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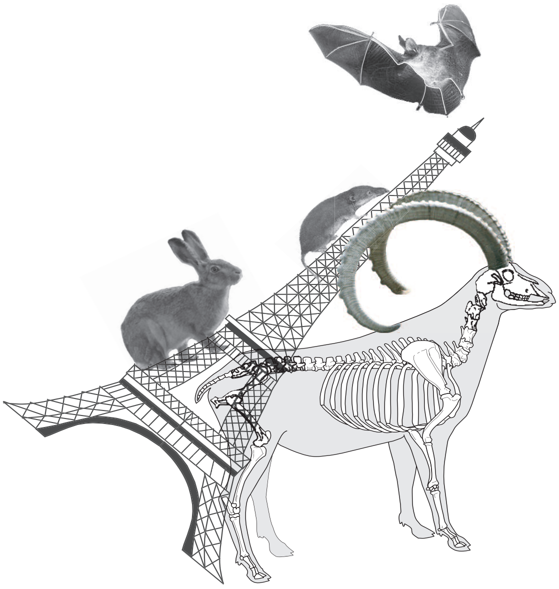
ECM 2011

VIth European Congress of Mammalogy

Université P. et M. Curie - Muséum national d'Histoire naturelle

Paris, France - 19 to 23 July 2011



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Tuesday 19 July

09:00 - 16:00	***EXCURSION to Parc des Félins of Melun (charged to participants upon reservation)***
14:00 - 18:00	**Registration of delegates *(Atrium, Jussieu Campus)***
18:00 - 20:00	**Opening session** ***(Amphitheatre F1, Jussieu Campus)***
18:00 - 18:15	**Welcome** - *Christiane Denys & Stéphane Aulagnier* - Opening of the congress
18:15 - 19:00	*François Moutou* - “About mammals and diseases”
19:00 - 19:30	*Sabrina Renaud* - “Evo-Devo and morphometrics: an insight into the evolutionary processes”
19:30 - 20:00	*François Bonhomme* - “Of mice and men: what’s new since the Neolithics ?”
20:30 - 23:00	***WELCOME RECEPTION in the Grande Galerie de l’Evolution***

Wednesday 20 July

	AMPHI ASTIER	*AMPHI HERPIN*	*AMPHI 45A*	*AMPHI 45B*	*AMPHI 55A*	*AMPHI 55B*
09:00 - 10:30	**1 - Subterranean mammals**	**20 - Macroevolution**	**21 - Population ecology**	**4A - Shrews**	**22 - General session**	**19 - Ungulates genomics**
10:30 - 11:15	**Coffee break / Visit of exhibition area *(Atrium)***					
11:15 - 12:35	**1 - Subterranean mammals**	**20 - Macroevolution**	**21 - Population ecology**	**4A - Shrews**	**22 - General session**	**19 - Ungulates genomics**
12:35 - 14:00	**Lunch *(Administrative University Restaurant)* / Visit of exhibition area *(Atrium)***					
14:00 - 15:30	**1 - Subterranean mammals**	**15 - Postglacial recolonisation**	**21 - Population ecology**	**4A - Shrews**	**22 - General session**	**19 - Ungulates genomics**
15:30 - 16:30	**Poster session *(Atrium)***					
16:30 - 17:00	**Coffee break / Visit of exhibition area *(Atrium)***					
17:00 - 18:00	**1 - Subterranean mammals**	**15 - Postglacial recolonisation**	**21 - Population ecology**	**4A - Shrews**	**22 - General session**	**19 - Ungulates genomics**

18:30 - 20:30	***EXCURSION Paris by bicycle (charged to participants upon reservation)***

Thursday 21 July

	AMPHI ASTIER	*AMPHI HERPIN*	*AMPHI 45A*	*AMPHI 45B*	*AMPHI 55A*	*AMPHI 55B*
09:00 - 10:30		**12 - Phylogeography**	**21 - Population ecology**	**4B - Chromosome & evolution**	**22 - General session**	**9 - Landscape**
10:30 - 11:15	**Coffee break / Visit of exhibition area *(Atrium)***					
11:15 - 12:35		**12 - Phylogeography**	**21 - Population ecology**	**4B - Chromosome & evolution**	**22 - General session**	**9 - Landscape**
12:35 - 14:00	**Lunch *(Administrative University Restaurant)* / Visit of exhibition area *(Atrium)***					
14:00 - 15:30	**17 - Movement ecology**	**12 - Phylogeography**	**3 - Zoonosis ecology**	**4B - Chromosome & evolution**	**14 - Urban ecology**	**9 - Landscape**
15:30 - 16:30	**Poster session *(Atrium)***					
16:30 - 17:00	**Coffee break / Visit of exhibition area *(Atrium)***					
17:00 - 18:00	**17 - Movement ecology**	**12 - Phylogeography**	**3 - Zoonosis ecology**	**4B - Chromosome & evolution**	**10 - Circum mediterranean**	**9 - Landscape**

Friday 22 July

	AMPHI ASTIER	*AMPHI HERPIN*	*AMPHI 45A*	*AMPHI 45B*	*AMPHI 55A*	*AMPHI 55B*
09:00 - 10:30		16 - Introduced invasives	13 - Systematics barcoding	2 - Parasites	7 - Speciation	9 - Landscape
10:30 - 11:15	**Coffee break / Visit of exhibition area *(Atrium)***					
11:15 - 12:35	5 - Morphometry	16 - Introduced invasives	13 - Systematics barcoding	2 - Parasites	7 - Speciation	9 - Landscape
12:35 - 14:00	**Lunch *(Administrative University Restaurant)* / Visit of exhibition area *(Atrium)***					
14:00 - 15:30	5 - Morphometry	16 - Introduced invasives	13 - Systematics barcoding	2 - Parasites	7 - Speciation	
15:30 - 16:30	**Poster session *(Atrium)***					
16:30 - 17:00	**Coffee break / Visit of exhibition area *(Atrium)***					
17:00 - 17:45	**Poster session *(Atrium)***					
18:00 - 20:00	**Plenary lectures *(Amphitheatre F1, Jussieu Campus)***					
18:00 - 18:45	*Joseph Merritt* - "Life in the cold: winter survival strategies on small mammals"					
18:45 - 19:20	*Johan Michaux* - "Phylogeny and conservation genetics in Europe"					
19:20 - 20:00	*Ran Nathan* - "Bat Movement Ecology"					

21:00 - 02:00	***CONGRESS DINNER & PARTY on the boat Maxim's (partly charged to the delegates)***

Saturday 23 July

	AMPHI 45A	*AMPHI 45B*	*AMPHI 55A*	*GAM*
09:40 - 10:30	11 - Laonastes	8 - Miller	6 - Islands evolution	18 - Biodiversity erosion
10:30 - 11:15	**Coffee break / Visit of exhibition area *(Atrium)***			
11:15 - 12:35	11 - Laonastes	8 - Miller	6 - Islands evolution	18 - Biodiversity erosion
12:35 - 14:00	**Lunch *(Administrative University Restaurant)* / Visit of exhibition area *(Atrium)***			
14:00 - 15:30	11 - Laonastes			18 - Biodiversity erosion
15:30 - 17:00				Poster prizes CONGRESS CLOSURE

Sunday 24 July

08:00 - 20:00	***EXCURSION to Baie de Somme (charged to participants upon reservation)***

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Venue location map

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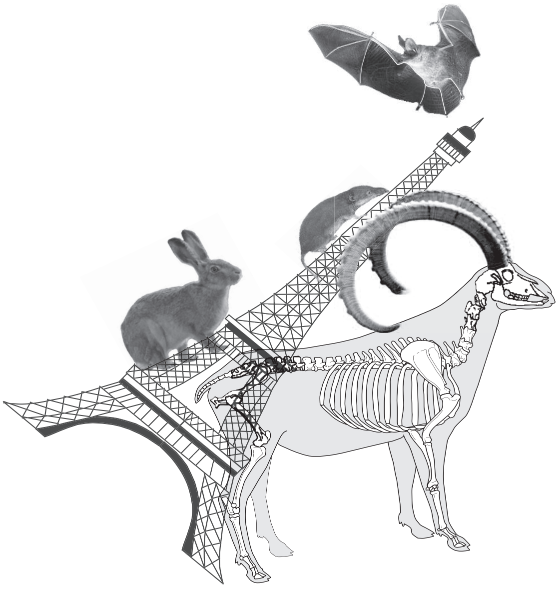

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Sessions’s Index

"We apologize for any involuntary omission or mistake which may have occurred inadvertently despite our efforts."

Plenary communications

“Of mice and men: what’s new since the Neolithics?”

F. Bonhomme

ISEM – Université Montpellier 2. Pl.E. Bataillon – CCO65 ; 34095 Montpellier cedex 05 ; France (francois.bonhomme@univ-montp2.fr).

The House Mouse *Mus musculus* is an emblematic mammalian species that has became a popular laboratory model in many fields actually well before its natural history was understood. *Mus musculus* was first described and characterised from rather peripheral parts of its range, and it is only recently that a comprehensive view of its global phylogeography has emerged. A picture emerges which suggests the Indo-Pak subcontinent and neighbouring Afghanistan and Iran as the area where *Mus musculus* originated and initially differentiated in a series of expansion/contractions during the Quaternary climatic oscillations. Molecular data suggest that the initial differentiation of the various present-day subspecies started possibly two interglacial periods ago. More recently, since the beginnings of agriculture and the first grain stores, the house mouse became commensal of humans some 12,000 years ago and has undergone since then a fantastic range expansion that has brought it almost anywhere at the surface of the globe. I shall review the state of our knowledge in the light of available data and discuss how *Mus musculus*, its subspecies and its allies, remain a prominent model for the study of differentiation and speciation processes.

Life in the cold: winter survival strategies of small mammals

J.F. Merritt[1], *D.A. Zegers*[2]

1- INHS, University of Illinois, Champaign, USA; (2) Department of Biology, Millersville University, Millersville, USA; (jmerritt@illinois.edu).

Winter-active small mammals residing in seasonal environments employ many different behavioral, anatomical and physiological mechanisms to cope with cold. We review research on survival mechanisms in cold employed by small mammals of the families Soricidae, Cricetidae, and Sciuridae. Elevated resting metabolic rate (RMR) is typified by winter- active small mammals; enhanced capacity for non-shivering thermogenesis (NST) is crucial for overwinter survival of soricids, cricetids and sciurids that exhibit social thermoregulation (i.e., *Glaucomys volans*). Shrews in the eastern hemisphere (Crocidurinae) evolved in warmer, more southern latitudes; some exhibit daily torpor and are known to nest communally. In the western hemisphere, shrews of the subfamily Soricinae evolved in more northerly latitudes; most do not enter daily torpor and do not exhibit communal nesting. The northern short-tailed shrew, *Blarina brevicauda*, and masked shrew, *Sorex cinereus* have northern distributions in North America and exhibit high metabolic rates, and demonstrate impressive changes in non-shivering thermogenesis. In contrast, least shrews, *C. parva*, exhibit a broader and more southerly geographic range unique among North American soricids, and like Old World crocidurines, *C. parva* exhibits low metabolic rates and employs communal nesting as mechanisms enhancing energy conservation. Laboratory studies of RMR ($V0_2$) at various Ta and group sizes showed an inverse relationship between RMR and numbers of huddling *C. parva,* supporting the classical explanation that reduction in metabolic rate is attributable to a reduction of surface-to-volume ratio.

Conservation genetics : new tools and hope for threatened species.

J.R. Michaux

Unité de Génétique de la Conservation, Institut de Botanique, Liège, Belgium; Centre de Biologie et de Gestion des Populations, Campus International de Baillarguet, Montferrier sur Lez, France. E mail : michaux@supagro.inra.fr

Conservation genetics is an applied and interdisciplinary science, involving the application of evolutionary and genetic methods to the conservation and restoration of biodiversity. This recent field of research encompass two major aims. The first one is the genetic management of small and fragmented populations in order to both maximize their genetic diversity and minimize inbreeding depression. The second is the delimitation of « Evolutionary significant units » (ESU) and « Management Units » (MU) and the resolution of taxonomic uncertainties. Moreover, it also helps to better understand the biology of threatened species and to look for potential particular biological characters explaining their fragility. The development of new molecular techniques allows to study endangered species using “non invasive” approaches. A small piece of tissue, some hairs, several drops of saliva or even faeces are now sufficient to analyse the genetic diversity and structure of the analysed populations as well as their isolation level. Using different examples of mammal species studied in our laboratory (European mink, Pyrenean desman, South East Asian endemic rodents, polar bear, wild cat…), I will explain the great interest, but also the limitations and constraints of this field of research. I will particularly emphasize on the risks of hybridization and outbreeding processes, the presence of invasive species or the interest of conservation genetics for reintroduction or translocation projects. Finally, I will conclude by discussing connections between conservation genetics and the wider field of conservation biology.

Movement ecology: general principles and application to fruit bats

R. Nathan

Elected Chairman, The Alexander Silberman Institute of Life Sciences. The Hebrew University of Jerusalem - Edmond J. Safra Campus at Givat Ram 91904 Jerusalem, ISRAEL (rnathan@cc.huji.ac.il)

Understanding and predicting the dynamics of complex ecological systems are best accomplished through the synthesis and integration of information across relevant spatial, temporal and thematic scales. Movements of organisms play a key role in various ecological and evolutionary processes, encompassing diverse phenomenon such as foraging within a specified region, dispersal away from the current home range, and seasonal migration across continents. Recent advances in mechanistic modeling and tracking technology have enriched our capacity to disentangle the key parameters affecting movement processes and to accurately characterize movement patterns. In lieu of this favorable background, movement ecology has recently emerged to facilitate the unification of movement research. Movement ecology aims at investigating the explicit links between the internal state, the motion and the navigation capacities of the individual and the external environmental factors affecting its movement. It links the four existing paradigms for studying movement – the random, biomechanical, cognitive, and optimality approaches, which have long been loosely linked to each other – and offers a cohesive framework as a unifying theme for developing a general theory of organism movement. In this talk, I will present the basic principles of the movement ecology approach, and will illustrate its application to study the foraging ecology and navigation capacity of fruit bats, and their role as seed dispersers.

About mammals and diseases

F. Moutou

Anses, Epidemiology unit, Laboratory for animal health, Maisons-Alfort, France(francois.moutou@anses.fr)

In public health, zoonosis are not new. Among infectious and transmissible diseases, it has been known for a very long time that if some of them look specific to human beings, others could be spread between species, including human beings, and under many different ways. However, the end of XXth century and the beginning of the XXIst century look a little special as if the discovery of some new such diseases was worsening our sharing of the planet with other species, in this case mammals. There may be another way, more optimistic, to analyze such a discovery, when in the same time all indicators show that biodiversity is severely decreasing. Figures like “62% of current human pathogens are zoonotic agents” or “nearly 72% of all new diseases described all around the world these past 20 years are of animal origin” are now common in many medical publications and symposia. New expression such as “the crossing of the species barriers” and the omnipresent “emerging infectious diseases (EID)” are everywhere, even in zoological congresses. Shall we worry, should mammals worry ? Answers to these questions should include data coming from microbiological and medical fields, certainly, but also others coming from epidemiology, ecology, conservation biology and zoology, here mammalogy (as for ECM 2011). The first step is to recall that if zoonosis are indeed of animal origin, human beings also. Certainly the emergence of AIDS was a big and sad surprise in the 1980s. Certainly HIV viruses are coming from SIV viruses. Without SIV, HIV could not have emerged but without Primates, SIV, HIV and human beings would not have been present either. In epidemiology today, bats (Chiroptera) are getting an extraordinary position, at the center or at the root of so many viral cycles, rabies, Nipah, Hendra, Ebola, SARS, just to mention a few examples. Should we see this so peculiar mammalian order as a threat or as a chance to try to understand new relationships with so many viral families ? The recent development of molecular biology tools like metagenomics gives today the possibility to explore the whole “virome” of mammal species. This is already under way with bats. The interpretation of the many data collected is not the easiest part. In every case, the emergence of a new disease involves many parameters, one of them, not to be underestimated, is consequence of the behaviors of human beings, modifying ecosystems, translocating invasive species, microorganisms included and still harvesting new species all around the world. In the same time and at the ecosystem scale, more and more publications highlight the fact that not or little modified ecosystems are in the better position to resist invasive species and have the higher resilience level. There could be a positive relationship between biodiversity and health, public health included. A last item could be devoted to suggest that biodiversity could also be analyzed at the individual level. If each individual could be seen as a symbiosis, knowing that for instance, at least 10% of human genome is made of endoviruses and that we harbor more bacteria that we have cells in each of our body, the real challenge in many cases would not be to eradicate but to live with. Will this really be understood and help mammals, other mammals ?

Evo-devo and morphometrics: an insight into the evolutionary processes

S. Renaud

Laboratoire de Biométrie et Biologie Evolutive, CNRS, Université Lyon 1, France (Sabrina.Renaud@univ-lyon1.fr)

Variation within a population is a key feature in evolution, because it can increase or impede response to selection, depending on whether or not intrapopulational variance is correlated to the change under selection. Drift may be favoured as well along these directions of greatest variance. Hence, main directions of variance have been proposed to constitute “lines of least resistance to evolution” along which evolution would be facilitated. Genetic variance is often considered as crucial, but the screening of selection occurs at the phenotypic level, and the phenotypic variance is not only the product of the underlying genetic variance, but also of developmental processes that may orient short and long term evolution by preferably generating certain phenotypes. Morphometric methods allow the quantification of intrapopulational variance and its comparison with directions of evolution. It can thus help to bridge the gap between the description of evolutionary patterns and the underlying processes, and insert questions such as parallel evolution in an evo-devo framework. Examples from tooth evolution in modern and fossil rodents will illustrate this approach.

Session 1 - Advances in studies on subterranean mammals

Invited & Oral Communication

Phylogeography and cryptic diversity in african mole-rats – the role of tectonics and the formation of the african rift valley

C.G. Faulkes[1], P.A.A.G. Van Daele[2], N.C. Bennett[3], F.P.D. Cotterill[4], G.F. Mgode[5], E. Verheyen[6]

1- Queen Mary University of London, School of Biological & Chemical Sciences, UK (c.g.faulkes@qmul.ac.uk); 2- Evolutionary Morphology of Vertebrates, Ghent University, Belgium; 3- Department of Zoology and Entomology, University of Pretoria, South Africa; 4- AEON, Department of Geological Sciences & Department of Molecular and Cell Biology, University of Cape Town, South Africa; 5- Pest Management Centre, Sokoine University of Agriculture, Morogoro, Tanzania; 6- Royal Belgian Institute of Natural Sciences, Brussels, Belgium.

African mole-rats (family Bathyergidae) are subterranean Hystricomorph rodents with high species diversity, and six extant genera distributed widely throughout sub-Saharan Africa. Using Bayesian methods in phylogeographic analyses of mitochondrial cytochrome-b and 12s rRNA DNA sequence data, we reveal how biotic evolution has been influenced by landscape evolution associated with the East African Rift System (EARS). While founding divergences within the mole-rat family appear independent of rifting, patterns of distribution of younger species correspond closely to physical barriers imposed by formation of the Gregory and Albertine Rifts, and associated palaeodynamics in climate and vegetation. In particular, the distributional ranges of *Heliophobius* and *Fukomys* reveal how their founding clades diversified across principal graben in the EARS. Further pulses of cladogenesis are responses to shifts in drainage across the Kalahari Plateau through the southwest extension of the EARS. As a result, a flock of no less then 15 vicariant species of *Fukomys* is confined west of the Rift Valley. Yet, a small number of isolated populations occur east of the Rift Valley in Tanzania, where *Heliophobius* is widespread and is the predominant bathyergid. Phylogeographic signatures in the Tanzanian *Fukomys* and geographically adjacent populations strongly suggest that vicariance in the Western Rift Valley subdivided ancestral populations and, together with climatic changes, played a role in isolating these extralimital populations of *Fukomys*. Molecular clock-based estimates of divergence times exhibit a remarkable spatio-temporal congruence with geological evidence, suggesting that cladogenesis reflects a focus of tectonic activity in the 'Mbeya triple junction' and Rungwe volcanic province between Lakes Rukwa and Nyasa.

Is evolution of blind mole-rats (subfamily Spalacinae) driven by climate oscilations? – New phylogenetic tree of the Eurasian blind-mole rats based on five mitocondrial gene

Y. Hadid[1], A. Németh[2], S. Snir[1], T. Pavlíček[1]; G. Csorba[3], Á. Major[3], E. Nevo[1]

1- Department of Evolutionary and Environmental Biology and Institute of Evolution, University of Haifa, Israel, Mt Carmel, Haifa, 31905; 2- Eötvös Loránd University, Department of Systematic Zoology and Ecology, Hungary, H-1117 Budapest, Pázmány Péter sétány 1/C; 3- Hungarian Natural History Museum, Department of Zoology, Hungary, H-1088 Budapest, Baross u. 13.

The taxonomy of the Eurasian blind mole-rats (subfamily Spalacinae) has been a problematic issue from the beginning. To date there has been no taxonomic system created that would be widely accepted among researchers. While some authors only recognize one single species, others believe that the real species richness is several tens-folds higher. To date there has not been a taxonomic tree created covering wide ranges of the subfamily based on molecular biological methods. In our research we investigated sequencies of 5 mitochondrial genes (12S rRNA, tRNA-Val, 16S rRNA, tRNA-Leu, NADH1, tRNA-Ile, 3742 base pairs in total) in 43 tissue samples from 40 populations of 29 taxa. Based on the results we drew the phylogenic tree of the group. We searched for (i) periodicities among lineage-specific stem ages and their correspondence with palaeoclimate periodicities, (ii) congruence between branching events and early palaeoclimate events responsible for origin of steppes and (iii) presence of branching events during humid/arid phases of the Quaternary climate cycles and their relationship with cycles intensity. Our data on ~4 kb of mtDNA sequence shown emergence of bmr during the Early Miocene (~19 Ma) when relatively opened, grass dominated habitats were established in the Eastern Mediterranean. During Miocene dry period was recognized anothe branching event ~7.4 Ma. Both of these datings are well supported by supported fossil evidence. Another split took place ~4.6Ma when the transformation of the ice free warm Earth Cretaceous climate to the bipolar glaciation system promoted establishment of the Mediterranean sclerophylous vegetation, and a process of glacial/interglacial cycles started, respectively. During Pleistocene the radiation events show periodicity corresponding to 100 kyr eccentricity bands. Significant majority of branching events took place during the dry phase of the climatic cycles in Quaternary and the amount of branching events significant increase between early and middle/late Pleistocene. Together, the molecular data provided a step to understand the role of the earth change from the warm, equable, mostly subtropical world that persisted from the Mesozoic to the early Cenozoic—to the Neogene (Miocene to present) ''cold house'' and associated climate variability.

Phylogeny of species and cytotypes of mole rats (spalacidae) in turkey inferred from mitochondrial cytochrome *b* gene sequences

I. Kandemir[1], M. Sozen[2], F. Matur[2], T. Kankilic[3], N. Martinkova[4], F. Colak[2], S.O. Ozkurt[5], E. Colak[1]*

1- Department of Biology, Faculty of Science, Ankara University, 06100– Tandogan, Ankara, Turkey, (ikandemir@gmail.com); 2- Department of Biology, Faculty of Arts and Sciences, Zonguldak Karaelmas University, 67100–Zonguldak, Turkey; 3- Department of Biology, Faculty of Arts and Sciences, Nigde University, Nigde, Turkey; 4- Institute of Vertebrate Biology, Academy of Sciences of the Czech Republic, Květná 8, CZ-603 65 Brno, Czech Republic; 5- Department of Biology Education, Faculty of Education, Ahi Evran University, Kırşehir, Turkey,

We described the genetic variation of cytochrome *b* gene sequences of blind mole rats in Turkey. We examined 47 individuals belonging to 10 cytotypes of three species (*Nannospalax leucodon, N. nehringi* and *N. ehrenbergi*) in the 402bp gene sequence. Cytotypes of *N. nehringi* with low diploid number of chromosomes in western Turkey formed a monophyletic group. On the species level, *N. nehringi* was paraphyletic as *N. leucodon* was included within the supported lineage that included all *N. nehringi* cytotypes. The divergence between two analysed cytotypes of *N. ehrenbergi* (2n=52, 2n=56) was 9.4%, which indicates that the population with 56 chromosomes could be considered a separate species, the recently described *N. ceyhanus*. The results of this study showed that the *Nannospalax* species complex most likely represents more species than currently recognised. We suggest that each cytotype of *N. nehringi* and *N. ehrenbergi* from Turkey should be investigated in detail as possible candidates for being separate species.

Expanding boundaries of chromosomal variability in mole voles *Ellobius tancrei*

I. Bakloushinskaya[1], *S. Romanenko*[2], *N. Serdukova*[2]; *A. Graphodatsky*[2], *S. Matveevsky*[3], *O. Kolomiets*[3], *E. Lyapunova*[1]

1- Koltzov Institute of Developmental Biology RAS, Moscow, Russia (irina.bakl@gmail.com); 2- Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia; 3- Vavilov Institute of General Genetics RAS, Moscow, Russia.

Subterranean mole voles, genus *Ellobius,* are an amazing model for studying chromosomal changes in evolution because of specific autosomes and unusual sex chromosomes. The wide variability due to Robertsonian translocations (Rb fan, 2n = 54–32) was described in Ellobius tancrei in Pamiro-Alay (Lyapunova et al., 1980; 1984, 2010). Using G-banding we revealed that Rb fan was formed mainly due to hybridization of high- and low-chromosomal forms, while applying Zoo-FISH method detected non-homologous translocations. Obtaining new material we discovered unknown form with a lowest 2n=30. According to new data, Robertsonian fan includes at least three different low-chromosomal forms, and a mixture of hybrid forms. Such diversity is caused by various chromosomal changes, like independent and repeated occurrences of Robertsonian translocations (single and multiple), hybridization, and, possibly, WARTs.

We got and analyzed hybrids of karyomorphs with monobrachial homology. Electron-microscopic and immunocytochemical analysis of synaptonemal complexes revealed formation of chains in meiotic prophase I of male and female F1 hybrids. Impeded segregation of such complexes leads to occurrence of unbalanced gametes and to dramatic reduction of fertility. Thus, our data support the monobrachial chromosomal speciation model.

Social evolution in subterranean rodents: does phylogeny matter?

A. Smorkatcheva,

St. Petersburg University, Universitetskaja nab 7/9, 199034, St. Petersburg, Russia (tonyas1965@mail.ru).

