45$, $p = 0.04$) and depended on animals sex ($F_{(1,43)} = 22.72$, $p = 0.00$). The total WBC number ($F_{(1,43)} = 8.15$, $p = 0.01$), as well as number of neutrophils ($F_{(1,43)} = 7.78$, $p = 0.01$), monocytes ($F_{(1,43)} = 4.98$, $p = 0.03$) and eosinophils ($F_{(1,43)} = 7.27$, $p = 0.01$) was higher in cats from the village. Also, the number of eosinophils in females was higher than in males, but only in the village ($F_{(1,43)} = 4.97$, $p = 0.03$). The ratio of neutrophils and lymphocytes did not differ significantly in these two locations ($F_{(1,43)} = 1.36$, $p = 0.25$), although it was extremely low in cats from herdsmen stations and varied highly in the village. Our results confirm that living in a high-density group of conspecifics leads to greater activation of the immune system of individuals. This study was supported by the Russian Science Foundation (18-14-00200).

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY

P42 AUTOMATIC TRANSPONDER READERS – A NEW TOOL FOR STUDYING ACTIVITY AND MOVEMENT OF SMALL MAMMALS

Zbigniew Borowski¹, Karol Zub², Jan Boratyński²

¹Forest Research Institute, Sękocin Stary, Poland

²Mammal Research Institute PAS, Białowieża, Poland

Passive implanted transponders (PIT-tags) are currently widely use in identification of individuals in animal studies and have successfully replaced most of old-time marking methods. The advantage of this technique is an automatic registration of an animal's presence and storage of collected data. However, the main limitation of the automatic systems is high power consumption. Thus, to reduce the energy loss energy-efficient motion detectors were applied. Newly implemented detectors turn on the power supply only when initiated by animal presence. Combination of transponder readers with camera-traps was used in order to estimate the proportion of marked and unmarked individuals in the population. In addition, this design enables the application of capture-mark-recapture (CMR) statistical models. In comparison with traditional methods, the new technique is by far more cost-effective and is particularly suitable for long-term data collection. To demonstrate usefulness of Automatic Transponder Readers we present data on activity, movement and mortality of small mammals (mice, voles, dormice, and weasels).

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY

P43 PLASTICITY IN DAILY ACTIVITY PATTERNS OF A KEY PREY SPECIES TO REDUCE PREDATION RISK

Esther Descalzo¹, Jorge Tobajas¹, Rafael Villafuerte², Rafael Mateo¹, Pablo Ferreras¹

¹Instituto de Investigación en Recursos Cinegéticos IREC, Instituto de Investigación en Recursos Cinegéticos IREC, CSIC-UCLM-JCCM

²Instituto de Estudios Sociales Avanzados IESA-CSIC

Some prey species can shift their daily activity patterns for reducing the predation risk. In turn, predators develop strategies to increase their chances of meeting and capturing prey. The European or wild rabbit (*Oryctolagus cuniculus*) is a key prey for many predators in Iberian Mediterranean ecosystems. Our aim was to test if rabbits can adapt their activity to different predation risks. Rabbits were translocated to a semi-permeable fenced plot and to unfenced areas of central Spain during two periods. We estimated daily activity patterns and relative abundance index (RAI) for both rabbits and carnivore predators using camera-traps. Rabbit daily activity differed between fenced and unfenced areas, being more nocturnal in the first scenario. Activity overlap between Egyptian mongooses (*Herpestes ichneumon*, strictly diurnal) and rabbits was low in all the areas in the first year, but overlap was moderate in unfenced areas in the second year, when RAI for Egyptian mongoose decreased. However, activity overlap between red fox (*Vulpes vulpes*, nocturnal and crepuscular) and rabbits in unfenced areas was high and moderate in the first and second year, respectively. Foxes were not detected in the fenced plot in the first year and were scarcely detected in the second year. These results suggest that rabbit nocturnal activity in the fenced plot was an adaptation to avoid the predation risk by the diurnal Egyptian mongoose depending on its relative abundance. Contrarily, rabbits in unfenced areas showed the typical daylight/twilight activity patterns as an adaptation to reduce the predation risk by the whole carnivore community. We conclude that rabbits adapt their daily activity patterns to reduce the predation risk depending on the pressure exerted by their predator species.

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY

P44 DOES THE TIME MATTER? INDIVIDUAL VARIATION IN THE ONSET OF ACTIVE SEASON IN EDIBLE DORMICE

Karolina Iwińska¹, Jan S. Boratyński², Kateryna Fyałkowska³, Zbyszek Boratyński⁴, Zbigniew Borowski³

¹*Institute of Biology, University of Białystok, Białystok, Poland; Mammal Research Institute, PAS, Białowieża, Poland*

²*Mammal Research Institute, Polish Academy of Sciences, Białowieża, Poland*

³*Department of Forest Ecology, Forest Research Institute, Poland*

⁴*Research Center in Biodiversity & Genetic Resources, University of Porto, Porto, Portugal*

As other heterothermic mammals, the edible dormice spend the majority of their life inactive. Hibernation shortens the active season and reduces mortality risk via predator avoidance. On the other hand, hibernation is associated with gonadal atrophy and thus negatively affects reproduction. That is why the end of hibernation and an earlier emergence in spring is crucial for reproductive success. Little is known about inter-individual variation in the timing of reproduction. In our research study for three consecutive years (2016-2018) we used an automatic logging system for ID tags mounted in nest-boxes. We observed clear sex-related differences in the pattern of the onset of an active season. Males, contrary to females displayed repeatable pattern with the timing of onset of the activity season. Results indicate that the time of the onset of active season is a consistent trait of dormice males. It suggests that females evolved flexible reproductive strategies related to resources availability, whereas males have more fixed life-history strategies. In accordance with the evolutionary trade-off, the males that start the active season earlier may increase reproductive success but also may have higher mortality rates. While males that emerge from hibernation later reduce their reproductive success but also increase survival.

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY

P45 EFFECT OF FIRE ON SMALL MAMMAL FORAGING BEHAVIOUR

Marina Morandini

University of Arizona

Climate change is increasing the magnitude of extreme environmental events, such as wildfire intensity and occurrence. These phenomena represent a challenge for wildlife, as if animals survived the disruptive event, they would need to adapt to a completely changed environment. In the summer of 2017, the Frye Fire burned 48.4 acres on Mt Graham, Arizona (USA), creating a mosaic landscape of different burn severity patches. We used Giving-Up Density to test small mammal foraging behaviour and the cost associated with it in different burn severities. In 4 different areas, we placed 5 trays filled with sand and seeds in completely burned patches, 5 in partially burned patches and 5 in unburned patches. Moreover, we placed one camera trap in video mode facing each tray to assess the species visiting the tray and their behaviour. The experiment was carried out between May and July in 2018 and 2019 for 3 days. 10 species visited the trays, 7 target (small mammals) and 3 non-target species. GUD was higher in burned areas than unburned or partially burned areas confirming that small mammals perceive a higher risk in areas where there is low vegetation cover. The analysis of the videos showed that even if chipmunks foraged in completely burned areas, the number of foraging bouts was higher than in unburned areas, probably as a consequence of the increased alert due to higher predator visibility related to the lower vegetation cover. These results show that small mammals visit highly burned areas while moving between less burned patches looking for food resources, but they modify their behaviour as a trade-off between gaining the food and minimize the predation risk. This is evidence of an adaptation of small mammal behaviour to a deeply modified habitat.