The subterranean rodents tend to occupy the opposite ends of the sociality continuum: most species are either strictly solitary or highly social. None of proposed models about the adaptive bases for sociality in subterranean rodents is fully consistent with this pattern. I suggest the scenario that explains the between-family social dichotomy, and I partially test it with phylogenetic comparative analysis. Social strategy of reproductive female in surface-dwelling ancestors might be a conservative trait that predetermined the directions of adaptive changes of social organization in different lineages. In accordance with my prediction, female social strategy had very high phylogenetic signal. Pairwise comparisons revealed no correlation between female social strategy and subterranean mode of life. Character state reconstructions suggested that two asocial subterranean clades, Geomyidae and Spalacidae, had asocial ancestors while nine fully social clades as well as Bathyergidae had social ancestors. The reconstruction for Ctenomyidae was ambiguous. The existence of the intrinsic dissimilarities between subterranean taxa seems to provide sufficient explanation for differences in social systems of their members without involving any selective forces. The comparative phylogenetic studies at the intra-familiar level appear to be appropriate for testing the hypotheses about the effect of subterranean environment on rodent social system. Each of the competing hypotheses may be valid, depending on ancestral female social strategy of focal group.

Evolutionary ecology of the western european moles. Combining genetics, fossil records, morphometrics and habitat modeling for the italian fauna

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Molecular data recently evidenced that direct ancestors of extant European moles originated during the early Pliocene, with two easternmost basal species (*T. altaica* and *T. caucasica*), an eastern clade (*T. stankovici* and *T. levanti*) and a western clade (*T. europaea*, *T. romana*, *T. caeca* and *T. occidentalis*). In Italy occur three of the western species: the widespread *T. europaea*, that is parapatric to the southern Italian endemism *T. romana*, and the southern European *T. caeca* that partially overlaps with both, but it is usually found at higher altitudes. The present distribution of these species suggests that both competitive exclusion and niche shift might be involved in the dynamics of inter-specific relationships. Suitable areas modeled through the Maximum Entropy algorithm for the sibling species *T. romana* and *T. caeca* were influenced by the water content in soil in spring and summer, and suggested a more xeric adaptation of *T. romana*. This is supported by its robust humerus adapted to dig hard soils, the extended inactive periods observed during summer drought, and the range shrinking and expansions of the fossil *Talpa* cf. *romana* during the Pleistocene. The large overlap of suitable areas between the two species (niche Identity test = 0,868) that at present are exclusively occupied by *T. romana*, suggest that this species is dominant in its optimal habitat range. By contrast the shifting of suitable areas of *T.caeca* toward moister soils, its small size and slender humerus would allow the explotation of suboptimal or unsuitable areas for *T. romana.*

The role of intestinal microbes in the evolution of blind mole-rats (Rodentia: Spalacinae)

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Eurasian blind mole-rats are regarded as an evolutionary model for active speciation and adaptive radiation. Cytogenetic and molecular biological mechanisms of speciation were studied in detail, however, the role of microbial communities in the speciation process has not been investigated yet. Mole-rat taxons live in and adapted to a variety of habitats (temperate steppes to deserts), characterised by different vegetation. Faecal samples were collected from two individuals of Judean mole rat (*Nannospalax* (*ehrenbergi*) *judaei*) during two experimental periods, when they were fed with different types of food (with high starch content and fresh green shoots). In the same time, we investigated the microbial communities in the appendices of 9 different species (17 individuals in total) collected from locations which covered the whole distribution area of the subfamily. For bacterial community analysis from faecal samples and cecal contents community DNA was isolated and molecular fingerprint analyses were performed for comparison of bacterial communities of all samples. Significantly different communities were detected during the different feeding regimes. It indicates that intestinal bacterial communities of mole-rats quickly adapt to the changing food resources. Multivariate statistical analyses of bacterial community fingerprint derived from the cecum of 9 mole-rat species resulted in groups of samples identical to host taxonomic groups. Moreover, the dendrogram topology deriving from cluster analysis of the microbial communities was very similar to the phylogenetic positions of mole-rat species based on mtDNA sequences and karyotypes. It suggests co-evolutionary changes of bacterial communities during the adaptive radiation and active speciation of Eurasian mole-rats.

Nitrogen fixation and gerbils’ impact to soil biological activity

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Nitrogen-fixing activity (NA) was detected in forestomach, cecum and colon of two coexisting gerbils’ species – *Meriones tamariscinus* and *M. meridianus*. The differences between NA levels of two gerbil species were significant. The highest levels were detected in colon of granivorous *M. meridianus* (up to 348.7 nM(C_2H_4)/g*h). Bacterial complexes of gastro-intestinal tracts (GIT) of gerbils were different, that correspond to their food preferences: *M. tamariscinus* forestomach was characterized by significant quantity of cellulolytic *Bacillus subtilis/licheniformis*; dominants in *M. meridianus* GIT were *Bacteroides*. In general, *M. meridianus* GIT was characterized by higher diversity of bacteria. NA levels in the burrows of *M. meridianus* were higher, than in control soil, and in the burrows of *M. tamariscinus* similar to control except the burrow chamber, where this level was 3 times higher. Denitrification levels in gerbils’ burrows and in control soil were significantly different and higher in the burrows irrespective of the gerbil species. There were no difference in CO_2 emission levels from the burrows and control soil. The main dominants of bacteria complex of *M. tamariscinus* burrows were *Bacillus* and *Paenibacillus*, and of *M. meridianus* - *Erwinia* and *Azospirillum*. Also the presence of *Bacteroides* spp., typical for GIT, should be noted. More than that, the essential increase of diazotrophs’ quantity was detected in burrows’ samples.

Twenty five years of Zambian Mole-rats in Europe

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Twenty five years ago, 1986, I brought to Germany several Zambian mole-rats, considered to be *Cryptomys hottentotus*, which later turned out to be a new species and a new bathyergid genus, denoted *Fukomys anselli*. Five years later, 1991, late Dr. Mathias Kawalika, sent ten specimens of the giant mole-rat, *Fukomys mechowii*, to me. Ten years ago, 1996, Dr. Andreas Scharff, my PhD student at that time, brought several silvery mole-rats, *Heliophobius argenteocinereus*, from Zambia. These animal imports started fruitful research on many aspects of biology and evolution of Zambian mole-rats, both in the laboratory and in the field. In the meantime, Zambian mole-rats are kept and bred, and intensively studied in several European laboratories, particularly in Belgium, Czech Republic, and Germany. This research ranges from studies on taxonomy, biogeography and phylogeography, field ecology, and behavioural ecology to studies in sensory biology, biology of reproduction, morphological and physiological specializations to burrowing and to life underground. Mole-rats have become established experimental models in the study of mammalian magnetoreception and have a big potential to become models for aging research.

Activity in african mole-rats: do different social systems imply different patterns of activity?

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The subterranean ecotope, particularly in tropical regions, is almost free of daily fluctuations in environmental factors that serve as zeitgebers of activity. The question arises as to whether there is circadian periodicity in the activity of its permanent inhabitants and, if so, how it is induced and maintained. Strictly subterranean African mole-rats (Bathyergidae, Rodentia) are excellent model organisms for such studies. We used radio-telemetry to follow the activity of three African mole-rat species with different social systems, the solitary silvery mole-rat *Heliophobius argenteocinereus* and two highly social *Fukomys* species, the giant mole-rat *F. mechowii* and the Ansell’s mole-rat *F. anselli*. Both solitary and social mole-rats showed circadian periodicity of activity. In solitary species, the fluctuation of soil temperature probably serves as zeitgeber of activity. However, the factors determining activity in their social counterparts are unclear. Interestingly, there was a significant difference in activity between breeding and non-breeding individuals within the particular families. Non-breeding mole-rats were synchronised in activity with each other and they are probably responsible for maintenance of the subterranean burrow systems. In contrast, breeding animals were much less active. Moreover, we found out that social mole-rats may adopt solitary habits during dispersion and then the pattern of activity is similar to solitary species. To conclude, we suggest that social factors play an important role as the determinants of activity in social mole-rats and are essential for the cohesion of the social unit. In solitary species, mole-rats are most active when environmental conditions are favourable.

Digging and biting in *Fukomys* mole-rats (Bathyergidae, Rodentia)

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African mole-rats use their jaw apparatus for digging large tunnel systems, feeding on geophytes and in inter- and intraspecific agonistic encounters. These chisel-tooth digging rodents thus require an efficient biting apparatus. Using bite force as a proxy for biting performance, functional and behavioural performance within colonies of these highly social mole-rats can be studied. For *Fukomys* mole-rats a caste system has been described based on the amount of work performed, where it can be hypothesized that variation in biting performance reflects variation in work behaviour. Behavioural observations were carried out in a colony of wild-caught *Fukomys micklemi*, in order to test whether distinct worker castes exist. Maximal bite force was measured and related to morphology and work behaviour, where also the relation between soil hardness, biting performance and work behaviour was explored. Individual mole-rats were allowed to dig in soils of varying hardness, with digging performance estimated as the amount of soil removed per unit of digging time. Although considerable interindividual variation in the amount of work was apparent within the colony, no distinct worker castes could be defined. These results suggest that a subdivision of the worker caste into frequent and infrequent workers, as reported earlier for *Fukomys damarensis*, does not reflect the pattern of continuous variation in work behaviour. Preliminary results show that digging performance was significantly lower in harder soil. For soft soils, no relation was found between bite force and digging performance. For harder soils however, digging performance shows a positive relation with bite force.

Stress in an african subterranean rodent – the giant mole-rat (*Fukomys mechowii*)

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We assessed physiological responses to different levels of stress in a socially living subterranean rodent, the giant mole-rat (Fukomys mechowii). We monitored heart rate and body core temperature of 10 individuals in different dyadic interactions and reactions to novel arenas. For this purpose we used transponders for body temperature and heart rate telemetry developed by Respironics Mini Mitter (USA). After surgical implantation into abdominal cavity the Mini-Miter system enables to monitor simultaneously locomotory activity, and the mentioned physiological parameters without any movement restriction of the animal under study. Experiments showed that during confrontation with a strange individual the heart rate increased from 200-350 beats per minute up to double values. The body core temperature ranged roughly between 33 degrees C in resting individual and 36 degrees C in high locomotory activity after confrontation. During exploration of a new arena the monitored parameters increased slowly and stayed under confrontation stress level markedly. The intraspecific variability was higher in confrontation stress level than in exploration level. Based on the determined parameters we get more real insight into biology as well as the social system of mole-rats.

The perception of sex differences in the contact calls of mandarin voles (*Microtus mandarinus*)

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Mandarin voles are subterranean rodents, distributed in grassland of Central Asia. They live in extended family groups with prolonged pair bond (Smorkacheva, 1990) and exhibit high vocal activities. Previously it was shown significant differences between male and female contact calls (Kunchevskaya *et al*., 2010). In this study we tested whether voles can identify the sex of an unfamiliar conspecifics from playbacks of its contact calls. We investigated behavioral responses by males and females to playbacks of same- and opposite-sex callers. Subjects were 47 adult females and 43 adult males. Females demonstrated shorter latent period of reaction (Mann-Whitney U test: $U = 88$, $p = 0.04$) and higher level of exploratory activity ($U = 29$, $p = 0.02$) in response to female calls than to male ones. In turn males responded to the same-sex calls more strongly than that of the opposite-sex calls ($U = 77$, $p = 0.03$), and decreased the locomotor activity when presented with female calls ($U = 53$, $p = 0.005$). The results suggest that sex differences exist in the Mandarin vole vocal behavior in both the contact calls' acoustic structure and responsiveness to this sexspecific signal.

Mating behaviour of Zambian *Fukomys* mole-rats

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Mole-rats of the genus *Fukomys* are subterranean rodents that live in eusocial multi-generational families. Only the founder pair, the queen and the king, reproduces whereas their offspring remains reproductively quiescent while staying within their home family. Incest avoidance between parents and offspring and between brothers and sisters is based on individual recognition, most likely via olfactory signals. If two unfamiliar reproductively quiescent mature mole-rats (non-breeders) of opposite sex meet, in many cases mating takes place soon after their first encounter. Here, we describe the mating behaviour of two species of *Fukomys* mole-rats (*F. anselli* and *F. mechowii*) from Zambia. We paired 18 Ansell's mole-rats and 7 giant mole-rats, respectively, which were all non-reproductively active at the time of first testing. Since several attempted pairings were unsuccessful because of choosiness either of males or of females we tried different mating constellations. It was often the male that became aggressive during an encounter. Although in these cases the female occasionally attempted to appease the male e.g. by means of lordosis and soliciting, the trials were interrupted since the male's aggressiveness escalated. All pairs that showed increased interest and courtship behaviour were tested repeatedly (maximally three times a week over a period of 10 weeks); between the trials animals were put back to their respective family. Our tests resulted in 10 successful (out of 19) matings (seven pairs of Ansell's mole-rats, three pairs of giant mole-rats), and we analyzed dozens of copulations. We report on the frequency, duration, and specific features of copulations and anogenital grooming.

Visual systems and the role of vision in the visual system of african mole-rats (rodentia, bathyergidae)

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Using a variety of approaches and techniques, we have studied the visual system of subterranean mole-rats of the rodent family Bathyergidae, for which light and vision seem of little importance. The axial length of the eye varies between 2.6 mm in *Bathyergus suillus* and 1.5 mm in *Heterocephalus glaber*. The small superficial eyes have features typical of sighted animals and appear suited for proper image formation. The retina is rod-dominated but possesses significant cone populations (~ 10%). Three cone types are present: cones that express exclusively either short-wave sensitive opsin (20%) or middle-to-long-wave sensitive opsin (10%), and dual pigment cones that co-express these two opsins (70%). The total number of optic nerve fibres ranges between 6,000 in *Bathyergus suillus* and 2,100 in *Heliophobius argenteocinereus*. Visual acuity, estimated from counts of peak ganglion cell density and axial length of the eye, ranges between 0.3 and 0.5 cycles per degree. The retina projects to all the visual structures described in surface-dwelling sighted rodents. All other visual nuclei but the suprachiasmatic nucleus are reduced in size and receive almost exclusively contralateral retinal projections. The primary visual cortex is small and, in comparison to other rodents, displaced laterally. Behavioural tests have demonstrated a clear photoavoidance response to full-spectrum, blue and green-yellow light, but no reaction to ultraviolet or red light during nest building. Plugging of illuminated tunnels strongly suggest that vision plays an important role in predator avoidance and tunnel maintenance in the African mole-rats. However, rare surface activities can hardly be visually guided.

Poster Communications

Mate preference and fidelity in monogamous Ansell's mole-rats, *Fukomys anselli*, Bathyergidae

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Ansell's mole-rats are subterranean rodents living in multigenerational families, where only the founder pair (king and queen) breeds and their offspring remain in the natal family as helpers. Burda (1990) hypothesized that the female alone is not able to raise her offspring which implies that her mate must be socially faithful. Since in Ansell's mole-rats repeated copulations over a longer period of cohabitation are necessary for ovulation (Burda 1999), the fidelity of the male partner is expected. Here we tested this prediction and addressed the related question whether or not the presentation of a new female provokes enhanced sexual interest in males (Coolidge Effect).

In a behavioral partner preference test, the king chose between two females but had no direct access to them. Kings spent significantly more time near unfamiliar females than their own mates. If given the choice between an unfamiliar queen and her non-reproductive daughter, the kings preferred the queen. In contrast, queens did not differentiate between own mate and unfamiliar kings or non-breeding males.

In the second test we allowed the males to access the compartment of an unfamiliar female while their respective families stayed in adjacent but grid-separated compartments. Only the non-reproductive adult males seized the chance for copulation whereas the kings remained faithful. In reversed test conditions (i.e. females had access to an unfamiliar male), aggressiveness of the males impeded sexual encounters in most cases.

We postulate that the maintenance of Ansell's mole-rats' families depends strongly on the faithfulness of the kings.

Osteological correlates of the trigeminal system within talpidae

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Talpidae consists of small insectivorous mammals expressing a range of behavioural, environmental and dietary preferences. In addition, all its members rely on a highly developed somatosensation system making them a perfect study-group for investigating osteological correlates of the trigeminal nerves innervating the mandibular and maxillary regions of the head. Due to the tight association between nervous and bony tissue, osteological cranial morphology has been extensively used as evidence for the presence of nervous tissue and (by proxy) sensory adaptations in both living and fossil mammals. Here I report findings on whether (1) species reliant on tactile sensitivity such as semiaquatic forms express an increased calibre of the infraorbital foramina (IOF) - through which the second division of the trigeminal nerve exits the skull - in comparison to terrestrial species and (2) if the size of the IOF correlates with the calibre of the foramen rotundum. In addition, I investigated whether bony artefacts of V3 innervation differed between species e.g. (3) whether the relative calibre of the foramen ovale correlates with the size of the mandibular canal within the dentary and whether this is related to behavioural and environmental preferences independent of phylogenetic relatedness? IOF dimensions were recorded within a sample of 29 species of talpids (n=205) and individual skulls of species were µCT scanned in order to analyse the internal or otherwise inaccessible foramen rotundum, foramen ovale and mandibular canal. This new research indicates that fine scale differences in the somatosensitivity of closely related mammals are detectable within bony anatomy.

Burrow Configuration of *Allactaga firouzi* (Womochel, 1978) (Mammalia: Rodentia)

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The Iranian jerboa (*Allactaga firouzi* Womochel, 1978) was described in 1978 by D. R. Womochel based on four specimens collected from near the village south of Shah-Reza, Isfahan Province. The IUCN/SSC classifies the species as data deficient. The current knowledge of the distribution of *A. firouzi* shows that, the species inhabits unique habitats in Iran. The earth consisted of hard-packed, gray, sandy soil contained little organic material. Recently we found this species near the Mirabad village in 22 km south of Shah Reza-Abadeh highway (31° 56' 02'' N, 52° 02' 05''E; 2198 m). Fifteen burrows of Iranian jerboa were excavated in the study area during July and Aug of 2008, Jan and Feb 2009. Burrows were carefully excavated by a spade and small shovel so as to maintain the original organization of tunnels and associated structure. We studied active burrows namely the burrows that jerboas entered it. Statistical analysis to determine significant mean differences among inter-substrate and surface differences in burrow systems including; depth of nest chamber, number of entrance holes and the length of tunnels. The burrow systems of Iranian jerboa *A. firouzi* are comprised of temporary, summer and winter types. The length of tunnels were significantly different (ANOVA, P=0.00) in winter burrows. General burrow described for Small Five-toed jerboa *Allactaga elater* was similar with these burrows except having reproduction burrow. Results show that depth of nest chamber in third type of burrow was deeper than in temporary and summer (P=0.00, P=0.003 respectively).

Towards a modern classification of *Fukomys* (Bathyergidae, Rodentia)

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Within the genus *Fukomys*, morphological similarity contrasts sharply with the high level of variation at the chromosomal and molecular level. Seven major clades can be distinguished based on morphological and DNA markers: a "Sudanian clade" (*F. ochraceocinereus* clade) and six Zambezian clades (*F. bocagei*, *F. mechowii*, *F. whytei*, *F. darlingi*, *F. micklemi* and *F. damarensis* clades ("Zambezian" clades). Within each of these groups a considerable amount of variation in DNA sequence, chromosomal and morphological can be observed. An integrative approach is proposed to gain insight into the *Fukomys* classification and to define species boundaries. Firstly we argue for the use of an evolutionary species concept. Secondly, we apply the species concept views starting from a molecular framework, which allows to further clarify patterns of variation not only in chromosomal but also morphological and ethological data. The chisel-tooth digging African mole-rats require a highly efficient jaw apparatus, used for foraging and in inter- and intraspecific agonistic encounters. Understanding the proximate versus ultimate processes related to biting performance and cranial morphology are now hampered by the lack of information regarding the degree of sociality within different taxa, the effect of dominance hierarchies in biteforce studies, the fact that intraspecific morphological variation exceeds interspecific variation and finally the lack of ecological data for most taxa. The available data provide evidence for the existence of a number of new *Fukomys* species and indicate that further field sampling is required which should be supported from microsatellite marker analyses, chromosome painting studies and extended sampling of etho-morphological evidence.

Vocalisations in *Fukomys micklemi* (Bathyergidae, Rodentia)

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African mole-rats (Bathyergidae) are subterranean rodents which live in social groups. To enhance integration of individuals into a social group, the development of efficient communication signals is necessary. Communication in African mole-rats, however, is severely constrained by the properties of the subterranean habitat and by the specialized auditory system. This study focused on acoustic communication. The main aim was to construct a vocal ethogram. To this end more than 4000 vocalizations were recorded, of which 2208 were analyzed in spectrograms. In combination with information from molecular and morphological studies, ethological data will ultimately help to gain further insight into the complex species relations in the genus *Fukomys*. In one colony of *Fukomys micklemi* sound recordings were made and combined with behavioural observations, linking vocal communication to behaviour. An extensive vocal repertoire was revealed for *Fukomys micklemi*. Sixteen different adult specific calls and four juvenile specific calls were distinguished, based on their physical characteristics derived from the spectrograms and the associated behaviours. The adult specific calls were further subdivided into five call-categories: contact calls, mating calls, distress calls, agonistic calls and submissive calls. Certain call-types served multiple functions. As expected for subterranean animals, the vocalizations were situated in the low to middle frequency range. In general, the extensive vocal repertoire of *F. micklemi* is quite comparable to that of *Fukomys anselli* and *Heterocephalus glaber*, two other social species. The large number of call types contrasts with the limited vocal repertoire of solitary species.

Session 2 - Mammals and their Parasites

Invited & Oral communications

Asymmetry in mammals-parasites' interactions: what have we learned?

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Parasites are by definition strongly dependent on their hosts, and empirical and theoretical studies have emphasized the adaptation of parasites through maximization of their transmission success, but mostly in single host-single parasite systems. However, hosts face multi-parasitism and one recognizes that hosts should do their best in a wormy world. Although the determinants of parasite diversity have been greatly investigated in the last decade thanks to the development of comparative methods, parasite diversity has only recently been viewed as ecological and evolutionary forces on their hosts. Even in the fields of behavioral ecology and human ecology, parasite diversity has been recognized to play a significant role. Here, we aim at giving an overview of the recent findings and the new opened avenues. As hosts face multi-parasitism, this implies that hosts should response and adapt to the whole parasite diversity. This asymmetry in host-parasite interactions will be exemplified in mammals.

Long-term co-evolutionary history with parasites and MHC diversity in rodents

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Due to the central role of the major histocompatibility complex (MHC) genes in the vertebrate immune system, it is generally assumed that the main selective pressures affecting MHC diversity arise from parasites. A few studies, based on data compilation from the literature, have shown associated diversities of MHC alleles and parasites at the interspecific level. MHC diversity was generally positively correlated with parasite richness. This pattern suggests that species facing high parasite diversity are likely to experience relatively high selection pressures for maintaining polymorphism at MHC genes compared with species facing low parasite diversity. We revisited this assumption using data on ca. 2000 rodents from ca. 10 species and their helminth parasites sampled in several localities in Southeast Asia. We considered the DRB gene, which is the most variable of MHC class II genes. We conducted a phylogenetically controlled analysis to test the prediction that host species harbouring high parasite diversity should exhibit high levels of MHC genetic diversity. Statistical analyses were controlled for spurious correlation arising from effective population size by taking into account the genetic diversity of two markers supposed neutral as regards struggle against parasites (cytochrome b on the mitochondrial genome and nuclear microsatellites). Our results give a better insight of long-term selection pressures arising from the coevolutionary history of rodents and parasites.

Evolution of toll-like receptors 4 and 7 genes in wild Rodents (Murinae)

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Appropriate recognition of parasites is crucial for effective immune response, ensuring an activation of adequate defense mechanisms. In vertebrates, it has frequently been demonstrated that genes encoding proteins involved in the recognition of pathogens by the adaptive immune system are often subject to intense selection pressures. However, much less information has been provided on the selection acting on the genes of the innate immunity. The aim of this study is therefore to describe natural variation of innate immunity genes involved in parasite recognition in rodents and to look for signatures of past selection. We sequenced TLR4 and TLR7 genes, which are known as key receptors of innate immunity, for 23 rodent species within the subfamily Murinae in Europe, Asia and Africa. Overall, the phylogeny of rodents TLR genes correctly recapitulates the phylogeny of rodents. The sequence analyses show that vertebrate *Tlrs* are slow-evolving genes. Major parts of these two molecules are evolving under strong purifying selection, which is likely to be mediated by the constraint of maintenance of their function, i.e. the recognition of conserved structure of pathogens. However, we also found the signatures of positive selection in several amino acid sites of the ectodomain in both TLRs. This domain is specifically involved in the detection of pathogens. This pattern could be explained by episodic parasite-mediated selection during the evolutionary history of rodents.

Microparasites interactions in mammals natural populations: how to distinguish true interactions from those generated by co-circulation mechanisms?

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Numerous parasites simultaneously circulate within natural host populations and interspecific parasite interactions are therefore likely within a host individual. As those interactions can seriously impact the circulation of some parasites, their study is essential. Up to now, such studies mainly focused on human pathogens, using an individual-based and experimental approach. Field studies are much rarer, though they are necessary to detect interactions of interest and access infection and co-infection probabilities. The detection of interactions on the field with presence-absence data (i.e. serology) is actually complicated by methodological obstacles. Indeed, confounding factors can create statistical associations between parasites, making the detection of true (biological) interactions difficult. For example, if a transmission mode is shared by several parasites, some hosts will be at risk for several parasites at the same time. Using a methodological and population-based approach, this work aims at conducting a cross-cutting reflection on the issue of those false interactions. Its results are applied to the main viruses of the domestic cat (*Felis silvestris catus*), surveyed in fifteen rural cat populations sheltering both feral and domestic cats. Two main questions will be addressed: (1) Which conditions favor false interactions? ; (2) Which method(s) should be used to take factors generating them into account?

Patterns, mechanisms, consequences of gender-biased parasitism

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In this talk, we will consider patterns, mechanisms and consequences of gender bias in parasite infestation using rodents and their ectoparasites as a model host-parasite association. Regarding patterns and using fleas harboured by rodents in the Negev desert, we will show that parasite abundance, prevalence and species richness is often host male-biased, but it may also be female-biased or absent. Then, we will demonstrate that manifestation and strength of gender-biased parasitism may differ inter- and intraspecifically. In particular, the expression of gender-biased parasitism with the same host species may vary temporally (e.g., seasonally), spatially and in dependence of a parasite taxon. Using an example of a South African rodent host (*Rhabdomys pumilio*), we found that spatial variation in gender differences in parasite infestation was affected by parasite-, host- and environmental factors, although the set of factors affecting gender differences in infestation differed among higher taxa of ectoparasites. Gender differences in infestation by fleas and lice were affected mainly by parasite-related factors, whereas gender differences in infestation by ticks and, in part, by mites were affected mainly by host-related and environmental factors. Second part of our talk will deal with one of the mechanisms of gender-biased parasitism. Using data from laboratory experiments on fleas *Xenopsylla ramesis* exploiting rodents *Meriones crassus*, we will show that, in general, fleas perform better on male rodents. In particular, when feeding on male as compared to female hosts, fleas took more blood, digested it faster, produced more eggs and larger male offspring. In addition, female (but not male) fleas appeared to be able to distinguish between male and female hosts presumably by odour clue and select male hosts in Y-maze trials. Finally, we will consider consequences of gender-biased parasitism and will demonstrate that male rodent hosts drive infracommunity structure of their flea parasites.