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY

P46 THE FOOD OF THE YELLOW-NECKED MOUSE (*Apodemus flavicollis*) AND THE BANK VOLE (*Clethrionomys glareolus*) IN LABORATORY EXPERIMENTS

Peter Mühlböck¹, Frantisek Sedlacek¹, Bozena Sera²

¹Institute of Zoology, University of South Bohemia

²Institute of Landscape Ecology, Comenius University

A total of 48 individuals of the Bank vole and the Yellow-Necked Mouse (12 males and females each) were housed in cages with different soils for a period of 80 days and given a mixture of seven different tree seeds species (total of eight grams) on days 1 and 2 and later on days 21 and 22 respectively to find out differences in seed preference. Each animal was weighed every day and a new seed mixture was put after the old not consumed seeds were taken away. Each seed species was determined for proteins (N), lipids, glucose, starch and cellulose, moreover the Ivlev index of electivity was calculated for every day and seed species and then grouped for days 1/2 and 21/22 by a one-way ANOVA. A PCA-analysis was done with the data of the nutrients to find out food preferences more clearly. Both species didn't differ a lot at food selection, except of acorns (with lots of glucose and starch), of which the Yellow-Necked mouse showed much more consumption. In general the Bank Vole showed a slightly higher difference between days 1/2 and 21/22 than the Yellow-Necked Mouse, but both species had a high consumption rate for seeds with high-energy contents like lipids and proteins (beechnuts, seeds of spruce, pine or lime-tree). Seeds with high contents of cellulose (hornbeam) were mainly rejected as well as high nutritious seeds of sweet cherry, which had a hard coat outside. It seemed that secondary metabolites (tannins, polyphenoles) also play a role in food preference, too.

BEHAVIOURAL AND EVOLUTIONARY ECOLOGY

P47 DIFFERENTIATION OF ACTIVITY RHYTHMS BETWEEN TWO COMPETING WATER SHREW SPECIES, *Neomys anomalus* AND *Neomys fodiens*, UNDER LABORATORY CONDITIONS

Leszek Rychlik¹, Oliwia Sęk¹, Roula Al Belbeisi²

¹Department of Systematic Zoology, Institute of Environmental Biology, Faculty of Biology, Adam Mickiewicz University

²Department of Zoology, School of Biology, Aristotle University of Thessaloniki, Greece

Hypotheses about the decrease of conflicts between the two competing water shrew species, *Neomys anomalus* and *N. fodiens* [below denoted by AA and FF], resulting from differentiation of activity rhythms and space use were verified in a laboratory experiment. Eight animals (4 AA and 4 FF) were kept together for 2 months in an enclosure (2.8 m²) provided with nest boxes, feeding trays and water basin. Their activity was video-recorded and changes in the cycle of circadian activity of both species, usage of nest boxes and feeding trays as well as distances kept between active animals were compared between the early (first 24 hrs) and late (last 24 hrs) phase of animals' co-existence in the mixed group. During the early phase both species were equally active (48.8% of observed active animals were FF and 51.2% were AA), however, in the late phase the activity of FF was lower (34.9%) than that of AA (65.1%). This supports the prediction that smaller shrew species, with a higher metabolic rate, should display higher activity and more equally distributed activity bouts than large species. In the late phase, pairs of different species (F-A) were rarely active at the same time and kept long inter-individual distances. We also observed interspecific differences in the usage of nest boxes and feeding trays. At the same time, the number of conflicts between phases decreased. These results suggest that, over time, water shrews are able to develop mechanisms that reduce the number of interspecific conflicts based on changes in the rhythms of daily activity, maintaining distance between individuals and rare usage of the same shelters and feeding sites. On the other hand, the observed frequent simultaneous activity of AA individuals confirms the greater sociality of this species than FF.

MAMMALS IN ANTHROPOGENIC LANDSCAPE

P48 DOES THE TRAFFIC NOISE AFFECT FORAGING IN SMALL MAMMALS?

Paula Antonina Bednarz¹, Karolina Grzelak², Rafał Zwolak¹

¹Department of Systematic Zoology, Institute of Environmental Biology, Faculty of Biology, Adam Mickiewicz University

²Institute of Acoustics, Faculty of Physics, Adam Mickiewicz University

Noise generated by human activities has increased over the last decades as a result of human population growth, global transport and urbanization. Expertise from the diverse spectrum of disciplines is mandatory to improve understanding of the impacts associated with noise. The aim of our study was to test the foraging of yellow-necked mouse in relation to traffic noise. Our study was conducted in summer 2019 in Poznań, Poland. We used "giving-up densities" to examine the foraging of yellow-necked mouse (*Apodemus flavicollis*) and conducted road noise surveys to verify whether it influences the foraging. We also recorded abiotic variables such as temperature, wind strength, cloudiness, humidity, and moonlight. In 2017 (pilot data), there was no relationship between the noise level and foraging of small mammals. Here, we will present the results from 2019 field season.

MAMMALS IN ANTHROPOGENIC LANDSCAPE

P49 DISTRIBUTION OF DENS AND BEHAVIOUR ANALYSIS OF EURASIAN BADGER (*Meles meles*) INHABITING THE AREA OF WARSAW – PRELIMINARY STUDIES

Izabella Zapędowska¹, Mateusz Jackowiak¹, Jakub Gryz², Dagny Krauze-Gryz¹

¹Warsaw University of Life Sciences

²Forest Research Institute

Occurrence of badgers in the area of Warsaw is still poor-known phenomenon. The study was conducted in 2017-2019, although some data about badgers' dens location had been collected before. Location of dens was carried out in autumn, winter and early spring and it included all green spaces in the city. The located dens were registered in GPS device and regularly controlled. For registration of badger behaviour, camera-traps were used. Camera-traps were located near the dens and left there for 3-6 months. They were regularly controlled to change memory cards or remove them to another den's entrance. Sixteen dens in nine locations were found until the end of June, 2019 and most of them (87,5%) were located in forest area. Among them, eleven were used permanently and the rest were used periodically during the study. Average number of entrances per den was 8,3. In the result of the study about 47000 photos from camera traps were collected. In five dens, badgers cubs were observed. Similarly as in non-urban areas badgers presented nocturnal activity - from 4.00 PM to 5.00 AM with the highest intensity between 7.00-9.00 PM and 2.00-4.00 AM. Badger behaviour analysis was separated for juveniles and adults. Most of their time, adult badgers spent on digging (46%), sniffing (16%) and moving (16%). For juveniles, most of time was often spent on sniffing (42%) and social behaviour (35%) which has marginal meaning for adult individuals. Some time, juvenile badgers spent also on moving (10%). Observations of badgers were conducted throughout a year and activity decrease in winter was not observed.

MAMMALS IN ANTHROPOGENIC LANDSCAPE

P50 POPULATIONS OF SMALL MAMMALS IN URBANIZATION GRADIENT

Gortat Tomasz¹, Alicja Gryczyńska¹, Robert Meronka¹, Miłostawa Sokół¹, Michał Kozakiewicz¹

¹Department of Ecology, Faculty of Biology, Institute of Zoology, Biological and Chemical Research Centre, University of Warsaw

The urban environment created and strongly dominated by humans is characterized by very specific conditions, which significantly affects adaptation processes and the functioning of many animal populations. Taking into account the fact that currently urbanized areas account for almost 5% of the land area, and in the cities live more than 60% of the world's population, studies related to urban ecology become one of the most important in contemporary environmental biology. We studied population genetics, behavioral traits of individuals and relations host-parasite in two closely related mouse species – striped-field mouse (*Apodemus agrarius*) and yellow-necked mouse (*Apodemus flavicollis*) in the city of Warsaw in localities situated along the gradient of anthropopressure – from the city center out to suburban areas. With the increase of the degree of urbanization gradient (including light and noise pollution, high heterogeneity of the environment, numerous barriers – eg dense buildings, street network), the living conditions of studied species change rapidly. The results are the differences observed, among others, in the genetic structure of the population, behavior (including daily activity rhythm) and parasite-host relationships. The processes of adaptation to life in strongly transformed urban environment (synurbization) are more visible in the striped-field mouse – the species with long history of settlement in Warsaw (about 100 years) than in yellow-necked mouse – the species present in the city from about 25 years.

MAMMALS IN ANTHROPOGENIC LANDSCAPE

P51 *Borrelia miyamotoi* INFECTIONS IN URBAN-INHABITING *Apodemus* MICE

Alicja Gryczyńska¹, Miłoslawa Sokół¹, Tomasz Gortat¹, Michał Kozakiewicz¹, Maciej Kowalec²

¹Department of Ecology, Faculty of Biology, Institute of Zoology, Biological and Chemical Research Centre, University of Warsaw

²Department of Parasitology, Faculty of Biology, Institute of Zoology, University of Warsaw

Borrelia miyamotoi is a spirochete bacteria considered as a tick-borne relapsing fever (TBRF) causative agent. It has been found in several of the hard-bodied Ixodes tick species known to be vectors of *Borrelia burgdorferi* s.l. complex (the agents of Lyme borreliosis) and a range of other tick-borne pathogens. The *Borrelia miyamotoi* zoonotic reservoir is still not defined, but it is known that small rodents are the main pathogen hosts. Given that some species of this vertebrate group inhabit urban areas, the principal goal of our study was to determine their *Borrelia miyamotoi* infective potential in this specific type of environment. The investigations were performed in the city of Warsaw (Poland). The rodent-trapping locations were situated strictly in the city centre and in suburban areas. In Warsaw habitat *Apodemus* mice species (*A. agrarius*, *A. flavicollis*, *A. sylvaticus*) comprise in total 85% of the whole small mammal community. The *Borrelia miyamotoi* infection, ascertained based on bacterium DNA presence in the rodents' blood (n = 252), was detected only in *A. agrarius* and *A. flavicollis* (7 and 3.6%, respectively), but no statistically significant differences were found in the infection rate depending on mouse species. Our data are the first report showing the *Borrelia miyamotoi* infection in city-inhabiting rodents and consequently highlighting their role in spreading of tick-borne, medically significant zoonosis, which pose a high risk to public health in human-transformed environment.

MAMMALS IN ANTHROPOGENIC LANDSCAPE

P52 ATTACKED FROM TWO FRONTS: COMBINED EFFECTS OF ANTHROPOGENIC AND BIOTIC DISTURBANCES GENERATE COMPLEX MOVEMENT PATTERNS

Salvatore Valente¹, Anna Skarin², Paolo Ciucci¹, Alessia Uboni²

¹Sapienza University of Rome

²Swedish University of Agricultural Sciences

Currently, disturbances generated by human activities are nearly ubiquitous and they have the potential to interact with biotic disturbances in generating cumulative impacts on animal movement. However, that interaction has yet to be investigated thoroughly. Our study aims to fill this knowledge gap by assessing the combined effects of a human activity, i.e. military exercises, and a biotic disturbance, i.e. insect harassment, on movement rates of free-ranging semi-domesticated reindeer (*Rangifer tarandus*). From 2010 to 2012, we collected location data from GPS-collared female reindeer in the largest European military test range, situated in northern Sweden. Subsequently, we estimated movement rates and related them to presence/absence of military exercises, indices of insect harassment, and their interaction. We determined that military exercises and insect harassment indeed interacted in affecting reindeer movement. This result suggests that the effect of anthropogenic disturbances may be underestimated if not considered in combination with biotic factors. Insect harassment will likely increase in the future as a consequence of the predicted climate warming, especially pronounced in the arctic regions. Thus, evaluating its interaction with human activities is imperative, especially because of the growing interest toward natural resources and other land uses in northern ecosystems.

MAMMALS IN ANTHROPOGENIC LANDSCAPE

P53 GREEN-BLUE SPACES OF METROPOLITAN HELSINKI AS HABITATS FOR THE RACCOON DOG AND RED FOX

Mia Vehkaoja¹, Milla Niemi², Veli-Matti Väänänen¹

¹*University of Helsinki*

²*Metsähallitus*

The raccoon dog and red fox are well adapted to urban areas. During the last 100 years, especially the red fox has been urbanized, whereas the raccoon dog is more a newcomer in European cities. City forests and parks provide habitats and corridors for many species. In addition to forests and parks ditches, streams and rivers are essential environments for urbanized wildlife. We investigated the abundances of the raccoon dog and red fox in metropolitan Helsinki, Finland by camera trapping. Altogether 60 wildlife cameras were set to trap urban wildlife. Half of the cameras were set to green spaces and half to blue spaces with stream or river. We hypothesize that the abundances of both of the species differ between the corridor types. The abundance of the raccoon dog and red foxes were analyzed by comparing the data between the green and blue spaces and the abundance of domestic dogs and humans, as well as, landcover variables using generalized linear modeling in R. The raccoon dog and red fox abundances were higher in blue spaces than in green spaces. Furthermore, the two species coexisted in the same areas; the greater the number of foxes present the more raccoon dogs. The abundance of humans and domestic dogs did not have an effect on the abundances of either of the species. Because urban ecology framework contains both nature and man-made urban structure and sees them as a human-ecological system, it is essential to acknowledge assemblage of animals, and specify the minimum environmental needs they have for their habitats. According to our results more emphasize should be put to blue areas of cities, as they maintain higher abundances of red foxes. In addition, restricting population growth of the raccoon dog, as an invasive species, should be prioritized at blue areas.

MAMMALS IN ANTHROPOGENIC LANDSCAPE

P54 ATTITUDES TOWARDS MAMMAL REINTRODUCTIONS IN SOUTHERN EUROPE CORRELATE WITH SPECIES INVOLVED, PEOPLE'S WILDLIFE VALUE ORIENTATIONS AND RELATIONSHIP WITH HUNTING

Rafael Villafuerte¹, Fernando E. Garrido¹, Miguel Delibes-Mateos¹

¹Instituto de Estudios Sociales Avanzados IESA-CSIC

Reintroduction programmes (RP) are increasingly launched to restore populations of wildlife species, including mammals. Most of these programmes are conducted by environmental agencies and thus funded with public budget. The social context is critical to the success of RP. In this study, we assessed variations in people's attitudes towards RP in function of: 1) the mammal species involved; 2) people's wildlife value orientations (WVO); 3) people's association with hunting. For this purpose, we interviewed 750 people (>18 yrs) in 2017 in Andalusia, southern Spain. We used a stratified consumer's panel attending to rural-urban areas, age and gender in order to achieve the most possible representation of the society in the study area. The survey was answered online or by telephone by those participants without internet access. Our results show that people generally were more prone to support the reintroduction of emblematic species like the Iberian lynx (*Lynx pardinus*) than that of species that are traditionally viewed by humans as conflictive like the wolf (*Canis lupus*). Furthermore, hunters were more supportive of reintroducing game species like the wild rabbit (*Oryctolagus cuniculus*) than the general public. People with a Mutualist WVO (who think that humans and wildlife should co-exist and live in harmony), are highly supportive to the RPs. However, individual with a more Utilitarian WVO (who think that wildlife should be used and managed for human benefit), are less prone to support RPs. Although the general public in Andalusia has a higher proportion of mutualists, special efforts should be done to improve utilitarian's support to RPs of emblematic and non-hunting mammal species.