Rodents and their parasites: various patterns associated with anthropogenic disturbances

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Rodent populations respond rapidly to the environmental changes from anthropogenic origin. While some populations have decreased with species recognized as endangered, some others are well known to colonize highly disturbed biotopes, possibly following humans and being introduced in new territories. Rodents are also hosts and vectors of a variety of pathogens causing serious diseases in humans. Several studies have revealed higher prevalences of microparasites and macroparasites in hosts living in highly disturbed habitats compared to those living in less disturbed ones. Unfortunately, data related to parasite species richness are scarcer and mainly concern helminth parasitism. While studying the ecology of the murine rodent species in Thailand, we decided to analyze the different published epidemiological studies conducted on these species in the same country. We show that the diversity of viruses is higher for rodent species living in the more human-dominated habitats, according to predictions. Nevertheless, bacterial species richness is not particularly higher in such habitats. Our study gives new insights on patterns of pathogen diversity in relation to habitat and stresses abusive generalizations in the ongoing debate on parasitic diseases and habitat disturbances. However, since human infection also relies on the exposure to vectors and pathogens, we put forward that human populations living in highly anthropized areas could be at higher risks for major rodent-borne viral diseases. This study was supported by the French ANR Biodiversity ANR 07 BDIV 012, project CERoPath, “Community Ecology of Rodents and their Pathogens in a changing environment”.

Ectoparasite communities of two closely related rodent hosts

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Here we present data on the ectoparasite fauna of two closely related rodent hosts, *Apodemus sylvaticus* and *Mus spretus*, sampled in the same localities. The study was conducted in Northern Spain during one year, in a crop land area patched with natural vegetation belonging to the Mediterranean region. Both species of mice share the area with other rodent and insectivore species, but constitute the predominant species of the small mammal community. Their role in the studied ecosystem is very similar, with individuals of both species occupying the same biotopes. In the 161 hosts captured (79 *A. sylvaticus*, 82 *M. spretus*), we recorded more than 4000 ectoparasites belonging to 34 species of arthropods.. Around half of the taxa were found in both hosts, although their abundance and prevalence varied. Of the remaining taxa, 11 species were only present in *A. sylvaticus* and 4 only in *M. spretus* (2 and 1 respectively with high enough abundances so as not to be considered ocasional presences). Thus, parasite communities of both mice species show statistical differences in composition. Since both hosts share the same habitat and population dynamics, ectoparasite abundance, prevalence and community differences could be related to specific factors such as behaviour or immunity. Results are discused according to each species' biology in the frame of evolution of patterns in the diversity of parasites among related hosts.

Comparative phylogeography of cestodes (anoplocephalidae) of arvicoline rodents in the holarctic region

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We review the molecular phylogenetic analyses of anoplocephalid cestodes and their arvicoline hosts in the Holarctic region. The parasites represent the genera *Paranoplocephala*, *Anoplocephaloides* and *Microcephaloides*, and hosts belong to the genera *Lemmus*, *Dicrostonyx*, *Microtus* and *Myodes* (*Clethrionomys*). These parasites are generally fairly host-specific. Cytochrome oxidase I (mtDNA) sequences were the basic tool in the analysis of cestode phylogenetics, accompanied in some assemblages by 28S or ITS1. The host phylogenies, based mainly on cyt *b* sequences (mtDNA), were extracted from published sources. Among arvicoline-carried anoplocephalid cestodes, colonization of new lineages has been the predominant mode of diversification. There is some evidence for allopatric divergence following host shifts, particularly in *Anoplocephaloides.* Within species or between closely related species of parasites, parasite divergence may or may not correspond to that of the hosts. High host specificity may have enhanced strict phyletic coevolution in some of the assemblages. The presence of phylogeographic structure in a parasite in the absence of corresponding host divergence may reflect "cryptic" divergence or inadequate sampling (or both) of the latter. Each anoplocephalid taxon in different arvicoline species shows an independent response to the host phylogeography, and there are no concerted common responses.

Sexual dimorphism in resistance and tolerance in the European populations of the wood mouse *Apodemus sylvaticus*

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Hosts can adopt two defences strategies when challenged by parasites, namely (a) to resist and limit parasitic burden or (b) to reduce the harm caused by a given parasite load , this latest strategy being referred to tolerance. Health or fitness deterioration in less tolerant individuals with increasing parasite burden would be faster as compared with more tolerant ones individuals. We studied Mediterranean populations of the wood mouse (*Apodemus sylvaticus*) and its helminth parasites and we assessed resistance (using PHA test and spleen size) and tolerance (using body condition) in males and females and testes size in males. While helminth infection did not differ between the two sexes, females and males differ in measures of the immune system. Females seemed to invest more in immune defences with the increase of parasite load, intensity or diversity. Conversely, males seemed to be more tolerant with less important loss of body condition when parasitic loads increase compare to females. All these results sustain sexual dimorphism in tolerance and resistance in wild animals and stressed that measuring only parasitic loads could be insufficient to detect any underlying sexual difference in the two strategies that evolved to face multiple parasitic attacks in natural systems.

Parasitic manipulation of appetite

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One common physiological phenomenon that is involved both in infectious and malignant processes is the reduction in appetite – disease anorexia. Potential candidates for inducing disease anorexia include various neuro-endocrine products that are known to regulate appetite in healthy animals including humans. These include leptin, ghrelin, cholecystokinin, insulin and somatostatin. Leptin a 16 kDa cytokine that has complex physiological effects including appetite regulation and is similar to other cytokines associated with the inflammatory response. An increase in plasma levels of leptin, both when associated with inflammation and when occurring in healthy organisms, has been shown to suppress appetite in several kinds of vertebrates. We wanted to test whether a parasitic infection with *Cysticerus fasciolaris* the larvae of the heleminth parasite *Taenia taeniaformis* would affect the levels of appetite regulating proteins such as leptin, gherlin, and neuropeptide Y (NPY). From an evolutionary perspective it would be more adaptive for an organism that is internally parasite within its host and that is constantly growing to stimulate the appetite of the host instead of causing its suppression. Infections with *C. fasciolaris* are rather common in wild Yellow-necked mouse (*Apodemus flavicollis*). The infection is thought to be asymptomatic and is considered harmless, however the eco-physiological effect of the infection is not well known. In the present experiment we investigated the effect of an internal parasite infection with *Cysticerus fasciolaris* on the plasma levels of appetite regulating neuro-endocrine substances leptin, ghrelin and neuropeptide Y (NPY) in wild Yellow-necked mice. We found that infected mice had significantly lower plasma levels of leptin and increased levels of NPY compared to the healthy subjects. Ghrelin levels were not associated with the occurrence of the parasites, however, these levels strongly correlated with the levels of NPY. This study suggests a possible manipulation by the parasitic larvae of the appetite regulation in infected subjects.

Poster Communications

Infestation of *Apodemus flavicollis* (Rodentia, Muridae) with ectoparasites in Transilvania (Romania)

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Apodemus flavicollis is the most widespread and abundant rodent in the woodlands of Romania. It inhabits all types of forests as well as open areas in their vicinity. Data on ectoparasites harboured by *A. flavicollis* were collected from 339 animals captured in 10 areas across Transylvania, beginning with the year 2004. Prevalence of ectoparasites was 78.2%. Four groups of ectoparasites were found, namely Acarina (including Ixodoidea), Siphonaptera, Anoplura, and Coleoptera. Among parasite taxa, mites (Gamasidae and Trombiculidae) were most common, followed by fleas, ticks, lice, and beetles. The effect of a number of biotic and abiotic variables (locality, altitude, season, year, host age and sex) was tested using Pearson chi-square test of independence. Geographic position (altitude and site) did not affect significantly prevalence of the ectoparasites when all taxa were pooled together. Time (season and year), on the other hand, has a significant effect with a decrease in prevalence from spring to winter. The considered variables differently affected the parasites taxa. Prevalence of fleas did not depend on any factors. Among mites, prevalence of *Trombicula autumnalis* depended significantly on host age and sex, being higher in males and breeding adults. Majority of rodents harboured parasites belonging to the same taxon, although co-occurrence of mites and fleas was common. Nevertheless, the Fager index revealed no significant association between these two taxa.

Contribution to an inventory of pathogens agents in rodents of Algeria

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The infectious agents transmitted or hosted in rodents are more and more numerous and they cause a real public health problem everywhere in the world. The aim of this work is to contribute to an inventory of these pathogens agents in this animals and their transmission to the man or to another domestic or wild animals. Among the pathogens agents detected in these animals, we quote: The Lyme borreliosis, Tick-borne Recurrentis Fever Borreliosis, Rickettsiosis, Ehrlichiosis, Bartonellosis, Plague, Leishmaniosis. This small list is a little apercu of this agents which circulating in rodents in Algeria.

Low-scale geographical variation in the ectoparasite community associated with a wood mouse population

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The study of ectoparasites associated with wood mice (Apodemus sylvaticus Linnaeus, 1758) has been covered extensively in the literature. However, while the relationship between some parasitic groups or species and this host is well documented, studies looking at the host's whole parasitic community are scarce, yet essential in order to determine ectoparasite diversity patterns related with the spatial distribution of the host. Here, we show the results of a study that examines low-scale variation of the parasite community of a population of A. sylvaticus. The study was carried out in a small, 20km long, pre-Pyrenaic valley in Northern Spain that comprises a marked north-south gradient of biotopes of forests, grasslands and crop areas, transitioning between Cantabric and Mediterranean climatic conditions. These biotopes are consecutively replaced along the river valley and the population of A. sylvaticus is maintained at high densities throughout the sampling area. More than 30 species of arthropod parasites were identified, mainly mites of the Prostigmata order. However, only 21 species were abundant enough to statistically analyze their distribution in the sampling area. Of these species, 12 show a significant geographic variation in prevalence, providing diversity differences among the distinct zones of the sampling area. Changes in vegetation, land use and farming industry are discussed as potential explaining factors for observed biodiversity patterns.

Anthropogenic disturbance and host-parasite associations: water pollution, acari abundance and bat immune response

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We investigated the effect of water pollution on the immune response of bats and on their infestation with ectoparasites. We used the bat *Pipistrellus kuhlii* and its Acari ectoparasites in the Negev desert, Israel, as a model system. We selected two sites where bats forage and drink that differ in the quality of the water they provide for bats: Ein Avdat (EA) – a complex of natural ponds, and Yeruham Lake (YL), a polluted anthropogenic lake. We hypothesized that the quality of water in sites where bats forage would influence ectoparasite abundance due to a reduction in immune function. We predicted that Acari abundance will be higher in YL than in EA. We found that adult female bats in YL harbored significantly more Acari than those in EA. We then used the bacterial killing ability (BKA) assay as an index of immune function to experimentally test the effect of water on bat immune response. We captured 13 female bats in EA and divided them into control (bats treated with EA water) and treatment (bats treated with YL water) groups. We measured BKA at day 0 and after 30 days of exposure to water. We found that BKA did not change in either group. Our findings suggest that in the system we examined, water pollution probably does not alter bat susceptibility to parasites and that other factors may be responsible for the higher Acari abundance in the YL bat population.

Helminth community of *Mastomys natalensis* in different agricultural patches in Morogoro, Tanzania

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Mastomys natalensis, the multimammate mouse, is a widely distributed African murid, a pest causing agricultural damage and acting as a reservoir of several human pathogens. Because some helminths can regulate host populations, they could be used as potential biological control for rodent pests. So far, the helminth community of *Mastomys natalensis* is still poorly known and has only been sporadically investigated across the continent. In order to gain insight into the ecology of the helminth community of *M. natalensis*, we sampled six localities evenly distributed along a 100 km transect between Morogoro and Berega, Tanzania, in December 2009. We crossed various agricultural patches that could potentially support different densities of *Mastomys*. Major agricultural areas are likely able to support a larger effective density of *Mastomys* than small patch scattered among dry bush land. In total, 329 individuals were dissected and screened for helminths. In this talk we present the results of the effect of host density and host intrinsic factors (sex, age, genetic, body mass index) on the composition and load of the *Mastomys*' helminth community. We also test for the potential interactions between Mopeia arenavirus and helminth parasites. A.Ribas attendance to ECM2011 was supported by 2009SGR403.

Ecological analysis of the helminth fauna of the iberian hare, *Lepus granatensis* Rosenhauer, 1856 in the province of Granada (Spain)

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A parasitological study of 487 Iberian hares, *Lepus granatensis* Rosenhauer, was carried out to analyze characteristics of helminth assemblages with respect to 15 biometric, sex-related, as well as climatic and sampling-related variables. Six helminth species were found: *Mosgovoyia pectinata* (Cestoda), *Trichostrongylus retortaeformis*, *Nematodiroides zembrae*, *Nematodirus* sp., *Passalurus ambiguus* and *Micipsella numidica* (Nematoda). Helminth infracommunities were mainly composed of *N. zembrae* and *M. pectinata* (62.4% and 17.2%, respectively), prevalence of other species was rather low (0.2-3.5%). The study of distribution of helminth species throughout the host, allows inferring a β-dominated model, in which individual hosts tend to be dissimilar. A significant seasonal variation was found in helminth assemblages, with maximum richness and abundance in the cold seasons. Abundance of *N. zembrae* showed negatively correlated with body condition of *L. granatensis*, especially in coinfestations with *T. retortaeformis*. In addition, parasitic burdens were found negatively correlated with reproductive status in female hares. These findings support the hypothesis that variations in the parasitic burdens of helminth species that are affecting Iberian hares throughout the year can exert an effect on the regulation of their populations.

Individual MHC variation and endoparasite infections in brown hares; L*epus europaeus*

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The genes of the major histocompatibility complex (MHC) are attractive candidates for investigating the link between adaptive variation and individual fitness. High levels of diversity at the MHC are thought to result from parasite mediated selection via any combination of three proposed mechanisms: heterozygote advantage, rare-allele advantage, and fluctuating selection. Differentiating between the three mechanisms is a difficult task and requires a comprehensive analytical framework examining multiple pathogens while at the same time controlling for confounding environmental and demographic variables. In our study, variation at three MHC class II loci (*DQA*, *DQB, DRB*) and 13 presumably neutral microsatellite loci is compared to infection intensities of *Eimeria spp*. and *Trichostrongylus retortaeformis* and several fitness parameters in brown hares. Samples were collected from hunting grounds in Lower Austria (n=291) and Belgium (n=227). There were large differences in MHC allele frequencies among the populations studied (D_{est}=0.594, p<0.001). We used a generalised linear mixed model to show significant associations between *Eimeria spp.* load and the variables age ($p<0.001$), body weight ($p=0.026$), body condition ($p<0.0001$), and whether individuals possessed a particular allele at the *DQA* locus ($p<0.0001$). For *Trichostrongylus* load, significant associations were detected only with body weight ($p=0.0062$) and sampling region ($p=0.033$). No associations were found between parasite load and microsatellite heterozygosity nor were there any significant associations between parasite species richness and MHC heterozygosity. Our results suggest rare allele advantage and fluctuating selection are the main forces acting to maintain high levels of MHC polymorphism in populations of brown hares.

Investigating the role of wild carnivores in the epidemiology of bovine neosporosis

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Neospora caninum is a protozoan parasite, primarily associated with bovine abortion and limb paralysis in dogs. Although many intermediate hosts of *N. caninum* have been identified the only definitive hosts discovered to date are carnivores. This study aimed to identify the role of wild mammal carnivores in the epidemiology of bovine neosporosis in Ireland. A bank of serum, faecal and brain samples was established to test for *N. caninum*: 197 American mink (*Mustela vison*), 157 red foxes (*Vulpes vulpes*), 62 pine martens (*Martes martes*), 50 badgers (*Meles meles*), 41 stoats (*Mustela erminea*), 32 otters (*Lutra lutra*) and 4 feral ferrets (*Mustela putorius*). IFAT tests on mink and fox serum showed a positivity of 0.88% (n= 141) and 0.99% (n= 101) respectively. All other serum tested negative. A DNA extraction and PCR assay technique found 5.96% positivity in foxes brain tissue (n= 151), 3.05% in mink (n= 197), 4.16% in otters (n=24) and 0% in pine martens (n= 8), badgers (n= 51) and ferrets (n= 4). This is believed to be the first time mustelid tissue tested positive for *N. caninum*. The need to test two relatively large (~ 200mg) targeted parts of the brain to avoid false negatives was also identified. All faecal samples tested negative (n= 311). The prevalence of *N. caninum* seems to be low in the Irish carnivores relative to studies carried out on the same carnivores in other countries, suggesting the local ecology of a species also has an important influence on its epidemiological role.

Session 3 - Mammal zoonosis ecology

Invited & Oral Communication

Plague ecology in kazakhstan: rodents and thresholds

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Plague, caused by the bacterium *Yersinia pestis*, is a widespread infection of rodents in Central Asia. In the deserts of Kazakhstan, its main host is the great gerbil *Rhombomys opimus*. The gerbils live in permanent burrow systems that are deserted during periods of low gerbil abundance but that become recolonized again when abundance increases. We earlier discovered that the proportion of occupied burrow systems is a good predictor for the occurrence of plague one to two years later, and below a given threshold proportion of occupied burrow systems, plague cannot invade or persist in an area. Such epidemiological thresholds have been an important theoretical concept although rarely proven, but usually are based on an assumption of random mixing of individuals. Since burrow systems are fixed in space, the spreading of plague can be considered a percolation process, which provides a more robust explanation for the observed threshold. The connection between burrow systems depends on the distance between them, but also on the movements of the rodents and, in fact, their fleas. Satellite images provide an unexpected and fascinating tool to study the relations in this system and the effects of landscape. We hypothesize that the thresholds framework, regardless of its underlying mechanism, is a useful approach to study not only temporal but also spatial and even evolutionary dynamics of infections, not only for plague but also for other infections in rodents.

Biome-specific rodent dynamics and hantavirus epidemiologies in europe

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Among emerging diseases, rodent-borne (robo) viral infections provide a prime example. In Europe, the incidence is increasing and more countries report robo infections. In the large collaborative EU project EDEN (Emerging Diseases in a Changing European Environment), we studied robo diseases from several points of view. Our most important aim was to understand the differences in human epidemiology in nephropathia epidemica, the most common hantaviral disease in Europe, caused by Puumala hantavirus (PUUV), between boreal and temperate Europe. We documented fundamental differences in the transmission dynamics of PUUV between these two biomes. The patterns in temperate zone are greatly affected by masting events, of which the frequency may increase due to warmer summers, while in the snowy boreal zone predator driven vole cycles shape the dynamics. Consequently, the underlying top-down or bottom-up causes of rodent fluctuations are different. We have further documented the role of landscape patterns (homogenous taiga vs. fragmented temperate forests) in rodent/virus dispersal, and in the presence or absence of host threshold densities for the PUUV occurrence. In addition, local environmental conditions (e.g. temperature and moisture) affect the virus survival outside the host, which may cause variation in indirect transmission. These results are essential for human risk evaluation with regard to both long-term and seasonal occurrence of PUUV in the environment. In conclusion, it is important to realize that within the same host/virus system, biome specific PUUV epidemiologies occur, which highlights the importance of geographically comparative studies in Europe.

Intensive forest management shaping small mammal communities –impact on puumala hantavirus transmission

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Nephropathia epidemica (NE) is the most common hantaviral disease in Europe and is caused by Puumala hantavirus (PUUV). Both the virus and its host, the bank vole *Myodes glareolus* are found in most of Europe, but the incidence of NE is by far highest in the boreal zone in northern and north-eastern Europe. This epidemiological pattern is partly a result of landscape configuration: forests are isolated patches in large areas of temperate Europe, but cover ~70% of land in the boreal zone. However, intensive management of boreal forests in Fennoscandia has lead to a mosaic-like landscape of different aged forests. As bank voles prefer mature forests as their primary habitat, we investigated whether the fragmentation of old forests has impact on PUUV transmission in its host. In this four-year study, we trapped small mammals twice a year in four different forest age classes. We show that PUUV infected bank voles occur in all forest age classes, yet numbers of total and PUUV infected bank voles were higher in mature forests. We also demonstrate that besides host density, the dilution effect, i.e. the presence of non-host species plays a role in PUUV transmission in boreal forests, suggesting a higher human disease risk in mature forests that are characterised by high bank vole abundance and low proportions of non-host species. Both the proportion of a superior (*Microtus sp.*) and an inferior (*Sorex sp.*) competitor were inversely associated with PUUV infection probability in bank voles.

Immunogenetics as a tool to assess hantavirus risk in wild rodents

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Immunogenetics, the analysis of genetic polymorphisms in pathogen recognition and immune regulation, is at the core of the study of host-parasite coevolution. We present here a synthesis of our works based on immune gene polymorphism to illustrate the power of this approach in improving our knowledge of rodent / hantavirus interactions and of zoonotic risk. Two candidate genes (encoding Mx2 protein and β_3 integrin) were first investigated at the inter-specific level. Sequence and/or expression polymorphism were compared among twenty murid species trapped in Asia, some of them being reservoirs and some others being non reservoirs of hantaviruses. Our results showed that SNPs as well as patterns of selection acting on these genes differed between these rodent species and could mediate their susceptibility to hantaviruses. Four candidate genes (*Mx2* gene and three genes from the Major Histocompatibility Complex) were next analyzed among populations of bank voles (*Myodes glareolus*), the reservoir of *Puumala virus* (PUUV). We revealed the existence of (i) positive associations between *Mhc* alleles and PUUV infection and (ii) negative relationships between *Tnf-α* or *Mx2* expression levels and PUUV prevalence. These results suggested that tolerance to PUUV could have evolved in endemic areas. Such tolerance could be selected in response to the costs of immune responses that are activated against PUUV. We will conclude on the advantages to combine this immune gene candidate approach with more recent analyses based on genome scan, to deepen our investigation of this intra- and inter-specific variability of rodent tolerance / resistance to hantaviruses.

Rodents, deer and ticks: how they interaction affects tick-borne diseases emergence and spread

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Tick borne diseases are of increasing relevance for human and animal health in Europe. The widespread tick *Ixodes ricinus* is nowadays recognised as competent vector for several emerging zoonotic pathogens. The prolonged tick activity due to climate change and the invasion into new habitat provide the opportunity for more intense pathogens circulation, as also observed by various combinations of co-infections indicating interaction of the transmission cycles. However, the observed pattern of infection of the ticks with various pathogens represent the outcome of complex interaction occurred among the various tick developmental stages and the vertebrate hosts on which the blood meal was taken. In this presentation a review on the ecology and epidemiology of some of the most common emerging tick borne diseases in Europe, especially tick-borne encephalitis, Lyme disease, Anaplasmosis and Babesiosis, will be discussed considering the variable effect of the interaction among the tick, small mammals and deer which role as competent/incompetent reservoirs change accordingly to the pathogen investigated.

Ljungan virus, an intriguing rodent-borne pathogen

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The Ljungan (picorna) virus (LV) was first isolated in 1998 from Swedish bank voles (*Myodes glareolus*)[1], and has subsequently been put forward as a zoonotic agent of several human (primarily gestational) diseases[2]. LV has been found in laboratory mice and rats, as well as many wild small mammal species, including mice, voles and lemmings, in Sweden, Denmark, Germany, USA, and most recently, Italy[3]. Interestingly, this rodent-borne virus causes symptoms in the rodents themselves[4]; hence, this virus is also interesting for its possible effect on rodent ecology and population dynamics[5]. Therefore, knowledge of the distribution LV among wild and domestic mammal species is crucial to assess its potential importance as a human and rodent pathogen. Here we provide a review of the current understanding of the ecopathology of LV and present the first results from southern Europe, including genetic variation within LV in northern Italy. We discuss the possible role of LV as a zoonotic agent, current projects exploring this, and possible future directions.

1. Niklasson et al 1999. Virology 255: 86-93.
2. Greene McDonald, A. 2009. Clin Microbiol Newsl 31: 177-182
3. Hauffe et al. 2010. J Wildl Dis 46: 262-266.
4. Samsioe et al 2006. Birth Defects Res (B) 77: 251-256.
5. Niklasson et al 2006. Oecologia 150: 1-7.

Leptospirosis in rodents from south-east asia: an insight thanks to real-time pcr

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Asia is recognized as a place where most of the (re)emerging animal diseases occur, some of them being zoonotic, such as leptospirosis. In South-East Asia, although leptospirosis is a major public health problem, it remains scarcely studied. Rodents are the main reservoir and humans get infected by contact with water contaminated with urine from infected rodents. Infections occur mainly in rural areas, but also during leisure activities. Through the project CeroPath (Community Ecology of Rodents and their Pathogens in South-East Asia), rodent trappings were organized in several locations of Thailand, Lao PDR and Cambodia in order to describe rodent species diversity and to screen these specimens for several bacterial and viral agents of diseases. The collected data should allow us to take into account landscape heterogeneity and to highlight the impact of rodent diversity (dilution effect) and abundance (density effect) on the risk of transmission of pathogens from rodents to humans. Here we focused on *Leptospira* to test these relationships. We will present the sensitive and reliable real-time PCR that we have developed for *Leptospira* detection in rodent kidneys. Two genes were screened, one common to all *Leptospira* species (16S ribosomal RNA gene), and another one being specific to pathogen species (LipL32 outer membrane lipoprotein gene). We will expose our results (prevalence and diversity of *Leptospira sp.* in South-East Asian rodents) analyzed with regard to rodent abundance and diversity among trapping locations.

Poster Communications

Sequence and expression polymorphism of *mx2* gene in wild rodents of south-east asia. Their potential role in susceptibility to hantaviruses

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Mx genes encode proteins that play a fundamental role in innate immunity due to their specific antiviral activity. Among the three functional regions of these proteins, the C-terminal domain leucine zipper (LZ) seems crucial in the interactions with viral nucleocapsids. Viral inhibition occurs shortly after virus entry into host cells by segregation of virus particles, preventing genome amplification and viral reproduction. In rodents, lab experiment researches suggest that the Mx2 protein could provide resistance against hantaviruses (family Bunyaviridae). We therefore developed a candidate gene approach to test the hypothesis that genetic variation at *Mx2* gene might underlie the variability of wild rodent species in their susceptibility to hantaviruses. Both sequence and expression polymorphism were investigated as they respectively influence the recognition of hantaviruses and the ability to limit hantavirus replication in cells.We will present the results recently obtained from thirty wild rodent species of the family Muridae (Rattini tribe, *Mus sp.*, *Apodemus sp.*), trapped in South-East Asia and Europe. SNPs and signatures of selection within the exons encoding the LZ domain will be discussed with regard to the hantavirus status of rodent species (reservoir / non reservoir). The variability of *Mx2* gene expression will be analysed at the inter-specific level, with regard to this hantavirus status, and at the intra-specific level for few species with regard to the infectious status of rodents (infected / non infected individuals).