GENERAL SESSION

P55 WHEN RESEARCH AND MANAGEMENT MEET: HOW TO SOLVE POLLUTION FROM INVASIVE ALIEN SPECIES

Panzeri Mattia¹, Francesco Bisi¹, Maria Vittoria Mazzamuto¹, Damiano Giovanni Preatoni¹, Lucas Armand Wauters¹, Adriano Martinoli¹

¹Università degli Studi dell'Insubria

Invasive alien species (IAS) are one of the greatest threats to biodiversity, ecosystem functioning and human wellbeing. One of the worst mammalian IAS in Europe is the raccoon (*Procyon lotor*), an opportunistic mesocarnivore native to North and Central America, but introduced in 27 European countries. Raccoons can impact bird populations, kill domesticated animals, cause damages to buildings and crops, and carry several disease agents. Here we report the steps taken in an eradication campaign of a population in Lombardy (Italy) under the "Nature Integrated Management to 2020 - LIFE14 IPE/IT/000018" project. During the first step we assessed the presence of raccoons through visual surveys (sightings or signs), interviews to stakeholders and official reports, followed by a 1-year trapping period in which we removed 30 animals. In the second step of the campaign, in an area of 120 km² (grid 1 x 1 km² cells), an intensive 3-month camera trapping survey detected raccoons in 6 different sites. We applied occupancy modelling to camera trap data to identify the habitat features that could influence the species presence and detection. This helped the following targeted 6-month trapping that resulted in the removal of other 30 animals. The final step of the campaign aimed to detect any remaining individuals by a combination of stakeholder interviews, visual surveys for raccoon signs and camera trapping. When raccoons were detected, traps were activated opportunistically to remove the last individuals. We discuss the results and highlight factors that can make the difference between failure and success of raccoon eradication, producing guidelines for future control campaigns of the species that will increase removal success, reducing the effort.

GENERAL SESSION

P56 HOW COARSE WOODY DEBRIS AND FOREST UNDERGROWTH VEGETATION IMPACT THE AREA USAGE OF BANK VOLES?

Emilia Kielan¹, Michał Kołakowski¹, Piotr Zegadło², Elżbieta Jancewicz¹

¹Department of Forest Zoology and Wildlife Management, Faculty of Forestry, Warsaw University of Life Sciences – SGGW, Poland

²Economic Institute for Empirical Analysis, Kozminski University, Poland

The aim of the study was investigating the bank vole's *Clethrionomys glareolus* area usage within the context of the habitat's local heterogeneity. We focused on two significant and often indispensable components of habitats for many species of small mammals - consideration of coarse woody debris and characterization of forest undergrowth vegetation cover. The research was carried out in 2017 on a 1-hectare research plot in the commercial forest stand of the Białowieża Forests. Field works consisted of 3 stages - a detailed inventory and calculating of coarse woody debris (CWD) coverage (lying logs and stumps), a detailed description of undergrowth phytocenosis within the research plot (dominant plant species, the average height of vegetation and the degree of soil coverage with plants) and telemetry studies of 9 individuals of the bank vole (4 males, 5 females). 339 bearings among all tracked animals were collected, mapped as a single point and linked with specific description of the research plot. Availability of places with specified features of vegetation and CWD cover was compared with animal bearings data within the research plot divided into squares of 5x5 m. It was found that bank voles clearly avoided places with low vegetation coverage. They were tracked most frequently in places with more than 75% of plant coverage (95% of all bearings) and chose places covered by plants higher than 50 cm significantly more frequently than random choice would suggest. Similarly, they were found more often in places with higher concentration of coarse woody debris (>1 m²) than their availability would suggest. This research was part of the project financed by the National Science Centre, Poland - 2017/25/N/NZ9/02944.

GENERAL SESSION

P57 FACTORS AFFECTING SPREAD OF SPARGANOSIS IN A CARNIVORE COMMUNITY IN NE POLAND – PRELIMINARY RESULTS

Eliza Kondzior¹, Marta Kołodziej-Sobocińska¹, Rafał Kowalczyk¹

¹Mammal Research Institute PAS

Sparganosis is a severe food- and water-borne disease caused by tapeworm *Spirometra* sp. with a complex life cycle with two intermediate and a definitive host, which may also involve paratenic hosts. We studied the spread of sparganosis in a carnivore community and analysed the influence of biological and environmental factors on prevalence and intensity of infections in two species of carnivores: a native – the European badger *Meles meles*, and invasive – the raccoon dog *Nyctereutes procyonoides*. A total of 529 animals of nine carnivore species from five locations were investigated. During necropsies *Spirometra* larvae were found in 165 individuals (31.2%) of seven species: American mink, badger, European polecat, pine marten, raccoon dog, red fox and river otter. Free of parasite were stone marten and Eurasian lynx. Badgers and raccoon dogs were characterised by the highest prevalence among all carnivores (37.6% and 32.2% respectively), with mean infection intensity significantly higher in badgers – 40 ± 57 (range: 1-276) than in raccoon dogs – 4 ± 4 (range: 1-23). No significant influence of the host sex on the level of infection was observed. Badgers showed an increase in the probability of infection and the number and size of larvae with age, while no such relationships were observed in raccoon dogs. It may be related to the longer coevolution of raccoon dog and *Spirometra* sp. in the area of their origin in Asia. Raccoon dogs reach the maximum rate of infection earlier than badgers, which may result from higher proportion of vertebrates in their diet and in food delivered to pups. Further research will be carried out to examine the relevance of the selected factors. The study was financed by the National Science Centre grant no. 2016/21/B/NZ8/02429.

GENERAL SESSION

P58 IDENTIFYING NEW POTENTIAL AREAS FOR THE ESTABLISHMENT OF THE INVASIVE RACCOON (*Procyon lotor*) IN EUROPE

Adrián Martín-Taboada¹, David Romero², José María García-Carrasco¹, Antonio Román Muñoz¹, L. Javier Palomo¹, Francisco Díaz-Ruiz¹

¹Universidad de Málaga, Departamento de Biología Animal

²Universidad de la República, Laboratorio de Desarrollo Sustentable

The concern about biological invasions is growing worldwide because implies a serious threat to biodiversity conservation, the high economic costs of management measures and, in many cases, involves a health risk for humans, since some species are host of pathogens that are transmitted to humans. The raccoon (*Procyon lotor*), a medium-size carnivore native from North America, is a good example of invasive species. Its high ecological plasticity has allowed it to adapt successfully to different ecosystems in Europe and Asia, where the species has been introduced due to: releases for hunting, fur farms escapes and more recently the pet trade. The successful raccoon's expansion in Europe poses a threat to biodiversity conservation. In this study we review and update the distribution of this species in Europe, with the aim of identifying new potential areas for the establishment of the raccoon in Europe. According to this updating of presences and a set of predictors variables (environmental and human activity), we applied the Favourability Function to detect favourable areas for the species. Anthropogenic variables have a significant relevance explaining the current occurrence of this invasive species. The favourability model detected central Europe and the United Kingdom as the areas with the best conditions for the species, being related to territories with a high percentage of urban area. This may indicate that the invasion pattern could still be reflecting the places of releases. In this sense, the favourable areas for the presence of the raccoon highlight unoccupied zones with high potential to be established in the near future. Our results provide useful information to increase the monitoring effort and develop prevention plans to optimize effective control measures.

GENERAL SESSION

P59 SOME NEW DATA ON THE MELANISTIC POPULATION OF THE COMMON HAMSTER *Cricetus cricetus* IN THE NORTHERN EDGE OF ITS RANGE

Alexander Saveljev¹, Natalia Feoktistova², Pavel Bogomolov², Alexey Surov²

¹Russian Research Institute of Game Management and Fur Farming, Kirov, Russia

²Severtsov Institute of Ecology and Evolution RAS, Moscow, Russia

The Common hamster (*Cricetus cricetus*) is legally on the list of hunting animals in Russia, but at the same time included in the regional Red Lists of nine regions of the European Russia and one in Siberia and listed in Appendix IV of the Habitats Directive, which provides strict legal protection in all EU countries. The causes of the global decline of the Common hamster are complex and not yet fully understood. Mortal material (n = 30, incl. 12 females, three of which reproduced) was obtained from July 25 to September 24, 2018, in Kirov region, Slobodskoy district, Devetyarovo village (N58.6209, E50.3587) at the northern edge of the species range. The population of hamsters in the Kirov region is historically characterized by total melanism as well as in the neighboring Perm region (E) and Republic of Tatarstan (S). Litter numbers and fertility were determined by placental scars (p.s.). Females of the current year of birth become maturity at a body weight of 290 g and give birth in the first decade of September (formerly so late reproduction was registered in southern edge of the range, e.g., in Simferopol city). Their fecundity is low (11 p.s.). One old female gave three litters per season (41 p.s.). The apparent fragmentation of the modern range makes it difficult for the genetic flow between local populations. In the course of our study, we found only one mt-haplotype that testifies either for a low genetic diversity at this part of the range or due to a limited sampling area. The study was funded by Russian Science Foundation (project No. 18-14-00093) and Presidium of the Russian Academy of Sciences, no 41, "Biodiversity of Natural Systems and Biological Resources of Russia."

GENERAL SESSION

P60 IMPLEMENTING PAYMENTS FOR ECOSYSTEM SERVICES – THE CASE OF BEAVERS

Stella Thompson¹, Mia Vehkaoja¹, Jani Pellikka², Petri Nummi¹

¹*University of Helsinki*

²*Natural Resources Institute Finland*

Payments for Ecosystem Services (PES) are market mechanisms used to actualize the monetary value of ecosystem services created by habitats or species. In a PES scheme, beneficiaries pay a resource manager (landowners in the case of beavers) to maintain or strengthen certain ecosystem services. Beavers (*Castor spp.*) produce a wide variety of ecosystem services, several of which could potentially offer high gains to society. Schemes related to water quality and supply along with greenhouse gas storage are potentially the most functional and applicable PES beaver schemes. PES offers a novel approach for incentivizing resource managers to tolerate beaver-induced damages on their lands in turn for pledges to uphold and safeguard beaver territories. The no-harm ideology rooted within PES schemes, to where resource managers may not weaken the production of ecosystem services on their lands, consequently guarantees nearby societies/communities continued access to services such as flood and drought mitigation. Certain beaver-produced services (e.g. increasing fish stocks) are local, while others affect larger geographical regions (e.g. water purification) or even global scales (e.g. carbon sequestration). In a beaver PES, landscape- or nationwideschemes may prove more workable than site-specific ones, as the mechanism must also consider the temporal dimension of beaver mobility in the landscape. Payment mechanisms could be set up by local communities or cities, or could be implemented by industries or companies, such as wastewater treatment facilities, which need to invest less money into their infrastructure when benefiting from beaver activity. Projects could be implemented as group contracts between several private and common resource managers.

GENERAL SESSION

P61 THE WIND IN THE WILLOWS: INFLUENCE OF BEAVER CONSTRUCTIONS ON ACTIVITY OF OTHER MAMMALS AND INTERACTIONS AMONG THEM - PRELIMINARY RESULTS

Zuzanna Wikar¹, Mateusz Ciechanowski¹, Adrian Zwolicki¹

¹Department of Ecology and Zoology of Vertebrates, University of Gdańsk, Gdańsk, Poland

European beavers *Castor fiber* are one of the few species that are capable of remodeling ecosystems and their influence comprises wide spectrum of organisms, including other semiaquatic mammals. Beaver constructions by themselves might be attractive roosts for the latter ones. Beavers, otters *Lutra lutra*, american minks *Neovision vison* and *Ondatra zibethica* often coexist and high population density of beavers positively influences density of other species, although there are antagonistic interactions between mentioned mammals. Our aim is to determine influence of beavers constructions on distribution, activity, intra- and interspecific interactions of otters, american minks, muskrats and water voles *Arvicola amphibius*. We've conducted studies since 12.2018 in nature reserve „Drużno Lake“, which is optimal habitat for beavers and has one of the largest densities of this species in Poland. For initial studies we used 6 trap cameras, 3 near beaver lodges and 3 in control sites, located 100 metres from the closest lodge. Number of mammal species next to lodges is higher (at least 16) than in control sites (7). Also activity of those species, not only semiaquatic, is higher next to beaver constructions – otter's 3,5 and american mink's 26 times higher. Muskrat was second most frequently recorded species after beaver, absent in control sites and present only next to lodge where minks were never recorded. Interestingly, red fox *Vulpes vulpes* activity was 14 times higher near lodges, not only during winter when canals were frozen, but also in spring.

GENERAL SESSION

P62 ECOLOGY AND ECOLOGICAL ROLES OF LONG-TAILED MARMOTS IN AN EXTREME HABITAT IN EASTERN PAMIR

Marcin Zegarek¹, Aleksandra Zarzycka², Piotr Chibowski², Małgorzata Suska-Malawska²

¹*Mammal Research Institute, Polish Academy of Sciences*

²*Faculty of Biology, University of Warsaw*

Social, burrowing, herbivorous animals are known to affect their environment and provide services for co-existing species. Their role as a key-stone species has been well documented in grassland habitats around the world. Little is known about the ecological functional roles in extreme high-mountain arid habitats. We conducted a study in the foreland of the Ujsu Glacier in Eastern Pamir Mountains (4200 m a. s. l.) inhabited by long-tailed marmots (*Marmota caudata*) in July 2019. We are studying following topics: (1) The effect marmot activity on soil nutrients, nitrogen and carbon content in plant biomass and plant distribution (2) Identification of vertebrate and invertebrate species co-occurring with marmots, using burrows for shelter or its unique habitat for development (3) The importance of marmots in the diet of predators, based on scat analysis (4) Marmot long-term diet using stable isotopes of bone collagen (5) Factors influencing habitat selection of long-tailed marmots such as relief, slope stability and soil type. Preliminary results will be presented at the conference. We hypothesize that long-tailed marmots act as a pioneers: they increase nutrient availability by enhancing the nutrient cycle consequently increasing the biodiversity and biomass of plants. The inside of burrows provides a humid, stable microhabitat, used by insects to complete their live cycle. Using camera traps, we observed other mammals and birds using burrows of marmots as temporal shelter. Our poster will show preliminary results This work was financially supported by the National Science Centre of Poland. Grant number is 2017/25/B/ST10/00468.