Host switch in hantaviruses: can puumala in *myodes* spill over to lemmings

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During WW II, approximately 10,000 German soldiers and 1,000 Finnish soldiers based in Finnish Lapland suffered a disease resembling Nephropathia epidemica, caused by Puumala hantavirus (PUUV). PUUV is carried by the bank vole (*Myodes glareolus*) and spread to people through the inhalation of infected aerosols from rodent excreta. Human incidence is correlated with bank vole density. However, the timing of this epidemic was atypically in spring. It coincided with the peak density of the Norwegian Lemming (*Lemmus lemmus*) and started 2-3 weeks after the lemming spring migration. Veterans from this epidemic still carry hanta antibodies. These facts suggest that a hantavirus in lemmings caused the epidemic. We have screened over 500 lemmings from peak populations but have not found a specific hantavirus from *L. lemmus* even though Topografov hantavirus is known from Siberian lemmings and can easily experimentally infect *L. lemmus*. Consequently, we tested the hypothesis that PUUV spread from sympatric bank voles to lemmings during the lemming migration into taiga, and that lemmings spread it to humans. It is known that host switches have occurred in the evolution of arvicoline hantaviruses. We attempted to infect lemmings with PUUV from the excreta of recently seroconverted bank voles in a laboratory environment. Three methods were employed; (1) transferring peat and bedding material from vole cages into lemming cages, (2) swapping voles and lemmings between cages, and (3) placing vole urine onto lemming nostrils. So far, we have not been able to infect *L. lemmus* with PUUV. The source of the WW II epidemic remains an enigma.

Statistical modeling and prediction of HFRS incidence in the Udmurt Republic, 1973-2009

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Puumala (PUUV) Hantavirus is agent that causes hemorrhagic fever with renal syndrome (HFRS) in humans. HFRS is widespread within temperate/boreal zone of Europe and ranked first on incidence among all zoonotic disease in Russian Federation. It is highly endemic in Udmurt Republic (UR) with an annual incidence up to 56.1 per 100,000 inhabitants (which is an order of magnitude higher than the average for Russia, 5.7). The bank vole is the main reservoir of PUUV. Based on time series of HFRS incidence in UR (1973 – 2009), monitoring data of bank vole population in the vicinity of Izhevsk (56°50′N 53°11′E) and applying regression modeling we built a set of simple predictive models which not only are in a good agreement with data, but also would provide early forecasting of HFRS outbreak. We utilized the first part of our time series (1973–2006) as training set for parameters estimation, and the last three years (2007-2009) have been used for verification. There is s-shape increasing trend and almost regular (“cyclic”) 2-4 (mainly 3) year’s periodicity in HFRS incidence. The earliest predictor for HFRS outbreak is the high yield of lime nuts in the preceding year. We hope that our models could be used for sufficiently accurate forecast of human risk to HFRS at least by 0.5-1 years ahead.

Detection of Dobrava-Belgrade hantaviruses among *apodemus* mice in hungary and northern croatia

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Dobrava (DOBV) hantavirus belong to the genus *Hantavirus*, family *Bunyaviridae* and carried by yellow necked (*Apodemus flavicollis*) and striped field (*Apodemus agrarius*) mice. The goal of this study was to determine the real prevalence of DOBV in *Apodemus* rodents in Hungary and in Northern Croatia. Rodents were trapped in seven different locations during the summer and autumn seasons of 2005-2007. Rodents were dissected and lung tissues were used for hantavirus detection by SYBR Green-based real-time PCR. A representative DOBV strain (DOB/Pécs/242Af/06) was selected for protein expression. Truncated nucleocapsid protein (rNP50) was expressed in *BL21 Rosetta (DE3) pLysS Escherichia coli* cells using pET28a expression vector. Presence of antibodies against DOBV in the collected rodents was determined by ELISA reaction. During the study period a total of 125 *Apodemus* sp. (67 *A. agrarius*, 58 *A. flavicollis*) was tested for the presence of hantaviruses. DOBV were detected from 21 *Apodemus* rodents by RT-PCR and/or ELISA. Five rodents were RT-PCR and ELISA positive and also 5 animals were positive by RT-PCR only. 11 small mammals were ELISA positive only, while 104 rodents were negative with both methods. The real prevalence based on the results of these two detection techniques was 17% (21/125). In this study we concluded that prevalence of DOBV is much higher as it was expected before, and the parallel use of molecular and serological techniques is the most reliable way to estimate the real prevalence of hantavirus infections.

Mammals as carrier vectors of lyme borreliosis Spirochetae in romania

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Wild mammals are important reservoirs of *Borrelia burgdorferi*, the etiologic agent of Lyme disease, the most widespread vector-borne disease in the cool-temperate regions of the Northern hemisphere. Although the medical importance of this pathogen is generally restricted to humans and some domestic species, the understanding of the epidemiology of Lyme borreliosis consists in revealing the ecological relationships between pathogens, vectors and wildlife hosts. This spirochete has been isolated from a number of experimentally infected mammals, but the natural reservoirs and their importance in maintaining the pathogenetic cycle is largely unknown. Thus, our aim was to evaluate the prevalence, geographical distribution and genetic diversity of *B. burgdorgeri* s.l. in mammals of wild origin from Romania. Tissue samples (skin, heart, liver, spleen, kidney, bladder) have been collected from 268 mammals belonging to 28 species from various localities in Romania. Molecular detection of *B. burgdorferi* s.l. was achieved by nested PCR using OspA primers. Genospecies identification was done by RFLP. *B. burgdorferi* s.l. DNA was detected in 14 mammals belonging to 7 species, the most prevalent genospecies being *B. afzelii*, followed by *B. garinii* and *B. burgdorferi* s.s. Out of 14 positive individuals, the hearth tissue was positive in 93% of the cases, the skin in 80%, the liver in 30% and the spleen in 20%. Our report is the first world record for *M. lutreola* and *V. peregusna* as carrier hosts of the Lyme disease agent and the first study on the presence of *B. burgdorferi* s.l. in carrier hosts from Romania.

What is role of small mammals as paratenic hosts of *Toxocara spp.?*

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Roundworms of *Toxocara* genus are one of the most common intestinal helminths of domestic and wild carnivores worldwide. In the intestinal tract of definitive hosts, carnivores, adult worms spread eggs via the faeces into the environment. In the intestine of paratenic hosts (small mammals, humans) larvae hatch from eggs, migrate via blood vessels and then remain as somatic larvae in tissues. To obtain comprehensive picture on the role of small mammals in the natural foci of diseases, this group has been monitored in Slovakia since 2000. A serological screening was conducted in rodents and shrews in order to determine seroprevalence of antibodies against *Toxocara* sp. Material of small mammals were sampled in Eastern and Central part of Slovakia from different types of habitats, with varying degrees of anthropogenic pressure. During nine years of study (2000 – 2008), 3684 rodents (11 species) and shrews (6 species) were serologically examined using a modified ELISA method. Occurrence of antibodies were confirmed in XY mammal species, with the highest values of seroprevalence in *A. agrarius, M. spicilegus* and *A. flavicollis*. The impact of season, age and sex on the seroprevalence was analysed Research was supported by grant APVV-0267-10, VEGA 2/0043/09.

Session 4A - Shrews, Chromosomes and Speciation

Invited & Oral Communication

The astonishing diversity of chromosomal races in the common shrew (*Sorex araneus*)

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The karyotypes of the ten species included in the *Sorex araneus* or XY_1Y_2 group differ mainly because of alternative fusion of large autosomal arms. Similar karyotypic differentiation evolved between the chromosomal races of the common shrew, however, the autosomes of smaller size were involved in the alternative fusions. This comparison indicates that the present diversity of chromosomal races is a result of continual evolutionary process of karyotypic changes that started already in the common ancestor of the *Sorex araneus* group. Data presenting the heritage of the International *Sorex araneus* Cytogenetics Committee, ISACC show that currently 75 distinct races are recognized throughout the species distribution range from the Atlantic coast in Western Europe up to Lake Baikal in Siberia. This comprehensive pattern of geographic differentiation of the karyotype within single species provides an excellent database for further phylogenetic and evolutionary analyses.

Karyotype evolution of *Eulipotyphla.* The genome homology of *Sorex* species revealed by comparative chromosome painting and banding data

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The genus *Sorex* is one of the most prosperous genera of Eulipotyphla and characterized by a striking chromosome variability including XY1Y2 sex chromosome systems and exceptional chromosomal polymorphisms inside and between populations. To study chromosomal evolution of the genus in detail we performed cross-species chromosome painting of seven *Sorex* species with *S. granarius* and *S. araneus* whole-chromosome probes. It is discovered here that the tundra shrew *S. tundrensis* has the most rearranged karyotype among the *Sorex* species. We reconstructed robust phylogeny of the genus *Sorex* based on revealed conserved chromosomal segments and syntenic associations. About 16 rearrangements led to formation of two major Palearctic groups after their divergence from the common ancestor. Further chromosomal evolution of 12 species inside groups, including 5 previously investigated was accompanied by multiple reshuffling events: 39 fusions, 20 centromeric shifts and 10 fissions. The rate of chromosomal exchanges upon formation of the genus was close to average rate for eutherians, but several fold speedup in rearrangement's rate occurred during recent (about 6-3 MYA) speciation within *Sorex*. We propose that plausible ancestral *Sorex* karyotype consists of 56 elements. It underwent 20 chromosome rearrangements from the boreoeutherian ancestor with 14 chromosomes retaining the conserved state. The set of genus-specific chromosome signatures was drawn from human (HSA)-shrews comparative map (HSA 3/12/22, 8/19/3/21, 2/13, 3/18, 11/17, 12/15 and 1/12/22). The syntenic association HSA 4/20 that was previously proposed as a common trait of all insectivoran species, here is shown to be an apomorphic trait of *S. araneus*.

De novo chromosomal rearrangements in consequence to interracial hybridization in the common shrew

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Although thousands of specimens of common shrews *sorex araneus* have been examined over the huge species range, there is a tendency to recover *de novo* chromosomal rearrangements in hybrid zones and in particular among f1 hybrids. This includes all three *de novo* warts recorded in the common shrew and the first examples of robertsonian fission and reciprocal translocation in this species. Where meiotic data have been obtained, mi configurations have been consistent with the somatic rearranged karyotype, suggesting that the chromosomal mutation was either inherited or arose early in embryogenesis of the f1 hybrid. The results could reflect an increased tendency for chromosomal mutation in the hybrid zone that may be of considerable importance in the process of 'zonal raciation', the generation of new races in hybrid zones (Searle 1993). In particular, novel acrocentric forms in common shrew hybrid zones are thought to arise by robertsonian fission, and are then selected for (Searle 1986, 1993; White et al. 2010).

Karyotype reorganization and gene flow in inter- and intra-specific contact zones of the *Sorex araneus* superspecies

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Chromosome races of *Sorex araneus,* Moscow, West Dvina, Seliger, and Saint Petersburg representatives of three distinct karyotypic groups are morphologically similar. We have tried to detect chromosome races with nineteen microsatellite markers, eleven of which proved to be polymorphic. A total of 130 common shrews were collected in Valdai Heights and 7 caucasian shrews were collected in Krasnodar Territory. We found out surprisingly low level of genetic differentiation of chromosome races. It is to be noted that genetic differentiation within the races proved to be more strongly than among them. There were not specific alleles in any race of *S. araneus* whereas the gene flow in a contact zone of three chromosome races was limited. *S. araneus* and *S. satunini* were differed in six loci and L2 locus can be used as diagnostic marker. *S. satunini* showed low level of polymorphism and heterozygote deficit. It is most likely that translocation combinations of chromosomes can be supported by meiotic selection while microsatellite variability has neutral character, therefore molecular differences were not fixed in large glacial refugia. This work was supported by the RFBR (grants no: 09-04-00530-a).

The common shrew as a model of chromosomal evolution and speciation

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The common shrew (*Sorex araneus*) is one of the best studied species in terms of chromosomal variation. Throughout its Eurasian range researchers have revealed a changing karyotype with subdivision into chromosomally distinct races. The racial subdivision mirrors interspecific differences in the *Sorex araneus* complex and there is a distinct possibility that chromosomal rearrangements were important in speciation in this group and that studies of the interaction between current races may inform about the speciation process. Zones of contact and hybridisation between races may be important not only in understanding the generation of new species, but also in the generation of new races which may arise through selective processes within hybrid zones. The chromosomal variation in the common shrew has arisen very recently and it is possible to consider the mode of accumulation of new rearrangements during and perhaps subsequent to the postglacial range expansion of the species. The chromosomal data that have been collected on the species are not only survey results, but also detailed studies of meiosis and its consequences, of relevance when considering the fitness of hybrids between races. Further insights into colonisation history, adaptation and speciation have come from molecular and morphometric analysis. Overall, this species is providing extraordinary insights into evolutionary processes involving chromosomes thanks to both coordinated and independent studies by many researchers throughout the species range.

Chromosomal hybrid zones of the common shrew in european Russia

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The common shrew, *Sorex araneus* shows extraordinary intraspecies karyotypic variability due to Robertsonian and WART chromosomal rearrangements. Up to now over 70 chromosomal races have been described (Searle, Wójcik 1998; Fredga 2007; Pavlova 2010). The study of interracial hybrid zones contributes to our understanding of microevolution and divergence between intraspecies forms. The hybrid zone between the extremely different chromosomal races Moscow (*gm, hi, kr, no, pq*) and Seliger (*g, hn, ik, mq, o, pr*) was discovered in central European Russia and has been well-studied since (Bulatova *et al.* 2007, 2011). This hybrid zone is very narrow (width about 3 km) with a bimodal structure (deficit of hybrids) and can be considered a 'tension zone'. Recently a narrow hybrid zone (width about 1.5 km) was found between less different races Kirillov (*gm, hi, no*) and Petchora (*gi, hn, mo*). F1 hybrids were recorded on both banks of river (width 300 m) and even on a small island. From the prevalence of hybrids this could be classified a unimodal zone. As well as invoking hybrid unfitness to explain the structure of these chromosomal hybrid zones, behavioural factors (limited dispersal) may be involved (Shchipanov *et al.* 2008). Hybrid zones may be a source of chromosomal diversity. Although WARTs have rather rarely been described, they have been found in both zones (Pavlova *et al.* 2008; Pavlova, Bulatova 2010).

Mitochondrial DNA diversity in the hybrid zone of two chromosome races of the common shrew, Sorex araneus in poland

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We studied control region mtDNA sequence polymorphism in the hybrid zone of the common shrew that belong to Drnholec (Dn) and Bialowieza (Bi)chromosome races. We found 27 mtDNA haplotypes and significant genetic differentiation (Fst = 0.153, $P < 0.001$) in this very narrow hybrid zone. This indicates significantly reduced level of gene flow between the races and possible role of chromosomal incompatibilities. However, the phylogenetic analyses suggest that the Dn and Bi races could have originated from different sources and we found some evidence for a bottleneck in the Dn race, but not for the Bi race. This study challenges current knowledge concerning the Dn/Bi hybrid zone and shows the importance of choosing adequate markers for evolutionary surveys.

Ranges of chromosome races of the common shrew in europaean Russia

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New localities of the karyotyped shrews at the European Russia facilitate composing of inhabited ranges of 15 chromosome races (from 18 races inhabited the area). The eastern corner of the Russian plain is entirely covered by inhabited ranges of the races Kirillov, Moscow, Neroosa, Manturovo, Petchora, Sok, Serov, Yuriuzan', and Mologa (Penza). The distribution of races was not limited by great rivers and there are not any other natural barriers for distribution of shrews. Inhabited ranges of the majority of races covered several natural zones. In 11 localities interracial hybrids were found. Five zones were attached to riverbeds and localization of 6 hybrid zones was not attached to any environmental threshold. The western corner of the area, especially in the northern segment is scarcely covered by studies, and apparently new races could be found here. One is Poyakonda (Pavlova, 2010). The mutual distribution of races was studied in hybrid zones of Moscow and Seliger races near Seliger Lake (Bulatova *et al*., 2011), and in triple hybrid zone of Moscow, Seliger, and West Dvina races (Orlov *et al*., 2008). In all the cases the zone of intergradation was narrow (several km) notwithstanding the lack of external thresholds. And so the very races of the same species can output a barrier for spreading of a karyotype beyond the inhabited range of a race.

A network approach to study karyotypic evolution: the chromsomal races of the common shrew (*Sorex araneus*) as a model system

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Chromosome rearrangements are often hypothesized to play a causal role in speciation. Within mammals, there are well-documented examples of species complexes whose species are most clearly separated on chromosomal grounds, and other cases of individual species that are subdivided into chromosomal races. These systems potentially have much to say on the role of chromosomes in speciation. However, evolutionary relationships amongst the different forms have not always been easy to determine. Here, we present a new method to reconstruct chromosomal phylogenies using a network approach. This approach allows us to take account of

Robertsonian fusions, fissions and whole arm reciprocal translocations (WARTs), but also hybridization events, which are hypothesized to play an important role in the evolution of chromosomal races. This method is applied to a species showing spectacular chromosomal diversity, the common shrew (*Sorex araneus*), both at range-wide and at a regional scale when we consider the phylogeny of chromosomal races in Scandinavia.

Metrical traits of the lower jaw of three chromosome races *Sorex araneus* and *Sorex satunini*

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Three samples of common shrews (*Sorex araneus*) representing three chromosomal races (Moscow, West Dvina and Seliger) were examined using 26 morphometric variables and 4 indices derived from them. The size of each sample explained 20 individuals. For comparison the sibling species is taken also *Sorex satunini* Ogn., geographically replacing common shrew on the Caucasus. The races were found to differ in a number dimensions and proportions of the skull and lower jaw. Noted distinctions of the skull and lower jaw of three chromosomal races in the contact zone testify that even for such huge time interval as all postglaciation (15 000 years ago) the stream of genes has not led to full levelling morphometric features of races. Nevertheless it is possible to note some influence of a hybrid zone and rapprochement morphometric features Moscow and Seliger chromosome races. The sample *Sorex satunini* Ogn. significantly differentiated from samples of three chromosomal races in the contact zone.

Analysis of interracial and population variability in the common shrew *Sorex araneus* L., 1758 using geometric morphometry

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The *Sorex araneus* is a suitable object for observation of microevolutionary process in nature owing to the fact that this species has variability of karyotype and over 70 described chromosomal races. Twenty three races have the range distribution within Russia. The correlation between chromosomal and morphological characters is the subject for consideration. Previous studies showed that the interpopulation variability among different races was compatible with interracial variability or exceeded it (Searle & Thore 1987; Wojcik et al. 2000; Shchipanov et al., 2011). However, in the studies that used geometric morphometry (Polly 2001, 2003a, b, 2004, 2007) the possibility of differentiating between karyotypic groups but not races has been displayed. The differences in the skull, mandible and first lower molar shape among samples the chromosomal races Serov, Manturovo and Pechora of the common shrew were studied using geometric morphometry. Our results agree with the previous estimates on different levels of composing morphological and choromosomal distinctions.

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Poster Communications

Chromosome reorganization in the superspecies *Sorex araneus* (Mammalia)

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The taxonomic structure of the previous polytypic species of the common shrew, *Sorex araneus* Linnaeus, 1758, was reconstructed with the use of cytogenetic and molecular methods. Five cryptic species, united into the superspecies *Sorex araneus* were distingushed: *S. satunini, S. coronatus, S. granarius, S. antinorii*, and *S. araneus* s. str. Centric fusions of 16 chromosome arms (*a-c, f-r*), and centromeric shifts appear to be the major mechanism of chromosomal divergence in the superspecies *S. araneus*. The karyotypes of *S. satunini, S. coronatus* and *S. granarius,* are monomorphic, the karyotype of *S. araneus* is polymorphic in 37 centric fusions. The chromosome formula of *S. satunini* (2na=22) is: XX / XY_1Y_2, *af, bc, gh, ik, jn, lo, tu, m, p, q, r.* The following centric fusions are common in *S. satunini* and other species: *af* in *S. araneus*, *bc* in *S. araneus* and *S. antinorii, lo* in *S. coronatus* and *S. antinorii,* and *jn* in *S. coronatus*. The *ik* metacentric is known in five chromosome races of *S. araneus* s. str. Chromosomes *p, q,* and *r* were found to be metacentric in the complement of *S. satunini* and acrocentric in *S. araneus*, suggesting centromeric shifts. Five rearrangements in the karyotype of *S. satunini*: centric fusion *gh*, centromeric shifts in chromosomes *p, q, r,* and, probably, a paracentric inversion in chromosomal arm *h* are unique for this species. Obviously, in the process of the chromosomal evolution, a greater number of specific chromosomal rearrangements were accumulated in *S. satunini* than in *S. coronatus, S. granarius, S. antinorii*, and *S. araneus*.

Characteristics of cold intolerance in the house musk shrew (*Suncus murinus*)

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The house musk shrew (*Suncus murinus*) is a unique experimental animal that is thought to be cold intolerant. When maintained at low temperatures, it becomes hypothermic, immobile, and eventually dies. However, no circumstantial reports on this phenomenon are currently available. We therefore exposed house musk shrews to cold temperatures for 3 weeks to evaluate the effects of a cold environment. In addition, C57BL/6J mice were exposed to cold as a cold-tolerant group. No dramatic changes were observed in the cold-exposed mice, whereas about half of the exposed shrews became immobile or died in the early phase of the experiment. No marked changes were found in body weight, epididymal white adipose tissue (EWAT), or interscapular brown adipose tissue (IBAT) in shrews that became immobile or died during the early phase. Moreover, in this phase, immobile shrews easily recovered from deep hypothermia if warmed by hand. Some shrews also became immobile or died in the middle and late phases. In contrast to the early phase, these animals showed decreased body weights and atrophied lipid droplets in EWAT and IBAT. These results suggest that the house musk shrew is more susceptible to cold than mice are, and that reasons for their cold intolerance are a malfunction of awaking from daily torpor caused by low thermogenic activity and lipid depletion in BAT.

Variability of one-apex molars upper row of three species of *Sorex* genus from northern Belarus

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Variability in structure of the upper row of one-apex molars of *Sorex araneus, S caecutiens* and *S. minutus* from the collectings made on the territory of Berezinsky reserve has been studied. High variability of signs is registered for *S. araneus*. For the given species 10 variants of morphs are marked out. From them to the share of two basic ones (1st and 2nd one-apex teeth are equal and are much larger than others, 3rd and 4th vary among themselves in the sizes and are larger than 5th) fall 77,3 % from all sample. For *S. caecutiens* 6 variants of morphs are marked out. From them on a share of sign with insignificant decrease of the sizes from 1st to 4th one-apex molar fall 59,6 % from all sample. Variability of the sign for *S. minutus* was the lowest. Two variants of the morph which equally was present in investigated sample have been marked out. As a whole, the indicator of variability of the investigated sign for all three species from the territory of Berezinsky reserve is in limits of the descriptions mentioned for the Eastern Europe.

Session 4B - Chromosomes & Evolution

Invited & Oral Communication

Two decades of cross-species chromosome painting: the big picture

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Cross-species chromosome painting, also known as Zoo-FISH (fluorescence in situ hybridization), essentially describes the use of whole chromosome- or chromosomal arm- or region-specific painting probes to delimit homologous segments (i.e. chromosome or chromosomal segments with evolutionarily conserved synteny) in other species by means of FISH. Ever since its first introduction to animal comparative cytogenetics in 1990, human chromosome-specific painting probes have been the main workhorses in the field of molecular comparative cytogenetics among eutherian mammals due to the wide availability of commercial paints. The subsequent invention of degenerate oligonucleotide-primed PCR, coupled with chromosomal sorting by flow cytometry, has made it possible to generate painting probes for any given vertebrate species and to carry out multidirectional cross-species chromosome painting. The ever-increasing availability of probes from more than 100 mammalian species covering the major branches of the mammalian tree has revolutionized comparative cytogenetics. Notably, genome-wide comparative chromosome maps between humans and representative species of almost all 18 extant eutherian orders have been established. Such maps enabled the reconstruction of eutherian ancestral karyotypes and the land-marker chromosomal rearrangements characterizing each main phylogenetic lineage. In this talk, I will review the major contribution of cross-species chromosome painting to animal comparative cytogenetics and in particular, to the study of mammalian karyotype evolution. I will also share with you my point of view on the challenges facing the field of animal comparative cytogenetics in the era of whole-genome sequencing.

Genetic structure and formation of reproductive barriers in *Cricetulus barabensis sensu lato*

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Taxonomy of striped hamsters (*Cricetulus barabensis* group) is controversial. In particular taxonomic treatment of the three closely-related chromosomal races ('*barabensis*' – 2*n*=20, '*pseudogriseus*' – 2*n*=24, and '*griseus*' – 2*n*=22) is disputable. *Cyt* b gene sequence data demonstrated that divergence between them (2 - 4%) falls close to the lower limit reported for interspecific levels in rodents. The results of our laboratory cross-breeding experiments did not reveal effective reproductive barriers between any of the races. The present study focuses on '*barabensis*' and '*pseudogriseus*' which are both widely distributed in Mongolia and Southern Siberia. Based on a sample of more than 400 specimens representing nearly 60 localities, the rangewide pattern of intra- and interpopulation variation was examined with the use of molecular and cytogenetic methods. To detect natural hybridization, more focus was placed on populations inhabiting two of the putative zones of parapatry between "*barabensis"* and "*pseudogriseus"* located in southern Buryatia and central Mongolia. Although two specimens with an abnormal karyotype (2n=21) were found in the vicinities of Kharkhorin (central Mongolia), chromosomal data demonstrate a general lack of regular hybridization. Moreover, neither mtDNA nor Y-chromosome data revealed traces of gene flow between chromosomal races. At the same time both nuclear and mitochondrial markers demonstrated relatively high levels of inter- and intrapopulation variation in both races supporting their long-term parapatry without substantial gene flow. Thus, our data suggest that, despite the low level of differentiation and lack of post-mating barriers, the examined lineages are evolving independently and, hence, can be regarded as incipient species.

Investigating gene flow within and among metacentric races of the Western house mouse (*Mus musculus domesticus*) using mapped microsatellite markers

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While the standard karyotype of the house mouse consists of 40 acrocentric chromosomes, there are chromosomal forms with different combinations of autosomal metacentrics which represent the products of Rb fusions or derivatives of these (whole-arm reciprocal translocations). Where metacentrics are fixed within a population they define a metacentric race. Because each metacentric involves a reduction in chromosome number, the diploid number that characterises such races can be as low as 2n = 22 (nine pairs of metacentrics). Many of these races are part of Robertsonian systems, which are comprised of closely related, geographically proximate races that share metacentrics by descent. Fixed karyotypic differences between such chromosome races are expected to act as barriers to gene flow, particularly in the vicinity of the chromosomal breakpoint(s). We outline four approaches that we adopted to investigate how karyotypic differences impact genetic exchange between metacentric races of the house mouse using mapped microsatellite loci. Particular emphasis is placed on examining several chromosomes and multiple chromosome regions. Results are presented for studies involving multiple races from two different Robertsonian systems (northern Italy and Madeira), as well as wild-derived laboratory-reared individuals (both pure-race and hybrid mice).