AUTHORS

- Ahmed, Atidzhe 39
Aivelo, Tuomas 76
Ake, Kanako 181
Åkesson, Mikael 39, 40
Alberti, Federica 129
Al-Hajri, Afra 118
Al-Jabiry, Hayat 118
Allegrini, Claudia 141
Alpizar-Jara, Russell 53
Álvares, Francisco 42
Alves, Paulo C. 45, 53, 138, 176
Alvim, Thiago 161
Ambarlı, Hüseyin 47
Andruszkiewicz, Anna 94
Angeloni, Lisa 136
Angerbjörn, Anders 43, 49, 62, 99, 182
Antal, Vladimir 41
Antonucci, Antonio 185
Antwis, Rachael 144
Apollonio, Marco 79, 93
Archer, John 46
Aresta, Sandra 138
Arnal, María Cruz 47
Aronsson, Malin 73
Aspi, Jouni 40
Aulagnier, Stéphane 90
Babaev, Elmar 47
Baca, Katarzyna 130, 131
Baca, Mateusz 130, 131, 190, 191
Ballesteros, Fernando 114
Baños, Joaquín Vicente 93
Bañuls-Cardona, Sandra 130
Bárány, Annamária 111
Barbara, Zimmermann 97
Barbosa, Soraia 53
Barlow, Axel 129
Baron, Juliette 142
Bar-Oz, Guy 129
Barti, Levente 127, 128
Bartolommei, Paola 122
Baryshnikov, Gennady 129
Batova, Olga 156
Bednarz, Paula Antonina 200
Beer, Martin 153
Bego, Ferdinand 47
Beja, Pedro 53, 176
Belyaeva, Elena 129
Bencini, Cristina 122
Bendrey, Robin 189
Benesova, Marketa 41
Berezcki, Judit 50
Berlioz, Emilie 89
Berto, Claudio 130
Bielecki, Wojciech 179
Binelli, Giorgio 39
Bińkowska, Katarzyna 147
Bisi, Francesco 137, 207
Blanco, Jose Antonio 93
Bleicher, Sonny 54
Bocherens, Hervé 109, 110, 113
Bogdanova, Elena S. 121
Bogomolov, Pavel 211
Bolfíková, Barbora Černá 41, 165
Bonacchi, Andrea 122
Boratyński, Jan 194, 196
Boratyński, Zbyszek 196
Borkowska, Anetta 172
Borowik, Tomasz 93
Borowski, Zbigniew 74, 81, 98, 117, 172, 194, 196
Boubli, Jean 161
Bouet, Léa 97
Bown, Kevin 144
Brito, José Carlos 132
Brivio, Francesca 93
Broekhuizen, Sim 106
Brooke, Christopher 112
Browett, Samuel 65, 144, 154, 158
Brown, Peter 77
Brzeziński, Marcin 124, 147
Bubnicki, Jakub 95, 105

Bueno, Guillermo 91
 Bužan, Elena 47, 84
 Cabral, João Alexandre 138
 Cagnacci, Francesca 28
 Caniglia, Romolo 39, 45
 Cano-Martinez, Rocio 103
 Carmen, Cianfrani 72
 Carpio, Antonio 91
 Carricondo-Sanchez, David 96, 97, 103
 Carter, Stephen 100
 Castro, Diana 42
 Castro, Giuseppina De 185
 Chaimanee, Yaowalak 113
 Charbonnel, Nathalie 51, 52
 Chibowski, Piotr 124, 191, 214
 Chorba, Konstantina 171
 Churski, Marcin 95, 105
 Ciechanowski, Mateusz 213
 Cielniak, Krystyna 179
 Cinqu, Carlo 122
 Ciucci, Paolo 204
 Cocchiararo, Berardino 132
 Coissac, Eric 87
 Colyn, Marc 89
 Corduneanu, Alexandra 127, 128
 Coscia, Ilaria 65
 Coulson, Tim 78
 Courchamp, Franck 142
 Cozzolino, Roberto 122
 Crégut-Bonnoure, Evelyne 130
 Cremonesi, Giacomo 137
 Cromsigt, Joris 60, 86, 151
 Crooks, Kevin 136
 Csanády, Alexander 106
 Csorba, Gábor 50
 Csósz, István 127, 128
 Cuadros, Jennifer Paola Correa 77
 Cuenca-Bescós, Gloria 130
 Curran, Thomas 144, 158
 Cyril, Milleret 96
 Czajkowska, Magdalena 87, 172
 Czernik, Marta 87
 Ćirović, Duško 39, 133
 Dalén, Love 129
 Dammhahn, Melanie 58, 59, 139
 Delibes-Mateos, Miguel 57, 107, 146, 206
 Demartsev, Vlad 125
 Descalzo, Esther 107, 146, 195
 Desclaux, Emmanuel 130
 Devillard, Sébastien 100
 Devineau, Olivier 86
 Diagne, Christophe 142
 Diamante, Sara 72, 175
 Díaz-Ruiz, Francisco 57, 107, 146, 210
 Di Marzio, Mirko 185
 Diserens, Tom 105
 Djan, Mihajla 39
 Doan, Karolina 115, 130
 Domenico, Giovanna Di 185
 Drucker, Dorothee G. 110
 Duarte, José Maurício 173
 Duhayer, Jeanne 51
 Dumić, Tomislav 106
 Eccard, Jana A. 59, 119, 139
 Eddine, Ahmed 132
 Ehlers, Bernhard 153
 Eliášová, Kristýna 165
 Elmhagen, Bodil 71, 73
 Endo, Hideki 166
 Ericson, Helena Sif 39
 Eriksen, Ane 61, 83, 96, 97
 Erlandsson, Rasmus 49, 62, 182
 Ermakov, Oleg 149
 Erofeeva, Mariya 183
 Estay, Sergio 77
 Everest, David 154
 Fabbri, Elena 39
 Fabijanić, Nera 93
 Fadeeva, Tatyana 167
 Falkowska, Ewa 170
 Farahvash, Tarlan 172
 Farkas, Attila 47
 Febbraro, Mirko Di 72, 175
 Fedorca, Ancuta 39
 Feoktistova, Natalia 211
 Fernández-Gil, Alberto 162

Ferrari, Nicola 33, 153
Ferreira, Clara 53, 59, 176
Ferrerias, Pablo 107, 146, 195
Ferroglio, Ezio 93
Figura, Michał 41, 164
Filippi-Codaccioni, Ondine 51, 52
Findo, Slavomir 41
Flagstad, Øystein 40
Flajšman, Katarina 84
Földvári, Gábor 127
Földvári, Mihály 127
Foronova, Irina 129
Frantz, Alain 134
Freire, Teresa Vaz 53, 176
Fristrup, Kurt 136
Fritz, Herve 112
Fuchs, Boris 97
Fyałkowska, Kateryna 196
Fyfe, Ralph M. 110
Gačić, Dragan 47
Gaffi, Lorenzo 137
Gagat, Przemysław 192
Gagliardi, Alessandra 137
Galan, Maxime 52
Galaverni, Marco 39, 45
Galov, Ana 47
García-Carrasco, José María 210
García-Vázquez, Ana 114, 168
Garin, Inazio 51
Garrido, Fernando E. 206
Gasparian, Boris 129
Gasperini, Stefania 122
Ghazaryan, Astghik 39
Gillich, Benjamin 97
Giovacchini, Simone 185
Godinho, Raquel 39, 42, 46, 64, 132, 159
González-Fortes, Gloria 168
Gorini, ucrezia 97
Gortat, Tomasz 75, 163, 202, 203
Göttsche, Claudia 139
Górny, Marcin 115
Grandal-d'Anglade, Aurora 114, 168
Grau, José 165
Grimm, Volker 119
Grossmann, Kamila 177
Gryczyńska, Alicja 75, 163, 202, 203
Gryz, Jakub 35, 88, 102, 135, 201
Grzelak, Karolina 200
Guenther, Anja 119
Guilfoyle, Colin 34
Guisan, Antoine 72
Gumiński, Witold 110
Haapakoski, Marko 54, 55, 56
Hajji, Ghaïet M. 172
Hałat, Zuzanna 126
Haneda, Shingo 188
Hanniffy, Ruth 34
Hapunik, Ewelina 145
Harper, Lynsey 48
Harrington, Andrew 158
Hasselgren, Malin 49, 62
Helm, Charles 112
Herde, Antje 119
Herman, Jeremy 189
Herrmann, Mathias 101
Hillström, Lars 91
Hindrikson, Maris 159
Hofman-Kamińska, Emilia 110
Hofmeester, Tim R. 60, 106, 186
Hofreiter, Michael 129
Holmala, Katja 73
Horáček, Ivan 130, 131
Hornok, Sándor 127, 128
Hudson, Michael 100
Huet, Ophélie 148
Hulva, Pavel 39, 41, 165
Iacolina, Laura 38, 47
Isakov, Vladimir 167
Iwińska, Karolina 196
Jackowiak, Mateusz 102, 135, 201
Jackson, Joseph 144
Jaeger, Jean-Jacques 113
Jancewicz, Elżbieta 170, 174, 208
Jansen, Patrick 93
Jasińska, Karolina 35, 135
Jędrzejewska, Bogumiła 39, 64, 66, 85, 115

Jiménez, José 107, 146
 Jindrichova, Milena 41
 Johnson, Ronald 92
 Kaizer, Mariane 161
 Kaneko, Yayoi 181
 Kardynia, Paweł 116
 Karssene, Yamna 132
 Kauffman, Matthew 26
 Kerley, Graham I.H. 151
 Keuling, Oliver 93
 Kępka, Klaudia 116
 Khammes-Elhomsy, Nora 90
 Khammes-Talbi, N 90
 Kielan, Emilia 208
 Kimmig, Sophia 134
 Kindberg, Jonas 60
 Klees, Dick 132
 Klich, Daniel 178, 179
 Kloch, Agnieszka 70
 Knowles, Sarah 123
 Knul, Monika Vlasta 130
 Kojola, Ilpo 40
 Kołaczyński, Andrzej 117
 Kołakowski, Michał 208
 Kołodziej-Sobocińska, Marta 67, 145, 209
 Konarzewski, Marek 29, 74
 Kondoh, Daisuke 188
 Kondzior, Eliza 67, 145, 209
 Kopaliani, Natia 39
 Koprowski, John 32, 37
 Korine, Carmi 141
 Kostrzewa, Agata 35
 Kowalczyk, Rafał 65, 87, 105, 109, 110, 145, 209
 Kowalec, Maciej 203
 Kowalski, Gabriele Joanna 119
 Kozakiewicz, Michał 75, 163, 202, 203
 Krajcarz, Magdalena 130
 Krasnov, Boris 141
 Kratochvíl, Lukáš 36
 Krauze-Gryz, Dagny 35, 88, 102, 135, 201
 Križanović, Krešimir 47
 Krystufek, Boris 31
 Kuijper, Dries 95, 105
 Kunva, Sazia 160
 Kusak, Josip 39
 Kutal, Miroslav 41
 Kwiatkowska, Iga 184
 Kwon, Youngsang 92
 Laczko, Levente 50
 Lamberth, Curt 78
 Lambin, Xavier 53
 Lanszki, József 106
 Lawton, Colin 34, 155
 Lazar, Peter 47
 Leblois, Raphael 51
 Leer, Peter Van Der 132
 Lemanik, Anna 130, 131, 190
 Lenardić, Jadranka Mauch 130
 Leonard, Jennifer 162
 Leuchtman, Maxime 51, 52
 Liao, Wenfei 148
 Liberg, Olof 40
 Lima, Mauricio 77
 Lindén, Harto 73
 Linnell, John D.C. 60
 Lipecki, Grzegorz 190
 Lissovsky, Andrey 31, 149
 Llona, Ana C. Pinto 114, 168
 Lobo, Diana 46
 Loiseau, Anne 51
 Lönn, Mikael 91
 Loosen, Anne 86
 Lopes, Susana 132
 Loudová, Miroslava 165
 Loukatou, Nikolitsa 171
 Loy, Anna 72, 175, 185
 López-Bao, José Vicente 42, 114
 López-García, Juan Manuel 130
 Lucas, Ignacio 165
 Lurz, Peter W. W. 153
 Lvovskiy, Leonid 167
 Lyons, Leslie A. 45
 Maartmann, Erling 61
 Macdonald, David 118
 Mackiewicz, Paweł 115, 190, 191, 192
 Macpherson, Jenny 100

Madsen, Aksel Bo 106
Magyari, Enikő 111
Makowiecki, Daniel 110
Maletić, Vladimir 47
Manser, Marta 125
Månsson, Johan 61
Manzo, Emiliano 122
Marean, Curtis 112
Marino, Shealyn 153
Markov, Georgi 47
Marković, Zoran 130
Marnell, Ferdia 31
Márquez, Ana Luz 146
Marrese, Maurizio 185
Marsh, Kirsty 123
Martínez-Jauregui, María 146
Martinoli, Adriano 33, 137, 207
Martín-Taboada, Adrián 210
Mateo, Rafael 195
Mathews, Fiona 51
Mathisen, Karen Marie 81, 86
Matosiuk, Maciej 172
Matsui, Motozumi 188
Matsumoto, Naoya 188
Mattia, Panzeri 207
Mattioli, Stefano 172
Mattucci, Federica 39, 45
Mazzamuto, Maria Vittoria 33, 207
Mazza, Valeria 139
McDevitt, Allan 48, 65, 144, 154, 158, 161
McKenna, Megan 136
McKinney, Conor 34
Melo, Fabiano 161
Mendes, Tiago 53, 176
Merceron, Gildas 89
Meronka, Robert 75, 163, 202
Mestre, Frederico 53
Michler, Frank 97
Miękina, Barbara 130, 190
Mihalca, Andrei Daniel 127, 128
Milošević, Dragana 47
Mira, António 53, 138, 176
Mitchell-Jones, Tony 31
Miteva, Svetlana 31
Mitsainas, George P. 68, 171
Mizsei, Edvárd 50
Molloy, Victoria 34
Montgomery, Ian 144
Morandini, Marina 37, 197
Moreno, Marta Garcia 91
Morlin, Mel 189
Mortelliti, Alessio 122
Mos, Jeroen 186
Mostefai, Noureddine 132
Motokawa, Masaharu 166
Mühlböck, Peter 198
Muñoz, Antonio Román 210
Murelaga, Xabier 130
Müskens, Gerard 106
Mysłajek, Robert W. 41, 164, 184, 187
Nadachowski, Adam 130, 131, 190
Naidenko, Sergey 183
Németh, Attila 111
Németh, ttila 50
Neupane, Dinesh 92
Nguyen, Dinh Duy 166
Nguyen, Truong Son 166
Niedziałkowska, Magdalena 66, 85, 115, 191
Niedźwiecka, Natalia 41, 164, 187
Niemi, Milla 205
Nordli, Kristoffer T. 97
Norén, Karin 43, 49, 62, 99
Nowak, Carsten 39
Nowak, Casten 132
Nowak, Sabina 41, 164
Nowak-Życzyńska, Zuzanna 179
Nummi, Petri 148, 212
Odden, John 60
Odden, Morten 103
Ogura, Tadatoshi 181
Ohnishi, Naoki 44
Olech, Wanda 178, 179
Oliveira, Márcio 173
Olivero, Jesús 57
Olivier, Broenniman 72
O'Meara, Denise 144, 154, 155, 158