Evolution of a hybrid zone of mole rats (*Nannospalax*, Spalacidae, Rodentia) in Israel: molecular-cytogenetic analysis

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To determine peculiarities of *Nannospalax* hybrid zones, we investigated a hybrid zone located near the Miilya village and composed of Israeli mole rats with the most divergent (12 chromosome rearrangements) cytotypes of 2*n*=52 and 2*n*=58. All parameters of the "Miilya" hybrid zone fit the hybrid zone tension model. Cytogenetic and morphological analyses of hybrids and parental cytotypes in the "Miilya" hybrid zone showed:

1. A very high frequency of back-crosses and apparently of F_2 hybrids evidencing the fertility and viability of F_1 hybrids. This was further supported by the normal chromosome pairing and progression of germ cells through meiosis, as well as litter sizes in hybrid animals that were similar to those in the parental species.
2. Significant selection against heterozygotes for only one Robertsonian rearrangement.
3. The prevalence of heterozygote hybrids in the "Miilya" hybrid zone did not support our preliminary hypothesis of an advantage of homozygote karyotypes in a hybrid zone.
4. Clines of four Rb metacentrics, specific of the 2*n*=52 cytotype, were coincident and staggered from the cline of Rb metacentrics specific of the 2*n*=58 cytotype.

5. The natural barrier in the south and restricted gene flow in the north of the hybrid zone play important roles in determining the structure of the “Miilya” hybrid zone.
6. The width of the “Miilya” hybrid zone is maintained by dispersal and geographical barriers to parental gene flow.
7. Comparison of our results with previous data show a shift in the distribution of chromosome frequencies towards high chromosome numbers.

Chromosomal evolution and comparative genomics in mammals

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Chromosome reorganizations contribute to reshuffling the mammalian genomic architecture, providing new chromosomal forms on which natural selection can work. Such chromosomal alterations are caused by improper reparation of double strand-breaks. If this type of DNA damage occurs in the germ line, such chromosomal alterations would have high probabilities of becoming fixed and propagating in the population. In this context, mammalian phylogenomics (the study of the phylogenetic relationships using genomes) is opening new horizons for evolutionary biologists; the analysis of how mammalian genomes are organized and how chromosomal rearrangements are involved in speciation will help us to understand how mammalian species evolved. Reconstructions of the ancestral architecture of mammalian genomes are revealing interesting aspects of mammalian chromosome evolutionary history, such as the conservation of large genomic regions and the suggestion that evolutionary breakpoints are clustered in regions that are more prone to break and reorganize. In this paper, we will go through our current data in order to discuss the dynamics of mammalian chromosomal evolution by analyzing the genomes of different species.

Chromosomal polymorphism in *Gerbillus latastei* (rodentia, gerbillinae) from Tunisia

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The species belonging to the genus *Gerbillus*, characterized by numerous rearrangements of autosomes and by autosome-gonosome translocations, represent a model for chromosomal studies in mammalian evolution. Among these, *Gerbillus latastei* is one of the most polymorphic species. We performed a karyotypic analysis of three populations from Bouhedma, Faouar and Sidi Toui that exhibit a constant diploid number equal to 74 chromosomes, whereas the fundamental number of autosomes (FNa) ranged between 94 and 102. FNa differed systematically between populations, and within some populations between males and females. In the Bouhedma population, males and females shared the same FNa equal to 100. By contrast, in the population of Sidi Toui, the FNa was 97 in males and 95 in females. The same phenomenon was observed in the Faouar population where FNa was 99 in females and 102 in males. To assess the relationships among populations and chromosomal variants, an unrooted NJ tree was built using cytochrome b sequences of five populations. The topology suggested the absence of any clustering of populations and chromosomal variants. The superposition of population distribution with the climatic map showed that the distribution was random and not related to ecological factors. This study suggests that the variability in FNa is probably due to pericentric inversions. The apparent absence of a population structure could be explained by a recent origin of the chromosomal variants. However, further investigations involving more variable molecular markers, are needed to investigate the degree of gene flow between populations.

Chromosomal variation and fertility in wild house mice (*Mus musculus domesticus*) in Switzerland

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The Swiss Alps are well-known for closely situated populations of house mice (*Mus musculus domesticus*) which vary in their karyotype. This variation, due to Robertsonian (Rb) fusions, can lead to impaired development of germ cells in wild hybrids heterozygous for Rb fusions, making the house mouse a model in speciation studies. However, Swiss populations are poorly studied. We trapped fifty-nine wild house mice from three locations 10 – 20 km apart in the Rhine valley of Eastern Switzerland. They were shown to belong to three distinct chromosomal populations: 2n=22 (BUC), 2n=28 to 30 (WEI) and 2n=28 (VIL). Crossings between populations BUCxWEI were performed, with expected meiotic chain configurations of 3 and 9 chromosomes. Epididymal sperm counts were performed for male offspring. Hybrids had low fertility, some with no sperm found. Backcrossing of female hybrids to parent populations supported this, with few litters born. This suggests that gene flow between these populations would be impeded by chromosomal incompatibilities. In addition, genetic analyses using mitochondrial DNA, three Y-specific and 25 autosomal microsatellites indicated that most of the molecular variation was among populations, rather than among individuals within populations. As expected, we found little evidence of recent gene flow.

Evolution of chromosomes and speciation of Gerbils (Rodentia, Cricetidae, Gerbillinae) from the territories of the former USSR

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Gerbils of the Palaearctic are a relatively young group (known from the Pliocene) with around 145 species widespread in Africa, south Palaearctic, and south India. Comparative cytogenetics of many groups of species is still unknown. We studied G- and C- banded chromosomes of 7 species of the genus *Meriones*, namely *M. tamariscinus*, *M. persicus, M. vinogradovi, M. libycus, M. unguiculatus, M. meridianus (including M. dahly), M. tristrami,* and one of the genus *Rhombomys, R. opimus* (284 animals from 35 local populations) from the former USSR. G-banding comparisons identified many fusion/fission rearrangements. We were able to allocate 15 homologous biarmed chromosomes to two or more species. A high degree of similarity was found between two species of *Meriones*: *M. tamariscinus* (2n=40, NF=78) and *M. persicus* (2n=42, NF=78) on the one hand and *R. opimus* (2n=40, NF=78) on the other hand. We suggest that *M. tamariscinus* is a sister taxon to *Rhombomys* and *Meriones*. The modes of chromosomal reorganization between *Meriones* species are discussed.

The genome diversity and karyotype evolution of mammals

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The past decade has witnessed an explosion of genome sequencing and mapping in evolutionary diverse species. While full genome sequencing of mammals is rapidly progressing, the ability to assemble and align orthologous whole chromosome regions from more than a few species is still not possible. The intense focus on building comparative maps for companion (dog and cat), laboratory (mice and rat) and agricultural (cattle, pig, and horse) animals has traditionally been used as a means to understand the underlying basis of disease-related or economically important phenotypes. However, these maps also provide an unprecedented opportunity to use multispecies analysis as a tool for inferring karyotype evolution. Comparative chromosome painting and related techniques are now considered to be the most powerful approaches in comparative genome studies. Homologies can be identified with high accuracy using molecularly defined DNA probes for fluorescence *in situ* hybridization (FISH) on chromosomes of different species. Chromosome painting data are now available for members of nearly all mammalian orders. In most orders, there are species with rates of chromosome evolution that can be considered as 'default' rates. The number of rearrangements that have become fixed in evolutionary history seems comparatively low, bearing in mind the 180 million years of the mammalian radiation. Comparative chromosome maps record the history of karyotype changes that have occurred during evolution.

Evolution of the b-chromosomes in the field mouse *Apodemus peninsulae* today

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The Korean field mouse *Apodemus peninsulae* is characterized by unique karyotype variability because of additional B-chromosomes. The B-chromosomes form specific systems of five B-chromosome classes (from tiny micro-B-chromosomes to large two-arm variants) in various combinations. Dot-like micro-B-chromosomes may be primary proB-chromosomes of *A. peninsulae* in Siberia. From 4 to 30 micro-B-chromosomes were found in populations from the left bank of the middle Yenisei River. As a result of radioactive contamination, the frequency of breaks in hot spots of microrearrangements in the A-chromosomes increases as well as the frequency of primary micro-B-chromosome formation. The process of formation of micro-B-chromosomes *de novo* may be active in the populations of the Enisei River while the further reorganization of micro-B-chromosomes into macro-B-chromosomes does not occur. The increase in B-chromosome number accompanied by their morphotype change in *A. peninsulae* populations from Gornyi Altai (territory polluted with propellant) has been observed over 28 years (1980, 1986, 1988, 1990, 2002, 2006, and 2008). The B-chromosome index in the population of Gornyi Altai in 2002 equaled 6.5 which was 2.8-fold higher than the index in 1980; only macro-B-chromosomes were noted. In 2006, the ratio of B-chromosome morphotypes changed: along with macro-B-chromosomes, we found micro-B-chromosomes in this population. In 2006, the field mice displayed a significant increase in the mean number of micro-B-chromosomes. In 2008, the number of B-chromosomes in this population was still increasing (7.1) as was that of micro-B-chromosome number. A concept of a new type of genomic mutations in the number of B-chromosomes has been substantiated.

Chromosome evolution in Rodentia

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Rodents represent one of the best groups for the study of karyotype evolution. They have been traditionally well examined by methods of conventional cytogenetics which have allowed the detection of a high variety of karyotypes and rates of chromosome evolution. Here we present results of chromosome painting applied to major representatives of all five rodent suborders. We built comparative chromosome maps between the studied species and defined the chromosome associations characteristic of different taxonomic groups. Our studies confirmed that sciuromorph karyotypes are conserved and similar to the ancestral eutherian karyotype, while the major traits of karyotype evolution within the suborder included centromere shifts and heterochromatin amplification. Chromosome painting of castorimorphs and anomaluromorphs further confirmed their separate status from sciuromorphs due to characteristic human signatures identified in the karyotypes of both the beaver and springhare. The successful reciprocal chromosome painting between human and guinea pig allowed us to identify a high degree of genome reorganization in hystricomorphs. We failed to find chromosomal signatures in the guinea pig that have a phylogenetical value to resolve the relationships between suborders. The suborder Myomorpha is known for the highest number of species and record rates of karyotype evolution. We applied the sets of muroid probes to resolve the phylogeny within the taxon. The largest families, Muridae and Cricetidae, were thoroughly studied by involving a high number of species. The multiple chromosome rearrangements accompanying the radiation of this group allowed us to reconstruct the general scenario of karyotype evolution within the suborder.

Chromosomal changes and speciation in mammals

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Analysis of cytogenetic data following the methods and principles of cladistics appeared to be an important source of phylogenetic information often complementary to that inferred from analyses of molecular and/morphological characters. The cladistic treatment of cytogenetic data provided information on the distribution of chromosomal rearrangements in the trees within a temporary frame determined by the molecular phylogenetic analysis of the same set of the taxa. This approach allowed us to gain a new insight on karyotype evolution itself and on how chromosomal changes are linked to cladogenetic events. In numerous systematic groups analyzed such as rodents, primates and artiodactyls, the rate of fixation of chromosomal rearrangements (traditionally considered as reflecting the rate of karyotype evolution) is irregular within the same lineage along the different steps of the divergence as well as between intra-generic sister clades, being sometimes highly different in closely related taxa. This kind of explosive genome repatterning usually occurred within a short span of time and involved underdominant rearrangements only rarely observed in most mammalian taxa studied. This strongly suggests the primacy of population conditions (effective population size and degree of inbreeding) in the fixation of chromosomal changes and thus in determining tempos and modes of karyotype evolution. Consequently, superposition of extensive karyotype reorganization and genetic drift resulting from population bottlenecks are the most efficient promoters of speciation that is often very rapid and not accompanied by measurable genetic divergence, called the process of chromosomal speciation.

Poster Communications

Rapid chromosomal evolution in the mesic four-striped grass rat *Rhabdomys dilectus* (Rodentia, Muridae) revealed by mtDNA phylogeographic analysis

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The mesic four-striped grass rat *Rhabdomys dilectus* De Winton, 1897 is distributed in mesic regions of southern and eastern Africa. We carried out a molecular and chromosomal study of the northernmost populations of the species to provide insight into the subspecific boundaries identified within the species and to describe its genetic structure in Eastern Africa. Maximum likelihood, maximum parsimony and neighbor-joining methods were used to construct phylogenetic relationships among all the haplotypes belonging to the large part of the species range. Times of divergences were estimated assuming a relaxed molecular clock with two calibration points. We identified three well supported clades within *R. dilectus*. One basal clade corresponding to *R. d. chakae* (2n = 48) is found in South Africa. Two additional sister clades corresponding to *R. d. dilectus* (2n = 48 and 2n = 46) are allopatrically distributed in southern and northern parts of the species range. Genetic divergence among the three clades is relatively high (ranges 4.2-5.7%). A very divergent new karyotype 2n = 38, FNa = 60 was found in two high-altitude populations on Mt. Meru and Mt. Kilimanjaro. The karyotype differences consist in three Robertsonian fusions and one whole-arm reciprocal translocation (WART). Interestingly, the mtDNA phylogeny does not match the diploid numbers. In fact, the 2n = 38 specimens form a monophyletic group within a clade that includes specimens with the 2n = 46 karyotype that appears as paraphyletic. We estimated that the new karyotype originated in peripatry during the last phases of the Pleistocene.

Chromosomal rearrangements and DNA variability of grey Voles from northeast asia (Rodentia, Cricetidae, Microtinae)

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The vole, *Microtus maximowiczii* Schrenk**,** 1858 is a widely distributed species in East Asia inhabiting humid biotopes of the forest zone. Analysis of the chromosomal characteristics of Maximowicz's vole from Transbaikalia, Far East Russia, and Mongolia, including novel data from 12 local populations, enabled us to supplement information on the chromosomal polymorphism of this species (2n=36-44; NF=52-62). We reveal that populations are fixed for various chromosomal rearrangements (fusion/fission) and inversions in the three geographical regions. The revision of the chromosomal characteristics allows us to describe six chromosomal forms in the area investigated (Kartavtseva et al., 2008), one of which belongs to *M. gromovi* (Sheremetyeva et al., 2009). Subspecies *M. m. ungurensis* includes at least 4 chromosomal forms from Transbaikalia and Mongolia, designated as “A”, “B”, “V”, and “D”, while *M. m. maximowiczii* includes only the “C” chromosomal form, that was observed in the Amur region. Each chromosomal form has its own set of rearrangements. The vole, *M. maximowiczii* is evolutionary closely related to two species, *M. evoronensis* and *M. mujanensis* as supported by chromosomal characters and mtDNA. The relationships between the two species and the chromosomal forms of *M. maximowiczii* as determined by published allozyme and molecular data are discussed.

About the taxonomic position of 46-chromosomal forms of the common vole M*icrotus arvalis* sensu lato (rodentia, arvicolinae)

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The 46-chromosome common vole is represented two geographically separate karyoforms. Karyoform «obscurus» (NF = 72) occupies the Eastern part of the range of *M. arvalis* s. l., and karyoform «arvalis» (NF = 84) – theWestern one. Crosses between these karyoforms yielded fertile F1 hybrids, but F2 hybrids showed a sharp drop in fertility. To the east of the Russian Plain is a zone of contact and hybridization between these karyoforms. A comprehensive study of these karyoforms showed that they differ in molecular-genetic, chromosomal and cranimetric markers, as well as in the enzymatic activity of specific skin glands and scent. The ranges of the karyoforms "obscurus" and "arvalis" have been isolated for more than 100 thousand years. During this time, differences at the molecular-genetic, karyological, morphological and physiological levels have accumulated. These differences indicate that strong reproductive barriers developed between the karyoforms. These karioforms are on track to becoming species (in status nascendi); they can be regarded as two phylogenetically very close species: *Microtus obscurus* and *M. arvalis* sensu stricto. Expansion of *M. arvalis* s. str. into Central Europe occurred in the east during the last Ice Age (100 thousand years ago). Glaciation and obstruction of the Volga-Don basin impeded the penetration of *M. obscurus* into Eastern Europe. After the retreat of the Valdai glacier, the East European Plain was populated by ancestors of *M. arvalis* s.l. from different refugia: *M. obscurus* from the southern Urals, Caucasus and Crimea, and *M. arvalis* s. str. from the Balkans and Carpathians.

The barcelona polymorphism zone of house mouse revisited

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A Robertsonian (Rb) polymorphism zone of house mouse, *Mus musculus domesticus*, is located in the province of Barcelona and surrounding areas (northeastern Spain). This zone extends about 5,000 km^2 and is bounded by 40 chromosome telocentric populations. To date, metacentrics Rb(3.8) (4.14) (5.15) (6.10) (7.17) (9.11) (12.13) and mice with diploid numbers between 27 and 40 chromosomes have been reported. We conducted a spatio-temporal study of the zone, comparing data from 1996-2000 and 2008-2010 periods. Karyotypes were determined from bone marrow plates and stained for G bands. Analyses revealed a global increase of diploid number (2n) ranges, especially in the sites located at the centre of the polymorphism zone, a reduction of genetic population subdivision for all Rb fusions (F_{ST} and G_{ST} indices), and no correlation between the F_{ST} (1- F_{ST}) index and geographic distance between each pair of sites studied. These results indicated that during the last decade some significant variations in gene flow dynamics at general and local levels had occurred. The commensal character of mice and the increase of commercial traffic, mainly between peripheral and central farming areas, are probably promoting the passive transport of mice and therefore introgression events between sites. Despite the global increase in gene flow, local isolation events were detected in the zone, probably due to the replacement of farms by urban zones and to the changes in agricultural practices throughout the last years.

More is yet to be revealed on the robertsonian (rb) variability of the house Mouse *Mus musculus domesticus* (Rodentia, Murinae): new data on the rb system of epirus, Greece

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Several mammalian species are characterized by remarkable chromosomal evolution, occasionally of phylogenetic value. The house mouse, *Mus musculus domesticus*, demonstrates extensive fixation of Robertsonian (Rb) fusions in its karyotype, which results in a variation of the diploid chromosome number (2*n*) from 2*n*=40 to 2*n*=22. More than 100 Rb fusions exist, as a result of different combinations of acrocentric chromosomes. These have led to the formation of over 40 Rb races that are organized in complex Rb systems, each of which is characterized by a common phylogenetic origin. In Greece, three Rb systems exist, i.e. in Peloponnese, Sterea Ellada and Epirus, but very little knowledge is available for the third. Thus, a chromosomal study was performed on *Mus musculus domesticus* individuals from Epirus localities. The study showed that the individuals in the vicinity of Ioannina city were characterized by 2*n*=28-29, 31-32. We verified that the previously described Rb(3.10), Rb(5.12) and Rb(15.17) also exist in the Rb populations of Ioannina, constituting commonly occurring Rb fusions in this Rb system. Moreover, the discovery for the first time of additional Rb fusions (e.g. Rb(14.16) in individuals with 2*n*=32 etc.) corresponds to the reduction of 2*n* down to 2*n*=28. The examination of all available data reveals that a well established Rb system, at least 60 km wide, exists in Epirus, which has evolved independently from the two other Greek Rb systems. We believe that there is still much more to be discovered on the extensive Rb variation that characterizes *Mus musculus domesticus* populations of Greece.

A cytogenetic approach to taxonomy in colombian woolly Monkeys (*Lagothrix sp.*)

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The *Lagothrix* genus is represented in Colombia by two subspecies: *Lagothrix lagotricha lagotricha* and *Lagothrix lagotricha lugens.* However, there is controversy regarding the taxonomic classification within this genus, since a recently proposed reclassification suggested that these subspecies should be considered as distinct species. Cytogenetic markers can provide a valuable tool for species differentiation and taxonomic clarification and have been used successfully for this purpose in Neotropical primates. This study examined 18 captive individuals (6 *L. l. lugens* y 12 *L. l. lagothricha*) from zoos and rescue centers; the standard 2n = 62 karyotype was determined for all individuals through peripheral blood culture and G, C, R, Q and NOR chromosome banding. Two karyotype variants, also known as karyomorphs, presented a different fundamental number due to a pericentric inversion on chromosome pair 24. Within such karyomorphs, other polymorphisms were found in several pairs representing high levels of intraspecific variation which did not interfere with species diagnosis. A review of the taxonomy within this genus is thus recommended, especially at the species level.

Session 5 - Morphometrics and Evolution

Invited & Oral Communication

Domestic versus wild: How Geometric morphometrics can help investigate the domestication process in zooarchaeology

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Sus scrofa domestication process during the Neolithic has produced a vast array of domestic forms easily distinguishable nowadays from their wild counterparts based on morphological characters. More challenging is the reconstitution of the early step of pig domestication based on the phenotypic divergence among archaeological specimens. The fragmentation of the skeleton remains within the archaeological contexts is one of the main obstacles. To by pass this issue we rely on molar teeth as phenotypic markers since they are numerous and well preserved in archaeological remains and were previously found informative for the study of pig domestication. We explored the molar size and shape variability of modern and archaeological *Sus scrofa* both in their wilds and domestics from all over the western Palearctic, using 2D landmarks and 2D sliding-landmarks and Geometric Morphometric approaches. We investigated the biological factors potentially implied in the phenotypic variability within *Sus scrofa* through time and space using chronology, geography, sexe, captivity and age as factors of variation. The aim is to pinpoint the different phenotypes at the beginning of domestication process in the Near East and follow their dispersal along with the main route of the early Neolithic dispersal outside its cradle.

Ecological and evolutionary factors of dental polymorphism in the red fox and the arctic fox

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The influence of some ecological and evolutionary factors on the patterns of dental polymorphism across the geographic range of the arctic fox (*Vulpes* (*Alopex*) *lagopus*) and the red fox (*Vulpes vulpes*) were studied. Frequency of dental morphotype characters (groups of morphotypes from A to S) in 12 geographically separate populations of the arctic fox and 45 populations of the red fox were documented. Dentition in the arctic fox displays more specialized i.e. insectivorous and carnivorous features than in the red fox. The arctic fox shows simpler shapes of the premolars and lower molars, and more complex structure of third upper incisor and fourth upper premolar. Geographic variation of the dental polymorphism in the red fox is strongly influenced by geographic and climatic factors. The inter-population changes in tooth shape in the arctic fox are probably determined by food resources and evolutionary history of populations. Morphotype dental pattern seems to be a good tool in the phylogeographic studies. With respect to morphology, the arctic foxes from mainland populations of Eurasia and North America, are the most similar each other, followed by partly isolated island populations (Greenland, St. Lawrence Island). The most distinct forms are the arctic foxes from Commander Islands (*V. l. semenovi*, *V. l. beringensis*) where they exist in permanent isolation. The red fox shows distinct difference between the Palearctic and the Nearctic regions. In the Nearctic the most morphologically distant are the foxes from Kodiak Island (*V. v. harrimani*), whereas in the Palearctic the red foxes from Morocco (*V. v. barbarus*) and India (*V. v. pusilla*).

Does morphological divergence follow molecular differentiation during the house mouse *Mus musculus* (rodentia: muridea) sub-speciation?

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M. musculus has at least three distinctive subspecies, *M. musculus musculus, M. musculus domesticus* and *M. musculus castaneus*. It is supposed that this commensal species has evolved from a wild ancestor somewhere between Iran and India where the three subspecies are currently found in contact to each other (central region) and from where they have colonized the rest of the world (peripheral regions). In this study, a geometric morphometric analysis was performed on mandible of 32 populations of house mouse including all the three subspecies from both central and peripheral regions to investigate the inter- and intra-subspecies morphological differentiation. The study shows that morphological divergence between the three subspecies followed the genetic differentiation between these taxa, both in central and peripheral regions. *M. musculus castaneus,* however, is highly polymorphic and may represent, at least, two morphological groups in the central region. The study also suggests that the evolution of mandible morphology during the diffusion of each subspecies should have undergone different selective pressures. It seems that the Iranian mice have retained an ancestral morphology while the Indian ones are more like the derived populations. It may suggest the Iranian plateau as the cradle of the species from where the three subspecies has evolved through a centrifugal dispersion.

Size and shape variation in the skull and mandible among the genus P*sammomys* (R*odentia*, G*erbillinae*) in Tunisia

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This study focuses on two *Psammomys* rodents: *P. obesus* and *P. vexillaris*. The first is represented by samples from four different Tunisian populations localized in Sidi Bouzid (Center), Tozeur (South-West), Zerkine (South-East) and Faouar (halfway between the previous two). The sample of *P. vexillaris* is from Faouar where both species occur in sympatry. Previous studies, conducted by Benhamou in 2006, revealed cytogenetic and a statistical significant size differences between the two taxa, *P. vexillaris* is significantly smaller than *P. obesus.* The comparative study of these populations was then based on geometric morphometrics analysis of two main parts of the skeleton, skulls and mandibles. Regarding the size, the skulls and mandibles of *P. obesus* individuals from different regions, except those of Zerkine, are still larger than those of *P. vexillaris*. Concerning shape, the principal component analysis and canonical analysis of studied variables, separate three different groups: one composed exclusively of *P. vexillaris*, the second distinct population of *P. obesus* of Zerkine, while the latter includes the three remaining *P. obesus* populations. In conclusion, our morphometric analysis has clearly separated the two species *P. obesus* and *P. vexillaris*. The latter, strictly desert, has the much smaller and rounded head than its congener. Within the species *P. obesus*, intraspecific patterns of differentiation depend on geographic gradients; thus, the study has highlighted a divergence of the most eastern and isolated population, compared to the populations of central and southern Tunisia which remain comparable in situation of allopatry or sympatry.

Measuring phenotypes: from evodevo to conservation biology

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Even in the era of genomics, studying variation in phenotypes provides essential information for understanding evolution and biodiversity. Measuring phenotypic variation accurately is the first fundamental step toundertake this task. The quantitative description of organismal formsusing geometric morphometrics, often seen as a type of image analysis, is becoming standard practice in a variety of fields of biology thanks to theoretical and technological advancements of the last two decades. Using digital data from several well-represented orders of mammals, I will demonstrate how the application of modern morphometric methods enables to numerically explore topics as disparate as the occurrence of evolutionary constraints in morphological evolution and the phenotypic dimension of taxonomic identification in biodiversity studies.

Suid Taxonomy and Evolution: Disparity and Enlightenment

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Pigs (Suidae) are one of the one of the world's major food resources and one of the most widespread mammals. Despite this their taxonomy is poorly resolved. Traditional morphometrics have been used extensively to investigate the taxonomy of the suid family but in recent years the focus has shifted to phylogenetics, aimed at reconstructing the family's evolutionary history and speciation. This study aims to integrate phylogenetics with 3D morphometrics to investigate interrelationships between taxa in the family Suidae. Three dimensional geometric morphometric analyses of crania were used to investigate shape differences between with individual Suid species. Sixty-nine unilateral homologous landmarks from 485 specimens are compared and contrasted using multivariate statistics and the differences in morphology illustrated with morphing of 3D surface scans to the morphological relationships between species were then compared to the latest established phylogeny. Results show that this comparative approach gives a good taxonomic resolution and demonstrates clearly the relationship between species, as well as the biogeographic structuring of the more widespread species. The morphological and phylogenetic relationships between these species are not fully congruent, especially regarding the position of the African bush pig (*Potamochoerous*) which is different from the widespread *Sus scrofa* genetically but similar morphologically. When examined more closely it becomes apparent that like *Sus,* but unlike other African suids, *Potamochoerous* has retained its ancestral generalist morphology through stasis, whilst becoming genetically differentiated from the other generalists (*Sus*) through temporally accrued genetic divergence.

New insights into the microevolutionnary process of the Orkney vole *(Microtus arvalis orcadensis)*

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The endemic form of the common vole, present in the Orkney archipelago, UK, remains one of the greatest biogeographic puzzles in Europe. Its peculiar distribution is nowadays explained by a human-mediated translocation. The aim of the Orkney vole project was to readdress the question of its origin, dispersal and evolution using combined approaches of molar shape and mtDNA analyses on a large dataset of both modern and ancient samples, integrated with the extensive archaeological record from Orkney. In this paper, we will focus on the phenotypic microevolution behind the morphological characteristics of the Orkney vole using molar shape analyses with sliding semilandmarks approach. Results suggest that the Orkney vole uniqueness is the result of a fast and ongoing diversification process mainly driven by stochastic vicariance.

Age- and sex-associated variations in the directional asymmetry of root vole traits

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A population of *Microtus oeconomus* from South Siberia was studied. Males and females were analysed as separate samples. Using Student's paired t-test, directional asymmetry (DA) was demonstrated for the adrenal (595 males; 442 females) and the kidney (557; 410) weights, for the length of the hind paw (255; 205) as well ($p<0.001$ in all cases). Specimens in each sample were divided into four age groups (juvenes, subadultus, adultus, senex). With the use of non-parametric box-and-whisker diagram ontogeny dynamics of DA for these characters was studied. The differences in adrenal weight increased with age. Maximum of kidney weight asymmetry was during sexual maturation (age-group subadultus). The right hind paw was longer than the left in young and old voles. Sexual dimorphism for mean length of the hind paw was strongly expressed. The course of DA curves during development for all the examined characters were similar in males and females. Their similar course allowed us to hypothesize that the two sexes share a common genetic program during its establishment in ontogeny.

Poster Communications

Craniometric characteristics of golden jackal (*Canis aureus* l.)

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Aim of the research was to determine craniometric characteristics of two different population of golden jackal (Canis aureus L.) which exists in the coastal part of Croatia (Meditterranean population) and in the eastern part (Slavonian population), and to determine differences between sexes. The specimens had been hunted and collected in the period 2008-2010. Skulls of animals older then 2 years have been studied, of which 32 belonged to Slavonian, and 11 to Mediterranean population. In samples from Slavonian population, 13 (40,62 %) were females and 19 (59,37 %) were males, while the sex were not recognized in Mediterranean population. Standard cranial measurements were taken for 44 parameters on each skull; 32 parameters specifically on skull, and 12 on mandible. All measurements were carried out using digital calliper to an accuracy of 0,01 mm. Statistically significant difference ($P<0,05$) between two different populations of golden jackal was confirmed for these parameters: greatest neurocranium breadth, greatest inner height of the orbit, height of the occipital triangle and height of the vertical ramus of the mandible. Highly significant difference that reflects sexual dimorphism were confirmed for 31 parameters, out of which 19 parameters at significance level ($P<0,01$), and for 12 paremeters $P<0,05$. Coefficient calculated as a ratio between skull length and width was 1,88 in males and 1,89 in females, proved to be unreliable for sex determination in golden jackal.

Morpho-craniometry and determination of the sex at *Meriones shawii* (Mammalia, Rodentia) in the algerian southwest

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The revealing of the morpho-craniometrical differences between the male and the females individuals of *Meriones shawii*, was led in the El Bayadh region, southwest of Algiers. The biological material contains 84 alive captured individuals among whom 44 males and 37 females. A total of 21 cranial measures and 5 morphological measures were taken on the captured animals. The results reveal the presence of a highly significant sexual dimorphism in favour of the males which exceed females at the level of 3 cranial measures and 2 morphological measures. Besides, an equation of discrimination is established. She allows the determination of the sex of the animal from craniometrical variables which contribute most to the discrimination between males and females of *Meriones shawii*. By means of this function we can classify correctly 71.60 % of the individuals, according to their sexes, males or females.

Changes of red deer (Cervus elaphus, l.) pedicles with age at baranja danube`s region

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Deer antlers (Cervidae family) are fast-growing bones and the only bone formation in mammals capable of complete regeneration. Males of all species within the deer family (Cervidae) grow antlers, except for the genus Rangifer, where both males and females grow them. Antlers that are changed each year, grow from the frontal extensions – pedicles, that last a lifetime. Each year the last year's antlers are discarded so that the new ones can grow. The study was conducted in the east of the Croatian Danube region (Baranja) during three hunting seasons (2007/2008, 2008/2009 and 2009/2010). A total of 348 pedicles were observed for this study. The height and diameter of pedicles were measured. This paper identified significant changes in height and diameter of pedicles in relation to age and the correlation between height and diameter was also significant. Thus the regression coefficient of pedicles height and age is significant and $R = 0.65$ ($AGE = 15.25 - 0.18 \times height$) (height of pedicles decreases with age); also a regression coefficient of pedicle diameter and age is significant and $R = 0.85$ ($AGE = 0.25 \times diameter - 4.72$) (diameter of pedicle increases with age). Changes of pedicle height and diameter are significant and they have a regular relation to each other and to the age, which is why wildlife managers should seriously take them into account. These average values and mathematical expressions for determining age, given the level of significance, can be used to determine the age and classified into age classes (young males in 3, 4 and 5 years old, middle age males at 6, 7 and 8 years old and mature males 9 and more years old) in the region were the research were conducted.

Morpho-functional study of the vertebral column of small carnivoran: 3D landmark surface approach

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Vertebral column is a central element of the skeleton: it protects the spine and supports the muscles that allow the movements of the head and the limbs. Diet of specie or its feeding condition (i.e., locomotion) can be considered such as the main factor that owes its movements. The mammalian vertebral column and its implication for functional morphology are still poorly known and surveyed. The diet and therefore the feeding conditions (arboreal, semi arboreal, semi fossorial, cursorial, natatorial) imply constraints that impact the spinal shape, on which the locomotion relies. This exploratory study was carried out on 14 living species belonging to 10 families of the order Carnivora, known for their great diversity of species and the variability of their behaviors and ecology. The study of three-dimensional geometric morphometrics has shown qualitative and quantitative differences on the vertebral column in relation to the diet and the feeding conditions.

Craniometric analysis of Eurasian badger (*Meles meles* l.) from eastern Croatia

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Aim of the research was to determine craniometric characteristics of the badger (Meles meles L.) from eastern Croatia, and to determine differences between sexes. Most of the specimens had been either hunted or gathered as road kills, and were collected during 2009 and 2010. A total of 19 skulls of animals older then 2 years have been studied, out of which 13 (68,4 %) belonged to females and 6 (31,6 %) were males. Standard cranial measurements were taken for 42 parameters on each skull; 31 parameters specifically on skull, and 11 on mandible. All measurements were carried out using digital calliper to an accuracy of 0,01 mm. Statistically significant difference for distinguish sexual dimorphism was confirmed for the following parameters: basicranial axis, facial length, viscerocranium length, greatest mastoid breadth and height of the foramen magnum ($p<0,05$), and greatest breadth of the bases of the paraoccipital processes and zygomatic breadth ($p<0,01$). Higher average skull length (14,4 cm) and breadth (8,26 cm) were determined for males, in comparison to a female skull (average length 13,64 cm, breadth 7,62 cm). Coefficient calculated as a ratio between skull length and width was 1,71 in males and 1,79 in females. As the border value which could help in sex determination, coefficient 1,75 is defined (lower value for males, higher for females).

Variation of the dimension of Talpa's humerus occidentalis in the north half of Spain

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In the Iberian Peninsula *T. occidentalis* constitutes an endemic species, distributed in the North half in a mostly constant way, with the excepcion of the Norheastern quadrant, occupied by *T. Europaea*. Both species support a narrow simpatría in the Cantabrian Mountain chain from the oriental end of Asturias up to the province of Bilbao. In a wide study on the variation of size of the length of the humerus of *T. occidentalis* in the north half of Spain, it has been verified, according to the bibliography, the existence of populations of moles of small size whose morphologic characteristics of cranium and dentition are coincidental with those of *T. occidentalis*. The decrease of the size of the humerus concerns the populations of central and oriental Asturias, Cantabria and the North of Burgos. The length of the humerus of these small populations supports, opposite to T. occidentalis "normal", a level of significant discrimination. The determinant factors of the difference of size are being explained through hypotheses either by a selective competitive pressure on the part of *T. europaea* or by the influence of the ecological characteristics of the environment. The above mentioned hypotheses are discussed in this paper that concludes in the need to develope studies of analysis of DNA to establish the degree of kinship and to confirm its specific status.

Molar shape of the edible dormouse (G*lis glis*) in Turkey: unsuspected differentiation between european and asiatic populations

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The present study illustrates the potential of a fine-scale analysis of tooth size and shape variation in the edible dormouse *Glis glis* (Gliridae, Rodentia, Mammalia) using the first upper molar. Tooth shape was analysed using an outline analysis (elliptic Fourier transform), based on specimens across the key but understudied zone of Northern Turkey. Two main groups are obtained, i.e. Thrace and Northeastern Turkey, suggesting the occurrence of an Eastern refuge for the edible dormouse, possibly on the foothills of the Caucasus. The contact zone between the European and Asiatic groups is located eastwards from the Marmara straits, undermining its role as an efficient barrier but stressing the importance of climatic and vegetational factors. A secondary differentiation between populations from the Central Black Sea coast and easternmost regions was evidenced, related to climatic gradients and forest fragmentation.

Craniometric variation among the raccoon dog subspecies

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The raccoon dog, *Nyctereutes procyonoides*, is an endemic species in East Asia but can be found as far as Europe after being introduced by Russians in the early 20th century. Currently this species is divided into six subspecies depending geographic distribution. Recent studies have proposed that Japanese raccoon dogs should be classified as a distinct species from other subspecies because of its unique chromosome number. However, since there have been few studies using molecular markers and morphological characters, geographical variation among all raccoon dog subspecies remain unclear. To clarify the morphological variation among raccoon dog subspecies, we examined 488 skulls consisting of five subspecies from seven locations: Korea, Hokkaido, Honshu and Shikoku in Japan*,* Northern China, East Russia and Finland*.* Totally 51 craniodental traits were morphometrically analyzed. No significant variation was recognized among all raccoon dog populations using variation analysis. Student's *t*-test and principal component analysis indicated that, Finnish population has significantly larger and different from skulls compared to those of other populations. Variation analysis showed that Hokkaido populations were significantly different from other populations within the Japanese raccoon dogs. Our results indicate that Bergmann's rule could be one of the influential factors affecting the skull morphology of the Finnish and Hokkaido populations. This study suggests the revaluation of the taxonomic status of these subspecies and management of raccoon dogs.

Comparative variability of skull characters in sibling species *Microtus arvalis* and *M. Levis* (Rodentia, Arvicolinae) from central Chernozem region (Russia)

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According to cytogenetic analysis *Microtus arvalis* is represented by two karyologically distinct forms *arvalis* and *obscurus*. They are separated geographically. Taxonomic status of these forms is unclear. The focus of the present study is a comparative cranial analysis of three kariological group of common vole and reconsideration of the subspecific status for *Microtus arvalis arvalis* and *Microtus arvalis obscurus*. Here, we generalize data on skull measurements and nonmetric cranial traits in common voles to test inter-species differentiation in sibling species. Cranial characters were examined in about 169 individuals representing *Microtus arvalis* (forms *arvalis* – 62 and *obscurus* – 52) and *M. levis* (55). All represented specimens were kariologically dated. Data on males and females were pooled because in both species there were no significant differences among sexes in scull characters. The multiple discriminant function analysis fulfilled on the basis of 35 skull measurements. Our analysis indicated that karyotypic forms *arvalis* and *obscurus* belong to the subspecies.

When morphometrics meets genetics: the case of the common dormouse, *Muscardinus avellanarius*.

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The aim of the study is to apply geometric morphometrics to the study of evolutionary processes that might have driven intra-specific differentiation of the common dormouse *Muscardinus avellanarius* in Europe. The analysis of phenotypic features appears as a valuable complement to genetic analyses, providing a insight into evolutionary processes such as differentiation by vicariance or adaptation to different environments. Previous genetic studies based on mtDNA genes revealed a complex phylogeographic pattern for the common dormouse with the presence of two highly divergent lineages subdivided into geographic clades. We thus investigated whether this genetic differentiation leads to morphometric differences. We examined 150 museum specimens of dormouse from 34 localities in 12 countries. For each specimen, the size and shape of the first upper molar was quantified using an outline analysis based on Fourier methods. A geographic structure emerges from the morphometric pattern of differentiation, partially corresponding to the expectations based on the genetic results. The main differentiation, however, was unexpected and revealed a divergent Austrian cluster. This region was not documented so far for genetic analyses and morphometric data therefore challenge a more extensive sampling of this species that might reveal the existence of a further lineage.

Modularity and form variation of the cranium in the spanish robertsonian system of M*us musculus domesticus*

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The *Mus musculus domesticus* karyotype consists of 40 acrocentric chromosomes. Populations with metacentric chromosomes and reduced diploid numbers appear in several geographic regions due to the occurrence of Robertsonian translocations. A geographic area extending over 5,000 km^2 with seven different metacentrics and diploid numbers ranging from 27 to 40 exists in northeast Spain. Two main forces driving morphological evolution of mouse populations have been previously identified in this zone: chromosomal variation and isolation by distance. The effect of both factors in morphological changes of the ventral cranium was analyzed by means of geometric morphometrics and Mantel tests. Because the effect of isolating factors may depend on the morphological module, the analyses were also assessed separately in the two main units of the skull: the face and the neurocranium. Size of the cranium differed between animals with different karyotypes. In particular, the skulls of the animals with diploid numbers ranging between 28 and 30 were significantly smaller than the skulls of the remaining groups. Size changes in the face and neurocranium were highly correlated, indicating that size is an important factor contributing to morphological integration of the ventral cranium. Although significant shape changes were observed in each functional unit as well as in the whole structure, differentiation patterns in the two modules were not correlated. Shape changes of the face significantly correlated with geographic distance, while shape changes of the neurocranium were not correlated with geographic nor chromosomal distances. The results support the existence of two evolutionary modules in the cranium, the face and the neurocranium.

Morphometric analysis of teeth remains from the El Harhoura 2 cave: towards a better knowledge of fossil mice from Morocco

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Two species of mice inhabit Morocco today: *Mus spretus* is characteristics of West-Mediterranean undisturbed areas, whereas the cosmopolitan *Mus musculus domesticus* is typical for anthropogenic habitats. Little is known about the temporal dynamics of interaction between these species in North Africa, mainly because of the difficulty to distinguish them in fossil assemblages, and because of the rarity of detailed analyses of the local fossil record.

To tackle this question, we studied morphological variations in the fossil mice from El Harhoura 2 cave (Rabat-Témara, Morocco) using geometric morphometrics. Size and shape of the first upper and lower molars were quantified using a Fourier analysis of their outline. This approach has been proven efficient to discriminate between rodent species or populations. Modern (*M. spretus, M. m. domesticus*) and extinct Pleistocene species (*M. haouzi, M. hamidae, M. jotterandi*) from Morocco were used as reference. Our morphometric results evidenced a good discrimination between the *Mus* species used as reference. This allowed a refined interpretation of the mouse fossil record through the El Harhoura 2 section, ranging from the Late Pleistocene to the Middle Holocene. Most teeth from El Harhoura 2 appeared as morphologically close to *M. spretus*. It seems that only one species occurred all along the record, attributed to an archaic form of *M. spretus*. Yet, differences

between archaeological levels suggest the occurrence of local evolutionary processes within this species.

Some restrictions of the morphometric methods as applied to classification of fossil remains *Sorex* (Eulipotyphla: Soricidae) and *Microtus* (Rodentia: Cricetidae)

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The overlapping of quantitative characters even in quite distant species is still a problem for diagnostics. Thus, when working with a mixture of species such as *Microtus maximowiczii*, *Microtus middendorffii* (Arvicolinae) and *Sorex unguiculatus*, *Sorex isodon* (Soricinae) occurred in fossil remains from Far-Eastern cave deposits challenges the identification of samples that have the overlapping shape and size of molar (for *Microtus*) and mandible (for *Sorex*). The differences in the first lower molar (voles), mandible (shrews) shape and size among/within recent fossil samples were studied using traditional and geometric morphometry. As a result of the analysis made it was revealed that *M. maximowiczii* and *M. middendorffii* have almost full similarity of size and surface patterns m1. In case both the species are found in fossil remains (possible for Far East of Russia), they will not be correctly detected. The *S. isodon* and *S. unguiculatus* are very hard to be detected by mandible using traditional morphometry and any time faces difficulties with the identification of specimens using GMM and Cartesian Coordinates.

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Session 6 - Evolution of mammals on islands: generalities and exceptions

Invited & Oral Communication

The colonization of islands by land mammals: a multifactorial reality that shows the unwise use of models

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The colonization of islands by terrestrial mammals is a topic most analyzed by biogeographers and paleontologists. Researchers tend to look for specific key factors that best explain why, how and when non volant terrestrial mammals reached islands, and then use them to develop models. The subjectivity in the choice of key factors obviously leads to controversy and debate. Islands and insular faunas are extremely complex, multifactorial systems, which are the result of an intricate combination of facts, conditions and processes. They need to be investigated individually, on a case-by-case basis and with the widest multidisciplinary involvement, collaboration and exchange between specialists of different fields. Models are nice, but they are simplified representations of reality, and the more systems grow multifaceted, as happens with islands, the more models become approximate. A protocol of analysis is proposed which is essentially an ***evidence-based,*** wide-scale ***multidisciplinary*** approach to be adopted dealing with insular faunas. Geological and stratigraphical information, paleontological evidence, climatological factors, sea-level evolution, paleogeographic characteristics, ecological, physiological and environmental factors, behavioral characters and ecological preferences, genetics and densities of colonizing populations, as well as taphonomic, sampling and analytical biases, but also possible historical sources, are the many different lines of evidence that need to collected. The lack of any of these pieces of information may seriously affect the reliability of our interpretations and reconstructions, and of course of models that can be derived. Cases that are not supported by sufficient information should be filed as potentially misleading and dismissed for any modelling purpose.

Phenotypic variability in shrews

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The common shrew *Sorex araneus* Linnaeus, 1758 is an excellent example of morphological variation within a single species, with traditional taxonomy recognizing a large number of morphological subspecies. Since for the common shrew it is characteristic significant geographic variability of external traits which exceed even differences between species, the progress in taxonomy within the *Sorex araneus* group has been binded with using genetic and chromosome criteria. At the same time it was revealed that the common shrew displays phenomenal chromosome variability of the Robertsonian type (about 70 chromosome races have been described so far). As a rule differences in morphology do not conform to the geographical distribution of chromosome races of the common shrew and could be explained rather by differences of environmental conditions and/or remoteness of studied populations. Besides of wide geographic and chronographic variation phenotypic traits of *S. araneus* demonstrate more or less significant variation related with population abundance and biotope type, age and season. On the example of 3 Soricidae species (*S. araneus*, *S. minutus* and *Neomys anomalus*) we tried to evaluate a contribution of ecological, environmental and other factors in display of phenotypic variations in shrews.

Ancient DNA analysis reveals unsuspected phylogenetic affinities of the extinct *Malpaisomys* (rodentia, murinae), an endemic of the canary islands.

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The Lava mouse, *Malpaisomys insularis*, was endemic to the Eastern Canary Islands and became extinct at the beginning of the 14th century when Europeans reached the archipelago. First studies based on morphological characters remained inconclusive about *Malpaisomys* relationships within muroids. Like most insular species, this extinct rodent exhibits derived characters that make it difficult to establish its affiliation with continental species. Ancient mitochondrial and nuclear DNAs were successfully amplified from fossils of three lava mouse specimens. Phylogenetic reconstructions revealed unsuspected affinities of *Malpaisomys* with the extant mice. Topological alternative tests strongly support this placement among the Murini tribe even if close relationships within mice could not be solved. Molecular dating gave an age of 6.9 Ma for the origin of the *Malpaisomys*/mouse clade. Since the mouse species closest to *Malpaisomys* could not be identified based on this molecular dataset, some biogeographic scenarios could be drawn but have to be further investigated with a larger dataset. Taking into account the great morphological singularities of lava mouse, this study proposed a novel hypothesis to explain the differences of dental pattern between *Malpaisomys* and *Mus* which is probably related to island evolution processes.

Recent colonization and adaptation mechanisms of the house mouse (M*us musculus domesticus*) on the sub-antarctic Kerguelen archipelago.

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Recent invasions on islands give an opportunity for studying evolutionary processes during an early phase which allows a direct analysis of possible mechanisms of early adaptation. House mice (*Mus musculus domesticus*) are well known as commensal pest species and indeed, starting from Western Europe, spread across the globe in historical time. However, most of the Sub-Antarctic islands and in particular the Kerguelen Archipelago (48°25'-50°S; 68°27'-70°35'E) were successfully colonized no more than 300 years ago. During this time, mice must have adapted to extreme conditions such as cold climate, new food resources and a feral lifestyle. Using an extensive data set on genetic diversity of Western Europe and Sub-Antarctic populations, we have an excellent case to study the population genetics of island invasion, the subsequent spread to further islands and patterns of re-invasion. As expected, mice show a low genetic diversity due to founder effects and geographical isolation. Our data also suggest that an area colonized by mice is refractory to further introgression, possibly due to fast adaptations of the resident mice to local conditions. Interestingly, single step mutational derivatives of one of the major mitochondrial haplotypes were found several times in different southern hemisphere islands, suggesting an unusually high mutation rate or the putative presence of a selective sweep in the mitochondrial genome. Taking all together, these data suggest a rapid adaptation of the mice on the Kerguelen extreme life conditions.

Changes in genetic variability in island populations of two rodent species – yellow-necked mouse (A*podemus flavicollis*) and bank vole (M*yodes glareolus*).

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The studies were carried out on two islands located on Mokre Lake (N-E Poland) and on the lake shores in years 2003-2005 and in 2008. Microsatellite markers were used to estimate the level of genetic variability within studied populations. Molecular analyses were successfully performed for 199 individuals of *A. flavicolis* and 628 individuals of *M. glareolus.* In both species allelic diversity and heterozygosity of island populations were significantly lower in comparison with lakeshore population, which indicates the presence of the "isolation effect". Moreover, the genetic variability of island populations of both species showed deep changes over time, correlated with changes of their densities. The results obtained suggest that island populations of both studied species can occasionally undergo the demographic and genetic bottlenecks which are compensated by immigration from the lakeshore populations.

Endemic oak jungles for the dwarf elephants and ungulates of the mediterranean islands

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Dwarf elephants, hippopotami and deer characterised the endemic fauna of several Mediterranean islands in the Upper Pleistocene/early Holocene. Dwarfism seems to be the only alternative large-sized animals have to lower selective pressure when they move into insular settings. Most of all, it appears that the low availability of resources sets insular populations under the strict control of both genetic and ecological constrains. We should however not undervalue the importance of the selection exerted in relation to such specialisation by the principal characteristics of the physical environment. In the Upper Pleistocene, for example, the majority of the Mediterranean islands must still have been cloaked in the densely tangled vegetation that covered most of these environments before any human explorer set foot on them. These practically impenetrable botanic formations must have been home to an entire dwarf mammalian fauna that was particularly adapted to living, moving, feeding, resting and hunting each other in such an environment. This is still the case in certain relic fragments of the rain forests of western and central Africa, where peculiar biological elements, such as the last dwarf elephants, hippopotami, and other ungulates still survive.

Poster Communications

Majorcan rabbits and hares – colonization history inferred from mitochondrial DNA variation

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The Mediterranean islands have a history of human-mediated introductions that frequently resulted in a change of their faunal and floral representatives. While these histories are sometimes well documented or may be inferred and supported by paleontological studies, often the use of phylogenetic and population genetics reconstruction methods are essential for answering questions related to the evolutionary history of the insular species. In this study, the colonization history of the Majorca Island by wild rabbits (*Oryctolagus cuniculus*) and hares (*Lepus granatensis*) was inferred from sequence variation of the mitochondrial DNA control region of 25 rabbits and 25 hares. This variation was analysed in the framework of the known phylogeography of the continental populations. Both species showed a genetic diversity comparable to that of the continental population, suggesting introduction of multiple lineages. Indeed two highly divergent lineages of hares were found in Majorca which haplotypes were closely related to those from Cáceres and Zaragoza populations, each one likely corresponding to a single founder event. However, our results do not support the existence of a Majorcan *L. granatensis* subspecies. Rabbits, which were identified as belonging to subspecies *O. c. cuniculus*, were likely introduced from Iberian but also from French populations. We estimated that most of the founder events could have occurred during the Holocene and possibly after the first human settlements on the Island, which agrees with the assumption of man-mediated introductions. In all cases, the hypothesis that insular populations experienced a demographic expansion following a severe bottleneck was unclear. This study, while clarifying some aspect of the history of the colonization of Majorca by hares and rabbits, raised numerous other questions that should be addressed in future studies.

Session 7 - Mechanisms of speciation in mammals

Invited & Oral Communication

Can stability create change? Exploring the role of stable environments in species diversity

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Throughout the Quaternary, the flux of glaciers across continental landscapes altered climates and created refugial pockets where species persisted, often in isolation. Glacial patterns have changed significantly since the late Pleistocene, and mammals have responded to shifting climates in various ways. Often, vicariant processes and differences in dispersal ability are invoked to explain variation in geographic distributions and divergence of lineages while the effects of stable areas on diversity are largely ignored. Here, we use the contemporary distributions of related lineages (i.e., sister genera) to model climatically suitable habitats for each during the late Quaternary (21 kbp) to examine the effects of stable climatic refugia on diversification. Specifically, we compare the amount of stable area from the last glacial maximum to the present-day for each genus to see whether it can explain current species diversity within genera and explore the possible effects distinct biogeographic barriers have exerted on diversification. We focus on the Americas since they represent high connectivity through the Mesoamerican isthmus and contain a myriad of distinct habitats influenced by tectonic dynamism and topography. When combined, the influence from these barriers and information about shared areas of stable climate (or shared refugia) across genera may contribute much to interpreting historical scenarios about the diversification of mammalian lineages across continents.