O'Neill, David 158
Ordiz, Andrés 96, 97
O'Reilly, Catherine 154, 155, 158
Osawa, Takeshi 44
Oshida, Tatsuo 166
Osten-Sacken, Natalia 143
Pacheco, Carolina 64
Pacher, Martina 110, 129
Pagani, Luca 45
Paijmans, Johanna L. A. 129
Pálffy, József 111
Palme, Rupert 56
Palomo, L. Javier 210
Papaioannou, Haritakis 47
Papakosta, Malamati A. 106
Paupério, Joana 53, 138, 176
Pavlova, Svetlana 69
Pawełczyk, Sławomira 85, 115
Pazonyi, Piroska 111, 130
Pedra, Raquel 42
Pellikka, Jani 212
Peralta, Dinora 53, 176
Peres, Pedro Henrique 173
Pereswiet-Soltan, Andrea 190
Pertoldi, Cino 65
Petculescu, Alexandru 130
Péter, Áron 127, 128
Petrović, Karolina 93
Pettett, Carly 118
Pfeffer, Sabine 86
Piličiauskienė, Giedrė 110
Pinhasi, Ron 129
Piotrowska, Natalia 115
Piry, Sylvain 51, 52
Pita, Ricardo 53, 138, 176
Plis, Kamila 39
Podgórski, Tomasz 93
Pokorny, Boštjan 84
Politov, Dmitri 39
Pons, Jean-Baptiste 51
Pontier, Dominique 51, 52
Popczyk, Bartłomiej 178
Popović, Danijela 130, 131, 190, 191
Potušek, Sandra 47
Preatoni, Damiano 33
Preatoni, Damiano Giovanni 137, 207
Puechmaille, Sébastien 51
Queirós, João 138
Rachwald, Alek 117
Randi, Ettore 39, 45, 63, 65
Rasmussen, Gregory 181
Ratajczak, Urszula 192
Ratkiewicz, Mirosław 87, 172
Raulo, Aura 78, 123
Real, Raimundo 146
Rebane, Helen 182
Rezaei, Hamidreza 172
Rezić, Andrea 47
Ridush, Bogdan 115
Rieger, Siegfried 97
Risch, Thomas 92
Rocha, Rita 42, 132
Rodrigues, Carmen Ruiz 93
Rokx, Kira 105
Romeo, Claudia 33, 153
Romero, David 210
Romportl, Dusan 41
Roux, Elizabeth le 151
Rozentsvet, Olga A. 121
Ruczyńska, Iwona 65, 67, 145
Ruczyński, Ireneusz 126
Ruelle, Sandrine 100
Ruiz-González, Aritz 65
Ruscoe, Wendy 77
Rutkowski, Robert 163
Rychlik, Leszek 116, 120, 177
Saarma, Urmas 39
Sabino-Marques, Helena 53
Sacks, Ben 65
Safner, Toni 47
Sakamoto, Hideyuki 188
Salado, Isabel 162
Sales, Naiara 48, 144, 154, 161
Samojlik, Tomasz 110
Sand, Håkan 40, 61, 83, 96, 97
Sándor, Attila D. 41, 127, 128

Sandoval, Eluzai 173
Santicchia, Francesca 33
Santos, Sara M 53, 138, 176
Sanz-Perez, Ana 96
Saveljev, Alexander 149, 172, 211
Savinetskaya, Liudmila 156, 157
Scandura, Massimo 47, 93
Scarpulla, Erminia 148
Schirmer, Annika 139
Schley, Laurent 31
Schlottau, Kore 153
Schneiderová, Irena 36
Schulze, Vanessa 153
Schutgens, Esmee 105
Schwerk, Axel 178
Searle, Jeremy 53, 144
Sedlacek, Frantisek 198
Sera, Bozena 198
Seryodkin, Ivan V. 172
Shannon, Graeme 136
Sheftel, Boris 69, 120, 149
Shoocongdej, Rasmi 113
Shuttleworth, Craig 154
Sievert, Thorbjörn 54, 55, 56
Silva, Pedro 42, 159
Skarin, Anna 204
Skarpe, Christina 86
Skoura, Akylina 171
Skrbinšek, Tomaz 39
Smet, Koen De 132
Smirnov, Dmitri 149
Smith, Graham 93
Šnjegota, Dragana 39
Socha, Paweł 190
Sokół, Miłosława 75, 163, 202, 203
Soliño, Mario 146
Soriguer, Ramon 93
Spitzenberger, Friederike 31
Šprem, Nikica 47, 93
Sramkó, Gábor 50
Srinivasan, Mridula 150
Stachyra, Przemysław 164
Stakheev, Valery 149
Stanković, Ana 115
Statham, Mark 65
Steele, Michael A. 153
Stefaniak, Krzysztof 115, 191, 192
Štefanská, Lucie 36
Stenseth, Nils Chr. 27
Stewart, John R. 130
Stępnia, Kinga Magdalena 164, 187
Stipoljev, Sunčica 47
Stojak, Joanna 65, 66, 67
Strandburg-Peshkin, Ariana 125
Strier, Karen 161
Stronnen, Astrid Vik 64
Sulwiński, Marcin 74
Sundell, Janne 148
Sunde, Peter 97
Suraprasit, Kantapon 113
Surov, Alexey 211
Suska-Malawska, Małgorzata 74, 124, 191
Sykut, Maciej 85, 115, 191
Synnott, Rebecca 154, 155
Szewczyk, Maciej 41, 104, 164, 187
Szőke, Krisztina 128
Szyndlar, Zbigniew 190
Świsłocka, Magdalena 87, 172
Taberlet, Pierre 87
Tallian, Aimee 80
Tarnowska, Ewa 66
Tattersall, Glenn 125
Tchabovsky, Andrey 156
Thissen, Johan 31
Thompson, Stella 212
Thorsen, Neri H. 60
Titov, Sergey 149, 156
Tobajas, Jorge 195
Tokarska, Małgorzata 145, 160
Tomczak, Patrycja 164
Tomek, Teresa 190
Tomiyasu, Jumpei 188
Tönisalu, Grete 140
Tosh, David. G. 155
Tournayre, Orianne 51, 52
Trillat, Marine 52

Tumasian, Philipp 120
Uboni, Alessia 204
Ulrich, Rainer G. 153
Unnsteinsdóttir, Ester Rut 108
Väänänen, Veli-Matti 205
Vaissiere, Anne-Charlotte 142
Vale-Gonçalves, Hélia 138
Valente, Salvatore 204
Väli, Ülo 140
Vaquerizas, Patricia H. 57
Vasilieva, Nina 156, 157
Vasiliev, Nikita 157
Veenhuisen, Laura S. van 151
Vehkaoja, Mia 205, 212
Vekhnik, Victoria A. 121
Vekhnik, Vladimir P. 121
Velli, Edoardo 45
Venter, Jan 112
Versluijs, Erik 97
Vilà, Carles 162
Villafuerte, Rafael 57, 195, 206
Vohralík, Vladimir 31
Voipio, Helinä 56
Wabakken, Petter 40, 61, 83, 96, 97
Wallén, Johan 43, 49, 99
Wauters, Lucas Armand 33, 137, 207
Wereszczuk, Anna 106
Wertz, Krzysztof 190
Widén, Anna 82, 180
Wikar, Zuzanna 104, 213
Wikenros, Camilla 61, 83, 96, 97
Wilczyński, Jarosław 130
Williams, A. Christy 92
Wittemyer, George 136
Woodbridge, Jessie 110
Woznicova, Vendula 41
Wójcicki, Adam 98
Wójcik, Jan 65, 67
Yamaguchi, Nobuyuki 118
Yearsley, Jon 144
Ylönen, Hannu 54, 55, 56
Young, Robert 161
Zachos, Frank E. 172
Zalewski, Andrzej 106, 145
Zanet, Stefania 93
Zapędowska, Izabella 201
Zarzycka, Aleksandra 147, 214
Zegadło, Piotr 208
Zegarek, Marcin 126, 214
Zimmermann, Barbara 61, 83, 86, 96
Zuberogoitia, Iñigo 106
Zub, Karol 74, 94, 194
Zwijacz-Kozica, Tomasz 164
Zwolak, Rafał 200
Zwolicki, Adrian 104, 213
Zyka, Vladimir 41
Žeromska, Aleksandra 190, 192

ORGANIZERS:



Mammal Research Institute
Polish Academy of Sciences
Białowieża



UNIVERSITY
OF WARSAW

CeNT CENTRE
OF NEW
TECHNOLOGIES



Springer

PAN
POLISH ACADEMY OF SCIENCES

EXHIBITORS:

ECOTONE[®]
GPS TELEMETRY



 **VECTRONIC
Aerospace**
innovative technology for science and research
www.vectronic-aerospace.com

wildlife 
ACOUSTICS
BIOACOUSTICS MONITORING SYSTEMS

ECM8

8th European Congress of Mammalogy

23 - 27 September 2019, Warsaw, Poland

www.ecm8.org