Measures of linkage disequilibrium among neighboring snps indicate asymmetries across the house mouse hybrid zone

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Theory predicts that naturally occurring hybrid zones between genetically distinct taxa can move over space and time as a result of selection and/or demographic processes, with certain types of hybrid zones being more or less likely to move. Determining whether a hybrid zone is stationary or moving has important implications for understanding evolutionary processes affecting interactions in hybrid populations. However, direct observations of hybrid zone movement are difficult to make unless the zone is moving rapidly. Here evidence for movement in the house mouse *Mus musculus domesticus* × *Mus musculus musculus* hybrid zone is provided using measures of LD and haplotype structure among neighboring SNP markers from across the genome. Local populations of mice across two transects in Germany and the Czech Republic were sampled and a total of 1301 mice were genotyped at 1401 markers from the nuclear genome. Empirical measures of LD provide evidence for extinction and (re)colonization in single populations and together with simulations suggest hybrid zone movement due to either geography-dependent asymmetrical dispersal or selection favoring one subspecies over the other.

Differential sperm performance in hybrids coincides with Y chromosome invasion across the house mouse hybrid zone

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The house mouse hybrid zone is thought to be maintained by selection against hybrids, and it has been suggested that invasion of a Y chromosome across the Czech/Bavarian region, in defiance of Haldane's rule, is an example of genetic conflict outweighing this selection. However, no unfit hybrid phenotypes and no mechanism for the suggested genetic conflict have been identified in nature. Here we assess phenotypes of the haploid phase of the mouse lifecycle. Sperm characteristics of wild caught males were measured in a field laboratory set up in the Czech/Bavarian region, and the hybrid index of each male was later calculated using 1401 diagnostic SNPs. While sperm velocity and sperm count did not differ between parental mouse subspecies, they were significantly reduced in their hybrids. A reduction of sperm velocity in the center of the hybrid zone was associated with shortened sperm heads. Hybrid males carrying the invading Y chromosome have both increased sperm count and velocity compared those carrying the alternative Y. Based on the observed phenotypes we suggest selective advantages in the haploid phase likely explain a large component of both the selection against hybrids that maintains the distinction between the mouse taxa, and the genetic conflict that has allowed a Y chromosome to cross the taxon barrier.

Speciation by sexual selection – and the importance of ecology

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The spectacular diversity in sexually selected traits among animal taxa has inspired the hypothesis that divergent sexual selection can drive speciation. However, the evidence for this mechanism is stronger for some taxa than others, with effect estimates for mammals much lower than those for fish, insects and birds. In my contribution to this symposium I will discuss some explanations for this variation. In addition, I will talk about the importance of considering the ecological context in which sexual selection takes place. For example, sensory adaptation may change mating preferences through pleiotropy; and mate choice for locally adapted partners can accelerate divergent adaptation. Recent theory and data suggest that such interactions between natural and sexual selection may be particularly powerful in generating species diversity.

Testing the role of MHC class I as a premating reproductive barrier between two *Microtus* sister species.

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Mammals have the ability to distinguish and recognize other individuals through olfaction. Being their dominant sense, it is essential in social behaviours such as parent-offspring bond and mate choice. Mating is heavily influenced by social chemosignals secreted by individual conspecifics which can permit the assessment of the degree of relatedness of a potential mate, reducing inbreeding and maximizing the fitness of the offspring. One described mechanism that allow individual recognition concerns the Major Histocompatibility Complex Class I genes (MHCI). MHCI peptide ligands, originated by the proteosomal degradation pathway and secreted through urine, act as odour chemosignals of MHCI identity at the vomeronasal and olfactory receptors. Since this mechanism allows strain recognition in mice, we hypothesize that this principle may be applied to species recognition, particularly concerning female mate choice. As premating and postmating reproductive isolation are the primary forces responsible for generating and maintaining biodiversity, their study is fundamental to understand speciation. Therefore, we are testing the role of the MHCI as a premating barrier between two *Microtus* sisters: *Microtus lusitanicus* and *Microtus duodecimcostatus*. These species present very low cytochrome *b* divergence and occur both in allopatry and sympatry. Because the MHCI is unknown for these non-model species, we are isolating and characterizing MHCI alleles for the most polymorphic loci (H2-K and H2-D) and exons (2 and 3), using next generation technology.

A moving hybrid zone between intraspecific lineages in *Microtus arvalis*

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Understanding the mechanisms which lead to speciation remains a fundamental question for evolutionary biologists. The investigation of hybrid zones provides crucial information on the degree of differentiation between gene pools. Here we studied a secondary contact zone between two highly-divergent evolutionary lineages of the common vole *Microtus arvalis* (resp. Western and Central). The genetic structure of the contact zone was investigated with mtDNA, Y-Chromosome and autosomal markers for more than 500 individuals along two replicate transects. Mismatches between markers and Bayesian clustering provided evidence for hybridization. Cline analyses suggested a moving hybrid zone (non coincident clines) as well as the presence of a partial reproductive isolation mechanism. Combining landscape and genetic information allowed us to develop a historical scenario of the hybrid zone. It seems likely that the direct contact zone between the two lineages has moved into the West for the benefit of the Central lineage, leaving behind the cline of mtDNA markers at the initial contact zone. We conclude that the speciation process in this system is not completed but it seems to be relatively advanced.

Pattern of gene flow across chromosomal hybrid zones in the house mouse *Mus musculus domesticus*

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The West European house mouse, *Mus musculus domesticus*, is a suitable model to investigate the role of chromosomal rearrangements in reproductive isolation. In fact, it exhibits a broad range of chromosomal polymorphism due to Robertsonian (Rb) fusions leading to various types of contact zones between different chromosomal races. We analyzed the chromosomal structure and estimated gene flow in two different contact zones in central Italy to evaluate the role of Rb fusions in the speciation process. Microsatellite loci variation was analysed in 235 mice sampled from 31 localities. In the hybrid zone between the Cittaducale race (CD: $2n = 22$) and the surrounding populations with standard karyotype ($2n = 40$), telomeric and pericentromeric loci were selected on six chromosome arms in order to estimate the amount of gene flow in these chromosome regions. The analyses show a differential gene flow, which seems more restricted near the centromeres of Rb chromosomes. A different pattern was observed at the contact between two metacentric races, the Cittaducale race (CD: $2n = 22$) and the Ancarano race (ACR: $2n = 24$). Here, the clear genetic differentiation between the races suggests the absence of gene flow. We discuss the obtained results considering the “hybrid dysfunctions” and “suppressed recombination” models of chromosomal speciation.

Genetic characterization of *Myodes rutilus* from Russian far East

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Electrophoretic study of 25 putative loci in *Myodes rutilus* from 12 localities of Far Eastern Asia detected most interesting pattern of geographic differentiation in hemoglobin. A total 67 samples and 290 specimens were collected for more detailed analysis of Hb geographical distribution. As before two different geographical groups were found. Hb A was found in samples from Kamchatka peninsula Magadan region, Sakha-Yakutia, Middle Priamurye. Hb B was fixed in the samples from Hokkaido-island Sakhalin-island, Bolshoi Shantar-island, Amur estuary and mainland coast of Tatar strait, but also in the samples from right bank of the Amur-river on Lower Priamurye and from coastal zone of eastern Sikhote-Alin. Both Hb A and Hb B were found in populations of two geographical regions. One of them locates in Lower Priamurye on right bank of the Amur-river. In Primorye, the western Sikhote-Alin locates another one. The data partly agree with result of CytB investigation (Ivasa et al, 2002). Only 49 specimens and 7 samples and 3 loci were used to start the study of geographic variation of microsatellites. Cg1F11 Cg2C5 and Cg2D3 loci (Ricalainen, 2008) were highly polymorphic and highly heterozygous. In each of the geographic groups both common and unique alleles were presented. Ways and reasons for geographic differentiation Hb discussed

Evidence of recombination suppression in vlei rats, *Otomys irroratus*

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Chromosomal speciation is controversial partly because new data suggest that chromosomal rearrangements may play a limited role in genetic diversity and speciation. Here we provide evidence for the role of rearrangements in incipient speciation using data derived from the extensive karyotypic analysis of an endemic Africa rodent, *O. irroratus*, which is known to have a variable diploid number (2n=23-32). Karyotypic data from 55 specimens collected at 7 localities in South Africa were analysed using conventional banding (G- and C-banding) and chromosome painting probes derived from *Myotomys unisulcatus*. The cytogenetic data was supplemented with mitochondrial *cyt b* and morphometric data. Of the 55 specimens analyzed, 47% contained inversions on 4 autosomes (OIR1, 4, 6 and 10) which were present singly in specimens (i.e., none of the specimens contained all 4 inversions concurrently). These inversions were found in both homozygous and heterozygous state over a wide geographic range suggesting that they occur as floating polymorphisms within this species. This is supported by both mtDNA *cyt b* and morphometric analysis that show no evidence of divergence between carriers and non-carriers. Given the potential role of inversions in post-mating isolation (through production of aneuploid gametes), the prevalence of inversions as floating polymorphisms (and lack of genic and morphological difference) in vlei rats suggests that they are not underdominant and they are probably retained in the population through suppression of recombination in centromeric regions of the rearranged chromosomes.

Poster Communications

Genome-wide architecture of reproductive isolation in a naturally occurring hybrid zone between *Mus musculus.domesticus* and *M. m. musculus*

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A hybrid zone where two house mouse subspecies (*M. m. musculus* and *M. m. domesticus*) meet occurs across central Europe. Several transects from different parts of the hybrid zone have been studied, revealing evidence that the hybrid zone is a tension zone resulting from dispersal of parental types and selection against hybrids. While these studies suggest a large role for the sex chromosomes, as well as multiple regions of autosomal chromosomes, they have not provided a sufficiently detailed analysis of the genetic architecture of reproductive isolation due to insufficient marker coverage on a genome-wide scale. The goal of our study is to detect and characterize genomic regions in house mice underlying reproductive isolation. We used 1401 markers evenly spaced across the genome to analyze the genetic interactions such as Dobzhansky-Muller incompatibilities across two transects. Using genotype data from 1301 mice collected from two different transects, we employed cline theory to assess genome-wide variation in patterns of introgression. Using genotype data from mice collected from two populations, one from each transect, we also used information on linkage disequilibrium to identify regions of the genome under putative selection. The results of these two analyses in combination with knowledge of biologically relevant gene content reveal regions of interest and our preliminary results suggest an important role of spermatogenesis genes in reproductive isolation between these taxa.

Session 8 - Miller and other European mammalogists contributions a century ago

Invited & Oral Communication

Gerrit Smith Miller – contributions to European Mammalogy and the value of natural history collections

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A century after the publication of his *Catalogue of the Land Mammals of Western Europe*, Gerrit Smith Miller's contributions to European mammalogy endures. His work was a landmark treatment of the European fauna and laid the groundwork for subsequent mammalogists. Miller served in the US National Museum as Assistant Curator of Mammals from1898-1909 and Curator until 1940. He produced 400 monographs and other contributions to scientific journals, including *Catalogue of the Land Mammals of Western Europe in the British Museum, List of North American Land Mammals in the United States National Museum, List of North American Recent Mammals,* and *The Families and Genera of Bats*.

Miller's vast array of specimen-based work underscores the fundamental role that natural history collections have played in building our understanding of the natural world. The relevance of collections to basic discovery endures, as they have evolved since Miller's time (now including tissues, cell suspensions, parasites, etc.) and our tools for extracting information from specimens have improved exponentially. While still utilized for systematic and taxonomic questions, museums and associated web-based databases (GenBank, GoogleEarth) are now relied upon heavily to answer questions related to environmental change (e.g. climate change, habitat conversion, emerging pathogens, pollutants, biodiversity loss, introduction of exotics), as they are the primary resource that unequivocally documents historic conditions and provides critical baseline data. These databases also provide a window into environmental biology for the next generation of biologists. As in Miller's day, museums remain centers of research and training for future generations of environmental scientists.

In the footsteps of Gerrit S. Miller: André Meylan, Ernst von Lehmann, and the rediscovery of *Sorex coronatus* (Millet, 1828)

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The 1912 publication of the "Catalogue of the Mammals of Western Europe" by the American zoologist Gerrit S. Miller (1869-1956) was a milestone in the exploration of European mammal diversity, not only in size (1020 pages), but also in its concept and contents. With keys to species, full lists of synonyms, detailed descriptions, measurements, and figures of skulls the book contained all components of a modern monograph and stimulated the work of generations of European mammalogists. Miller's work was based on morphology, and cryptic species were easily overlooked. The purpose of this talk is to review the work of two European zoologists, André Meylan (University of Lausanne, Switzerland) and Ernst von Lehmann (Museum Koenig, Bonn), who both and independently studied the polymorphism of the Common shrew *Sorex araneus* L., 1758, using the classical methods of Miller and adding the study of chromosomes, a new technique at that time. Their slightly different approaches, enforced by their students Jürgen Olert and Jacques Hausser, led to the discovery and final recognition of Miller's shrew *Sorex coronatus* (Millet, 1828), a species which had rested in synonymy for almost 140 years.

The contribution of Edouard-Louis Trouessart to Mammalogy

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Edouard-Louis Trouessart (1842-1927) is one of the major figures of European Mammalogy. He started first medical studies and passed his thesis of medicine in 1870 in Poitiers. Then in parallel to his medical work he was a real naturalist and frequented regularly the Natural History Museum of Angers were he was nominated as director from 1882 to 1885. After that he started to visit the Museum of Natural History in Paris and became professor in 1906 at the death of Oustalet. He was at the head of the « Mammals and Birds » section of the Museum between 1906 and 1926, after Etienne & Isidore Geoffroy St Hilaire, Milne Edwards Henri and Alphonse Oustalet. He published more than 300 scientific and diffusion articles and has named about 30 new species for science. Among his major works one finds in 1884 a book on Fauna from France, in 1885 the first edition of the "Catalogue of modern and fossil Mammals" reedited three times, which can be considered as one of the first reference book for mammals classification and an early precursor of Simpson (1945) and Mc Kenna and Bell (1997) or Wilson & Reeder (1993, 2005). In 1910 he publishes the "Fauna of European mammals" as well as the European Birds catalogue in 1912 and a book devoted to biogeography. Trouessart was a systematician and had made of Taxonomic classification his main aim. His impressive work at the interface between biology, palaeontology and biogeography at the beginning of XXth century is worth to be known.

S.I. Ognev and the formation of Theriology in Russia

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Intuition of a taxonomist based not just on a vision but on a large experience. S.I. Ognev (1886–1951), one of the famous Russian biologists, was both an armchair scholar, and a great field researcher. Combination of excellent knowledge of natural habitats and morphology formed a unique insight. Taxonomic position of a surprisingly large fraction of forms classified by Ognev in the early and mid-XXth century got confirmed recently by modern molecular genetic approaches. Ognev's "Fauna Mosquensis" (1913) became the most comprehensive study of mammals of European Russia after Pallas. Ognev examined over 3000 specimens, it was the first case of serial collecting for small mammals. Throughout his life, Ognev's work involved two important components: biological observation in nature and study of geographical distribution. He also used a wide network of correspondents who provided him with valuable biological data. This effort resulted in seven volumes of "Mammals of eastern Europe and northern Asia" and "Mammals of the USSR and adjacent countries" published during 1928–1950. This fundamental work included detailed description of taxonomy, morphology, geographical range and biology for 264 mammalian species and 635 forms. 4879 pages were illustrated with almost 2000 photos and drawings of skulls, teeth, and a huge number of maps made by the author; 56 color figures were drawn by famous animal painters. Ognev also authored books on ecology and field photography. It is impossible to overestimate the significance of Ognev's input into mammal studies, his "Mammals..." remains one of the most cited works nowadays.

How stable are phylogenetic roots? Contributions of russian mammalogists a century ago and overlooked from nowadays

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Among the Russian mammalogists of XX century whose contributions to the study of systematics, distribution and phylogenetic relationships of Palearctic mammals was outstanding one can mention Ognev, Geptner, Vinogradov, Gromov, Argiropulo and some others who enriched our knowledge of mammal diversity at the regional and continental scale. Unfortunately, it is impossible within the frame of short communication to highlight equally the input of each of the prominent scholars in the field. Therefore, I will limit my talk to illustrate the contribution of Russian zoologists of the past century to the example of the study of subfamily Arvicolinae, including voles and lemmings. This group was always a hard nut for systematics from one side and a good model to test the suitability of any new methods and evolutionary hypothesis on the other. All possible methods of study were successively applied to the group which also has rich fossil record. Among Russian scientists the greatest contribution to the study of the group belongs to I.Gromov. His papers and comprehensive monograph (1977), had strong influence on several generations and to a great extent determined the further lines of research and classification of taxa within the group. In a couple of years (2013) we shall commemorate the 100th anniversary of Gromov's birth, therefore it is an appropriate moment to overlook his ideas from the viewpoint of recent knowledge.

Mammalian taxonomy in Europe over the last century: convergences and divergences in number of recognized species

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A century ago E. L. Trouessart (1910) and G. S. Miller (1912) provided first comprehensive taxonomic revisions of European mammals. Particularly Miller's "Catalogue of the Mammals of Western Europe" influenced the taxonomy and nomenclature more than any other single contribution to European mammalogy. A list of 198 species, as recognized in 1912, was reduced to 130 species in the influential revision of the Palaearctic mammals (Ellerman & Morrison-Scott 1951). The estimate of species richness remained at low number until late 1960s but started to grow steadily since late 1970s. Although the most recent revisions (Wilson & Reeder 2005, IUCN Red List 2008) converge towards Miller and Trouessart in number of species, the similarity index based on species composition lists decays as a function of time separating the two revisions. Therefore, the greater the time period between the two revisions, the more dissimilar their taxonomic lists tend to be, irrespective of differences in the number of species recognized. Species turnover index among species lists is the highest for lagomorphs and rodents, hence these two orders had the most dynamic taxonomic history over the last century. Of the 179 species in Wilson & Reeder's compilation, 21 names were proposed since Miller's Catalogue, i.e. during the last century.

Session 9 - Mammals and landscape

Invited & Oral Communication

Population dynamics and habitat selection of rodents in a complex desert landscape

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Population fluctuations of 13 rodent species were monitored for 18 years in the central Negev Desert, Israel, in an area 110 sq. km in different habitat types including sand dunes, open gravel plains, rock cliffs, loess hills and dry river beds. Analysis of factors affecting population dynamics of 9 common and abundant species demonstrated that densities of most rodent species in the late summer, after the end of reproduction, were determined mainly by total precipitation during the previous rainy season. Rodent densities in the winter, before the reproductive season, were determined mainly by their densities in the previous (late summer) season. Rodent populations in dry river beds (wadi) demonstrated either no or negative correlations with total rainfall, suggesting episodes of population crash due to flash winter flooding. For all species occurring in more than one habitat, densities, at least in some habitats, were correlated with their contemporary densities in other habitats. For these species, processes of density-dependent habitat selection were indicated using isodars analysis. Interspecific competition affecting species distribution at the micro-habitat scale has no effect on population dynamics at the macro-habitat scale. Generally, population dynamics of desert rodents were determined by the complex interactions of extrinsic (rainfall) and intrinsic mechanisms but were modified by density-dependent habitat selection.

Landscape effects on small mammal communities and population dynamics

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In a fascinating article, Delibes-Mateos et al. (2011) pint point that small mammals such as the European rabbits, the plateau pikas, the prairie dogs have been traditionally perceived as pests and targeted for control on a very large scale despite their importance as key-stone species in their native ecosystem. This is also the case for many species of voles in Eurasia and North America (see e.g. Giraudoux and Raoul 2010). However, although a considerable number of studies have been undertaken at local and other scales to understand the mechanisms of vole population outbreaks and cycles, few of them provide basic concepts and useful elements that can be used by ecosystem managers on the scales requested. Lidicker (1995) and Barret & Peles (1999) wrote the first books providing a landscape ecology perspective to small mammal studies. During the 90s, a number of studies have shown that small mammal population management could be grounded on knowledge on the effect of landscape on population dynamics. Here we present results obtained from the long term and multi-scale study of two grassland species, *Microtus arvalis* and *Arvicola terrestris* to illustrate this approach. We describe at which scales landscape variables were found relevant to explain population dynamics and the consequences of the observed population dynamic patterns on the vertebrate community (other small mammal species and predators including species of conservation value). We argue that long term observational studies at various scales are of primary importance to understand the role of small mammals in regional ecosystems and essential to put experimental studies into relevant context. Such knowledge is critical to provide managers with useful concepts for integrated sustainable landscape management, to protect biodiversity and also for pest and disease control.

Barrett, G.W. and J. Peles eds., 1999. Landscape ecology of small mammals. Springer, New York. pp 347.
Delibes-Mateos, M., A.T. Smith, C.N. Slobodchikoff and J.E. Swenson. 2011. The paradox of keystone species persecuted as pests: a call for the conservation of abundant small mammals in their native range. Biological conservation in press.
Giraudoux, P. and F. Raoul. 2010. Ecologie du paysage, perturbations anthropogéniques et transmission de l'échinocoque alvéolaire, In:(eds M. Gauthier-Clerc, F. Thomas), Ecologie de la santé et biodiversité. De Boeck, Bruxelles. pp. 211-226.
Lidicker, W.Z.J. ed., 1995. Landscape approaches in mammalian ecology and conservation. University of Minnesota Press, Minneapolis. pp 215 pp.

Targeting habitat management in fragmented landscapes: a case study with arboreal rodents.

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Improving the quality of habitat patches in fragmented landscapes is a main conservation target; nevertheless few studies have examined patch management in relation to the surrounding landscape. Tackling such an issue needs a cross scale approach that takes into account the hierarchical nature of landscapes. We here show the results of a cross-scale study focusing on the distribution patterns of 3 arboreal rodents (*Muscardinus avellanarius*, *Sciurus vulgaris*, *Rattus rattus*). The overarching goal of this study was to understand the strength of patch scale determinants of distribution, following the appropriate control for relevant landscape properties (e.g. habitat loss vs habitat subdivision). We show how, after controlling for uncertainty in the detection of the species and for the role of landscape properties, patch scale variables still played an important role in determining occupancy patterns of arboreal rodents. For some species variations in the values of patch structure variables increased presence probability only with moderate levels of habitat loss, highlighting the fact that habitat management should be targeted towards precise landscape conditions. In other cases the effect of patch variables was particularly strong therefore variations in the values of patch variables always brought substantial modification in the value of presence probability. Overall these results strongly suggest that habitat management should never be carried out irrespective of the properties of the surrounding landscape, rather, it should be carefully targeted towards specific landscape contexts (e.g. above a certain amount of habitat) where it is more likely to be effective.

Impacts of forestry on voles and small predators in Finland

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It has been hypothesised that the steep decline of grouse populations in Finland is caused by forest management by increasing the number of predators favouring voles from genus *Microtus*. The two most common and widespread vole species in Finland are the bank vole (*Myodes glareolus*) and the field vole (*Microtus agrestis*). Due to different environmental requirements, forestry affects *Myodes* and *Microtus* voles differently. It has often been suggested that after clear cutting *Myodes* species will decline and *Microtus* voles increase. *Microtus* voles are especially important for numerous predators because of their high local densities. We monitored voles in commercially used forests in four successional forest phases (10 stands with 5 small quadrats in each phase) in Taivalkoski in northern Finland biannually in 2006–2010. Field and root voles (*Mi. oeconomus*) were caught mainly from reforestations but spread also to older forests in low numbers in 2010 when densities were high. Bank voles used all four successional phases but relative densities were highest in mature forests especially in low years. As *Microtus* vole densities were also low, vole densities in all younger successional phases were overall low. We also investigated the habitat use of small predators using wildlife triangles and the results compared with vole abundances will be discussed.

Habitat suitability modeling of murine rodents in South-East Asia: use of high resolution data at a local scale

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Understanding the ecological patterns that define the biotope of a given species is a fundamental step in the study of its niche. It allows the delineation of its suitable habitats. Nevertheless, it does not determine its presence also conditioned by the interactions with animals, humans, parasites or other extrinsic factors. Locally, studying the arrangement of landscape features is necessary for such habitat suitability modeling but requires high resolution data.

In a study of murine rodents (rats and mice) diversity in South-East Asia (www.ceropath.org), we analyzed their habitats at a local scale. Rodents were trapped, identified and described in seven study sites in Cambodia, Laos and Thailand. Sampling was rigorously conducted to investigate the different biotopes and the diversity of species in each location. We acquired high resolution satellite images (Spot V at 2.5 meter resolution in Panchromatic mode and at 10 m in Multispectral mode). We used object-oriented classification (eCognition® software) to better consider landscape features and integrate textural and topographic variables to the analysis of images. We present here how we modeled the suitable habitats of different species trapped for the project. We finally discuss the use of high resolution data in species ecological modeling and the perspective for the study of the impact of environmental changes on species dynamics.

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Seasonal habitat use by red deer and rabbits in a heterogeneous landscape: competition or resource partitioning?

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Red deer (*Cervus elaphus*) and rabbits (*Oryctolagus cuniculus*) can often be found living in sympatry across Europe. These two herbivores differ significantly in size, and some evidence suggests that the larger herbivore may displace the smaller one through competitive interactions and indirect effects. In Mediterranean environments, seasonal fluctuations in the availability of resources make potential competitive interactions between these two species especially important. The aim of this study was to determine seasonal habitat use of red deer and rabbits in a heterogeneous landscape, and assess whether competitive interactions or resource partitioning may be taking place during the most resource-limited times of year. The study was carried out in a game estate in Central Spain. A total of 104 sampling points were distributed across three main habitats: open, scrub and ecotone. Relative abundance of each species was assessed by pellets counts in pre-cleared 1 x 5 m quadrats, and environmental variables were measured at each point. Results suggest that although both species exhibit seasonal changes in habitat use, rabbit changes are more pronounced. There was some degree of overlap during winter, and differences started to appear in spring, when rabbits use mainly ecotone areas and deer prefer open areas. Rabbit habitat use shifts again in summer, when they prefer scrub areas, while deer remain in open areas. Results are discussed in the light of dietary habits, resource partitioning and potential indirect interactions. We conclude that a heterogeneous landscape and rabbit plasticity favour the coexistence of both species under Mediterranean climatic conditions.

Where to eat? : prey availability and habitat choice by hedgehogs (*Erinaceus europaeus*) in a rural irish landscape

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The European hedgehog is a characteristic member of the Irish fauna yet there has been little previous research on this species in Ireland. In order to investigate home range and seasonal habitat use, 24 hedgehogs were caught and radio tracked in a mixed agricultural landscape in Co. Cork, Ireland, from June 2008-2010. The density of surface invertebrates was monitored in arable and pasture land throughout this period. Males had a mean home range of 56 ± 0.67 ha (100% minimum convex polygon), which was significantly larger than females (16.5 ± 0.49 ha). Male home range encompassed that of a number of females and was at its maximum during the breeding season (April to July). In both years activity was concentrated in pasture during the breeding season and in a 15 ha arable field after this time. Previous studies, in the UK and Denmark ranked preference of arable land as the lowest, but such was clearly not the case in this study. Use by hedgehogs of arable land in the present study coincided with a rise in mollusc density. Hedgehogs concentrated their activity in areas with greatest prey density. Furthermore, contrary to previous studies, hedgehogs consistently foraged in the centre of both arable and pasture fields. This is the first analysis of habitat use by hedgehogs in Ireland and presents some novel differences to studies elsewhere in Europe. It is suggested that these differences are related to prey distribution. Reasons for the observed pattern of prey remain unclear and warrant further study.

Stressful living close to roads? increased physiological stress levels in wild wood mouse (*Apodemus sylvaticus*) populations beside a motorway

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Linear infrastructures such as motorways produce several effects on mammal populations being recognized as a major cause of habitat fragmentation, habitat degradation and biodiversity loss. However, it is unknown whether motorways lead to an increase in physiological stress levels in animal populations. We analyzed faecal corticosterone metabolites (FCM) in wild populations of wood mouse (*Apodemus sylvaticus*) inhabiting at different distances (0 m, 500m and 1000 m) from the AP-51 motorway in Spain. Wood mice were captured with Sherman live traps, and fresh faecal samples from 424 captured individuals were collected and analyzed in the laboratory. The quantification of FCM concentrations was performed by competitive enzyme immunoassay using ELISA technique. Results showed motorway increasing FCM concentrations, individuals living close to the motorway showed higher levels of FCM (90.1 ng/g dry faeces) than those ones captured further (73.5 ng/g). Factors like sex and breeding condition also significantly explained the variation in FMC concentrations showing females and breeding individuals higher FCM levels. In addition, weight of animals was positively related with FMC concentrations, but neither cover and height of vegetation nor cattle presence influenced FCM levels. Our study is the first one demonstrating a significant impact of motorways perturbation on wood mice physiological stress levels. As mice are used world-wide as research models, our results could open new perspectives to test human influence on the natural environment and trade-offs of species in degraded ecosystems. This could benefit to biodiversity and also maintain healthier wild animal populations.

Spatial genetic structure of yellow-necked mice *Apodemus flavicollis* in north-eastern Poland

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Understanding the impact of landscape features on the spatial distribution of genetic variation is one of major objectives of landscape genetics. The yellow-necked mouse is a common forest rodent, widely distributed in Europe. Although preferring mature deciduous forests, the yellow-necked mice are characterized by high mobility in heterogenous landscape. To evaluate how environmental factors are influencing metapopulation dynamic of this species in north-eastern Poland we conducted intense sampling in seven large woodlands (optimal habitat) and on transects between them that included small woodlots (suboptimal habitat). Analysis of 13 microsatellites revealed a high level of genetic variability and strong dependence on geographic distance (isolation by distance). A bayesian clustering method (Geneland) divided individuals into 4 subpopulations, indicating clear genetic isolation of three, distantly located forests and defined three clusters within continuously trapped individuals across the heterogenous landscape. The analysis of mtDNA (247 bp fragment of the cytochrome b) revealed 24 distinct haplotypes. We found that three European subclades, known from other studies, are present in north-eastern Poland. Samova recorded 4 or 5 subpopulations, largely concordant with thosebased on microsatellite markers. An explanation of the observed spatial genetic structure will be undertaken by testing the dependence of genetic subdivision (Fst) on environmental variables (climate, cover type, size of the forest etc.).

Grouping dynamics of feral goats in Ireland: social segregaton and habitat use

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Feral goats (*Capra hircus*) are widely distributed in Ireland. Legally, they fall on the ill-defined border between domestic and wild but there is evidence for a rare landrace. However, with the release of domestic stock, it is near impossible to find feral herds without characteristics of introgression with improved dairy breeds. Very few studies have been carried out on feral goats in Ireland. GPS and/or VHF collars were attached to adult females from independent herds to locate the herds and examine home range and habitat use. Each herd was located once a month and group composition recorded hourly. By examining different herds in two distinct landscapes we compared the grouping patterns of these feral herds and related it to social segregation and habitat availability. Group sizes in the mountainous and boggy Beara peninsula (Cork, southwest Ireland) are significantly smaller than those in the exposed karst limestone region of the Burren (Clare, midwest Ireland). There are fewer male-only groups in locations where there is male-biased trophy hunting and mixed sex groups are significantly larger than either male-only or female-only groups. Group size varies seasonally, increasing in size during the late summer and early autumn rut period. This is more noticeable in the Beara than in the Burren, where large mixed herds can be found throughout the year. Home range (MCP) sizes of up to 10 km^2 were recorded but the largest range size does not correspond to the largest group size or to the highest proportion of bare rock habitat.

Genetic structure of rat populations infesting oil palm agricultural landscapes in southeast Asia

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In Southeast Asia oil palm cultivations represent one of the major components of agricultural landscapes. These plantations have replaced large forest areas thus contributing to habitat fragmentation and acting as putative barriers to gene flow. Since rodents' damages on oil palm can cause important crop losses, assessing the precise influence of landscape characteristics on rodents' population structures is a major stake for the success of integrated pest management. In this study, we propose to investigate the processes and patterns of rodents' gene flow within oil palm agricultural landscapes. Firstly, molecular barcoding approaches using COI (Cytochrome Oxidase I) sequences were used to characterize species composition in 17 plantations throughout Indonesia. Two species were hereby identified: *Rattus tiomanicus* and *Rattus tanezumi.* Secondary, genetic analysis of the *Rattus* population were carried out for individuals collected in three oil palm plantations characterized by very distinctive features: (1) containing *R. tiomanicus* in Riau (Sumatra), (2) containing *R. tanezumi* in Bangka, a small island located close to the East coast of Sumatra, and (3) the last one containing *R. tanezumi* and surrounded with large area of natural tropical forest in Papoua, the most eastern Indonesian island. Hundreds of rats were collected for these three localities and were characterized using eight microsatellites markers (*D10Rat20, Rr021, Rr114, D18Rat75, D11Mgh5, Rr068, D11Rat56, D5Rat83*). Statistical approaches (isolation by distance and Bayesian methods) were then used to evaluate the involvement of landscape features in shaping diversity and population structure of rats in oil palm crops.

Impact of human pressure and forest fragmentation on a social primate species: the case of Barbary macaques (*Macaca sylvanus*) in Morocco.

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Overexploitation of forests by humans can lead to highly fragmented populations in forest-dependent species which present a low dispersal power in relation to their behavioral and social life traits. Social organization is an important determinant of the ability of a social species to disperse between habitat patches and thus to survive in a disturbed and fragmented landscape. We tested the influence of habitat quality, landscape structure and human pressure on Barbary macaque densities in the largest wild population. Females are philopatric, living all their life in their natal group while all males disperse. Social groups are resident in stable home-ranges of about 3-4km². We estimated habitat quality of forest patches by the vegetation structure and the intensity of human pressure: overgrazing by livestock, cedar pruning by local population, clear-cutting in holm oak formations. Mean density was estimated to be around 9 ind./km², depending on the patch (0.2-23 ind./km²). We found that human pressure had a negative impact on densities while density responded positively to the increase of patch size. The survival of several small populations is severely compromised. As the Moroccan Middle Atlas is the main reservoir of this endangered species, we recommend changing forestry practices, reducing overgrazing within forests and stopping clear-cuttings in holm oak formations. Strict philopatry of females living in large cohesive groups on stable home ranges, and strong reliance on mature forests, seem to be key factors that predispose the Barbary macaque to local extinction because populations in forest fragments are likely to be entirely isolated.

Habitat and connectivity of the black snub-nosed monkey (*Rinopithecus bieti*) populations in Yunnan: a climate change scenario

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During the past 50 years the climate zonation of Yunnan Province, China, has shown a shift towards higher altitude and higher latitudes (Chen et al.2008). In the same time, human population increase led to the encroachment of intensive agriculture and cities on more natural areas. The black snub-nosed monkey (*Rinopithecus bieti*) is an endangered species of China endemic to Yunnan. It has 13 discrete population patches, totalling about 1,500 individuals (Long et al.1994 and 1996). They are distributed across a narrow mountainous region stretching between the Jinsha and Lancang rivers, from Mangkang in Tibet (29020'N, 98038'E) to Yunlong in Yunnan (25053'N, 99022'E). Based on satellite imagery and field surveys the present study analyzes the spatial distribution of the optimal habitats for this species and their connectivity. Results are compared to the population genetic characteristics (Liu et al. 2007) of the population patches. They indicate that some populations are isolated by highways and road networks, dense arable land, and residential areas. Climate and socio-economics scenarios were used to model land cover changes until 2050, predicting that cultivated land will increase of about 66% until 2050. Suitable habitats for the Snub Nosed Monkey will be reduced by 15%. Patch connectivity is currently under study using a least cost distance approach.

Chen JG, Xie MN, 2008. The Analysis of Regional Climate Change Features over Yunnan in Recent 50 Years. Progress in geography. 27(5):19-2. [in Chinese]
Long YC, Kirkpatrick RC, Zhong T, and Xiao L.1994. Report on the distribution, population, and ecology of the Yunnan snub-nosed monkey (*Rhinopithecus bieti*). Primates. 35:241-250.
Long YC, Kirkpatrick RC, Zhong T, and Xiao L.1996. Status and conservation strategy of the Yunnan snub-nosed monkey (*Rhinopithecus bieti*). Chinese Biodiversity.4(3):145-152.
Liu ZJ, Ren BP, Wei FW, Long YC, Hao YL & Li M. 2007. Phylogeography and population structure of the Yunnan snub-nosed monkey (*Rhinopithecus bieti*) inferred from mitochondrial control region DNA sequence analysis. Mol. Ecol. 16 (16): 3334-3349.

About the effect of artificial and natural barriers on space use and movements of four large African carnivore species: implications for spatial co-existence among competitors

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The effects of human-induced habitat modification on ecosystems and on the long term viability of single species have become a major topic in conservation biology. Since human impact on natural ecosystems is likely to increase in the future, it is necessary to understand how human activities influence i) species' spatial behaviour and ii) spatial equilibrium among sympatric species.
In this study we compared the effects of an artificial (fence) with a natural (river) barrier on space use and movement patterns of four sympatric African carnivore species. Long-term data on space use and movement were obtained using GPS radio collars on lions (*Panthera leo*), spotted hyenas (*Crocuta crocuta*), African wild dogs (*Lycaon pictus*) and cheetahs (*Acinonyx jubatus*) in the Okavango Delta, northern Botswana. Our results showed that lions and cheetahs were restricted in their movements and space use by the fence, while sympatric spotted hyenas and wild dogs were unaffected by the fence and repeatedly crossed it. In contrast, movements by these same species across the river were symmetrically inversed with the river being comparatively permeable to lions and cheetahs while representing an impermeable barrier to spotted hyenas and wild dogs. We conclude that the permeability of a barrier is species-specific and barrier-specific. Within species, barriers may for example affect dispersal, gene flow, and ultimately population dynamics and viability. Furthermore, since different barriers affect species differently, artificial barriers such as fences may shift the spatial equilibrium between species, for example by excluding some species but not others, and ultimately their co-existence.

Refugee species conservation – the European bison as an example

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Refugee species can be defined as those that can no longer access optimal habitat, but are confined to suboptimal habitats, with consequences of decreased fitness and density, and attendant conservation risks. Refugee species may be difficult to detect in the absence of information on prior habitat use and fitness, and their observed ecology will be constrained by the habitat limits forced on them. Identification of refugee species, characterization of pre-refugee ecology and the restoration of such species to optimal habitat is critical to their successful conservation. European bison, the largest terrestrial mammals in Europe, after extermination in the wild in 1919, were restored in the wild from captive survivors and nowadays occur in 30 free-ranging populations in Eastern Europe. European bison is typically managed in forest habitats. However, its evolutionary background, dental morphology, neonatal behavior, diet and microhabitat selection are characteristic of a grazing species inhabiting open, grass-rich habitats. So, European bison is probably an example of a refugee species. We hypothesize that a combination of increasing replacement of open steppe by forest cover after the last glacial period and increasing human pressure forced bison into forests as a refuge habitat. This process was then reinforced through active management of bison in forests as managers committed themselves to the "bison as forest species" paradigm. Finally, other potential refugee species suggest that the phenomenon of refugee species might be widespread and likely to increase under global change and that conservation planning should develop strategies to take this into account.

Bat fatalities at wind farms. A regional-scale approach

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Current expansion of windfarms across Europe requires to identify areas of potentially high impact on bats. Modelling may help to implement such sensitivity maps limiting the number of surveys needed to cover large areas. To evaluate the potential impact of windfarms on the bat community at regional scale we realized a combined habitat suitability map for two species especially at risk of collision, *Nyctalus leisleri* and *Pipistrellus pipistrellus*. The habitat suitability models were produced for the Molise region (central Italy) applying the maximum entropy algorithm on all available records for the species in the region. Species ecological requirements proxies were derived from digital layers (IV and V level resolution Corine Land Cover, 30-m resolution Digital Terrain Model, and 10-m hydrographical grid) using ArcGis 10. Suitable areas for both species and a 150 m buffer around turbine locations were then overlapped to define most vulnerable areas for planned and existing windfarms. Models for both species were statistically robust (AUC = 0.80 for *P. pipistrellus* and 0.83 for *N. leisleri*). Suitable areas for both species covered the 41% of the regional surface. The 63% and 73 % of the total surface interested by existing and planned windfarm in the region fall within suitable areas for both species. These results highlight the potential threat posed by both existing and planned windfarms to the bat community of the region, both in terms of habitat loss and collisions.

Assessing habitat connectivity of the lesser horseshoe bat using graph theory to explain its distribution

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The lesser horseshoe bat, *Rhinolophus hipposideros* was formerly widespread and quite common in north-western Europe, but has undergone a dramatic decline from the 1960s. The main hypothesis for this decline is a change of habitat quality. Recent works have stressed the importance of good connection between roosts and foraging areas by tree lines and well-structured hedgerows. Thus, landscape connectivity is assumed to be a key-factor for population sustainability. The present study is based on a case study in Franche-Comté (France). Its purpose is to model the distribution of the lesser horseshoe bat and to characterize the functional connectivity of its habitat. Graph theory is used efficiently in landscape ecology as a framework to model landscape connectivity (Galpern et al., 2011). In such approach, habitat patches defined as optimal for the focal species are considered as the nodes of a network. Connections between nodes are set up from ecological assumptions concerning the movements of the species within the landscape. The graph resulting from these connections allows quantifying the connectivity by means of different metrics. In the present case, patches were defined as composite objects requiring both places of potential roosts (i.e. small villages) and wooded environment. Among the different types of graph, we focused on the minimal planar graph, where all pairs of nearby patches are linked by the least-cost distance. This graph allowed computing several patch-based metrics including a parameter of dispersal distance. They were included in a species distribution model as explanatory factors in addition to other potential factors impacting movement and distribution as light pollution.

Galpern P., Manseau M. & Fall A. (2011) Patch-based graphs of landscape connectivity: A guide to construction, analysis and application for conservation. Biological Conservation, 144, 44-55.

Modeling the occupancy of sympatric carnivores in a Mediterranean ecosystem

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Site occupancy provides a reasonable estimate of population status and trends, and it also provides an unbiased, cost-effective alternative method for large-scale, multispecies monitoring programs. In this study, we used camera-trapping data to determine carnivoran occupancy and associated environmental factors in Serra da Malcata Nature Reserve, Portugal. The study was intended as a precursor of further long-term multispecies monitoring programs. We estimated carnivoran species occupancy using a likelihood-based method, using the software PRESENCE. The major conclusions of the study were: 1) fox occupancy tends to be independent of environmental factors, 2) stone marten occupancy is related with habitat variables, landscape structure and small mammal abundance, 3) common genet occupancy is related to broad leaf formations and prey density, and 4) mongoose occupancy is higher in extensive areas of shrub habitats. Methodologically, we demonstrated the importance of modelling detection probabilities for species with low or variable detection rates. In the future, monitoring programs could benefit from incorporating estimates of detection probabilities into their design and analysis.

Poster Communications

Bats Occupancy: "montados" vs. Exotic forest plantations, does it make a difference?

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Thousands of years of human intervention have shaped the Mediterranean landscape and made this region one of the biodiversity hotspots of the world. Nowadays, several threats peril the biodiversity of this region: land abandonment, introduction of exotic species, habitat modification and destruction, amongst others. The typical agro-forestry system known as "montado" in Portugal and wheat cropland were replaced by exotic forest plantations, mainly eucalypt *Eucalyptus globulus*, over the last 30 years, which covers nearly 26% of national territory and is subject to intensive management. Eucalypt plantations have a typical low plant diversity and complexity which is associated with impoverished fauna. In Portugal, studies on vertebrate biodiversity in single-species stands have provided evidence for negative impacts on avifauna and reptiles. In this study, we compared the bat species richness and occupancy between "montado" and eucalypt plantations (with different age stands and in clear-cut areas), transects of 1 km were conducted using an ultra-sound detector. Eleven species were detected and "montado" had the higher number of bat passes and species richness in contrast with the clearcut areas. We assessed the species occupancy using a likelihood-based method, using the software PRESENCE, for the most common species, like *Pipistrellus kuhli*. The probability of occupancy for the different species was most influenced by local-site variables when compared to landscape variables. Further studies are needed to investigate the bat use of the different habitat covers as well as the dispersal.

Spatial dynamics of *Apodemus agrarius* in a naturally fragmented landscape: islands of the river Tagliamento, NE Italy

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Landscape fragmentation implies a patchy distribution of resources and is well known to affect the spatial behaviour of small mammals. This study investigated the influence of landscape fragmentation on the spatial behaviour of the Striped field mouse (*Apodemus agrarius)* across the floodplain of the island-braided River Tagliamento in Italy. The aim of this investigation was to see whether males used larger home ranges with a larger number of core areas on islands than in the continuous riparian forest as a result of lower local densities and a patchy distribution of food and receptive females on the islands. Twenty-two male mice were radio-tracked in riparian forest and on islands over a period of 10 days and nights. In accordance with our hypothesis, home ranges were smaller in the riparian forest, but the numbers of core areas were not higher on islands. The size of the home ranges of the males was affected by the local density of receptive females and not by food resources.

Importance of river islands in mammal dynamics of the river tagliamento, ne Italy

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Recent research identifies the need for a new approach in studying the ecological dynamics of natural rivers, considering them as real landscapes and demonstrating the importance of their conservation for maintaining the vitality and the biodiversity of surrounding habitats. The aims of this study were to explore the composition of the mammal community inhabiting the banks and the islands of the island-braided River Tagliamento and to assess the role islands play in the seasonal dynamics of carnivores and small mammals, using a landscape ecology approach. Methods included seasonal surveys and live trapping of the banks and of 18 islands. Results proved the occurrence of 20 terrestrial and semi-aquatic mammals, including 16 species recorded on islands. Carnivores (*Vulpes vulpes* and *Martes foina*) visited islands independently of their size and isolation and their abundance on islands was higher in autumn and winter, therefore suggesting islands might play an important role during juvenile dispersal. Islands were inhabited by three species of mice: *Apodemus flavicollis*, *Apodemus agrarius* and *Apodemus sylvaticus*. Preliminary results indicate islands provide suitable habitat for small mammals but their seasonal dynamics appear to be regulated by fluvial dynamics and inter-specific competition rather than by landscape characteristics.

Landscape, water vole and common buzzard populations: do they correlate?

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Since the 1970s, changes in agricultural practices in French mountain areas have produced large homogeneous grassland ecosystems. This has led to population outbreaks of a grassland rodent, the fossorial water vole (*Arvicola terrestris*) which causes severe damages on harvests and economic losses. Predators are believed to be an important regulating factor of the water vole population dynamics. During 8 years, *A. terrestris* populations and their diurnal predators were monitored on 5 study sites in Auvergne. Here we focus on the common buzzard (*Buteo buteo*), the most abundant predator locally, and we examine if this species responds to vole population and landscape feature variations. Analyses were performed using generalized linear mixed effect models. Results showed positive relationships between *A. terrestris* and *B. buteo* densities in autumn without time-lag and in spring with a time-lag of one year. Furthermore, large abundances of common buzzard were associated with an important number of patches of forest and small size plots of grassland. In the literature and compared to open grassland, those areas have lower population densities and smaller fluctuations of *A. terrestris* in average. However, although our results were suggestive, here we failed to detect such a difference statistically, probably due to the relatively small sample size used in our study. This study confirms that the common buzzard favours fine grain landscape mosaic of wood and grasslands and that current or past abundance of water voles modulate the common buzzard foraging strategy. This has important consequences in term of pest control and biological conservation.

Effects of edges on small mammals communities in Dinaric beech-fir forest

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Small mammals were studied in Dinaric beech-fir forest, their edges, and adjacent meadow in the mountainous region in the central continental part of Croatia. Mammals were collected with pitfall traps along transect extending 60m from the edge into a forest interior and 60m into a meadow, and also along natural and human-induced forest edges. Abrupt edges were created during the construction of the highway, pipeline and transmission lines during different time periods. Therefore, natural process of succession has caused changes in vegetation structure and soil pedological properties, especially in patches of forest clearing. Small mammals were surveyed within the carabid beetle fauna study at 16 sites from April until November 2009. In total, 112 small mammals were captured. Species richness, abundance and diversity were significantly higher along abrupt edges than in the forest interior, which might be caused by the edge effect and particularly higher invertebrate prey offer. Successional changes in oldest clearing patches (under transmission lines) have caused expanding of ecotone and increasing abundance and diversity of small mammals. However, opposite trends were observed in youngest clearing patches (under pipelines), possibly due to scarce vegetation and karstic soil structure, and enhanced predation. Species richness and abundance of small mammals were higher in the forest sites than in the meadow. Abundance and diversity of small mammals vary seasonally in open habitats, most likely due to the vegetation growth causing widening of the ecotone zone.

Structure and diversity of small mammal communities of lowland forests in the rural central European landscape (case study from the Czech Republic)

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The aim of the study was to assess the impact of selected forest community types on the structure and diversity of small terrestrial mammal communities (SMC) in the intensively managed rural landscape of South Moravia. A total of 15 biotope types differing in their tree species composition, stand age, succession stage, herb layer character and composition, potential food supply and management were defined at three research plots. Over four years of monitoring a total of 11 small mammal species of differing associations to forest biotopes were identified, out of which only three were eudominant (D>10%). In general, *Apodemus flavicollis* (51.5%) was dominant, in fruiting tree stands its abundance amounted to over 80%. Younger stands with a well-developed herb layer were dominated by *Myodes glareolus* (up to 66%). Seven species were represented by less than 1%. Species diversity and community heterogeneity of individual biotopes were assessed with the help of commonly used indexes. Diversity was significantly higher in early succession sites (plantations), which owing to their small area (< 1 ha) demonstrated the ecotone effect. A significant difference between early and late succession sites was monitored in species richness as well. SMC faunistic similarity in individual biotopes was assessed by cluster analysis and species preferences for individual biotopes were confirmed by multi-factorial analysis. We also attempted to determine indicator small mammal species for individual biotopes. The significance of forest habitats in various succession stages proved to be important.

The work was supported by MSM 6215648902 and NAZV QH72075

Session 10 - Circum Mediterranean mammals

Invited & Oral Communication

The mediterranean fruit bat (*Rousettus aegyptiacus*): position and dynamics of range margins.

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The Mediterranean population of *Rousettus aegyptiacus* represent the only ofshoot of the chiropteran family Pteropodidae beyond limits of tropes. We summarized all distributional data and revised its current status in most regions of its Mediterranean range with particular respect to the situation along the range margins in the region. Distribution of *R. aegyptiacus* in the Palaearctic shows three different patterns: (1) supposedly continuous distribution in the Nile valley and delta (mostly linear in the zone of date palm plantations in a narrow belt along Nile), (2) densely patched (or locally continuous) distribution in thermo-mediterranean arboreal zone, in S Turkey, Cyprus, N Levant to central Israel, i.e. 10 to ca. 50 km wide belt along the sea shore, locally with particularly high population densities; and (3) clearly discontinuous distribution in desert zones (Egypt, N Sudan, Arabian Peninsula, southern Iran and Pakistan), characterized by mutually isolated patches of distribution in desert oases and smaller areas of relative humid habitats (southern part of Nile valley, Estern desert oases, western slopes of the Hijaz and Sarawat ranges of SW Arabia, Hajjar Mts. of NE Oman, southern slopes of the Zagros Range in Iran). Detailed fine-scale data on an isolated marginal population in Dakhla Oasis, Egypt, suggests considerable potential of the species for survival in small isolated populations. The dramatic decline documented from 2005 to 2010 in Cyprus, synchronous with expansion of ranges margins in Turkey suggests, at the same time, considerble capacity for range dynamics.

Feeding habits of the golden jackal *Canis aureus*, the mongoose *Herpestes ichneumon* and the Genet *Genetta genetta* L. 1758 in the area of Djurdjura (North of Algeria).

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We studied the diets of three species of carnivores (*Canis aureus* golden jackal, genet *Genetta genetta* and the Mongoose *Herpestes ichneumon*) in the North Slope Djurdjura National Park (Kabylie, Algeria). For this, we analyzed during an annual cycle feces collected. The location and number of feces collected were carefully plotted on a map to indicate places of defecation, but also their characteristics. The diet analysis shows a high elasticity of the plan for the 3 species with a predominance of mammals followed by arthropods and plants. Some seasonal variations are highlighted. The comparison shows that the schemes jackal has tended to take prey mammalian middle while the other two species have a preference for small mammals. The results show and confirm the general nature of the three and opportunistic predators. The low waste reveals the quality of habitat that is its low human impact and / or its richness and prey availability. The jackal collects preferentially the boar in all seasons while the genet is more specialized on the field mouse. Various indices (Shannon-Weaver index, evenness index) were used to reflect the main features of the various species studied.

Low genetic diversity of Eurasian lynx (*Lynx lynx*) from Croatia

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Eurasian lynx (*Lynx lynx*) is one of the most endangered mammals in the Mediterranean region. At the end of the 19th century it has been eradicated from most of the South European habitats, including the Dinaric Mountains. Dinaric population has been established again in 1973 by reintroduction of six animals from Slovakia to Slovenia, followed by their expansion to Croatia and Bosnia and Herzegovina. By rough estimates today there are 40 – 60 animals present in Croatia and population is strictly protected. Besides poaching, habitat fragmentation and lack of prey, loss of genetic diversity due to inbreeding is thought to be one of the causes of population decline in the past 10 years. The goal of this research was to evaluate the consequences of founder effect and inbreeding on genetic diversity of Eurasian lynx from Croatia. In the period from 1980 to 2010 a total of 15 muscle, 30 bone and 15 tanned-skin samples have been collected. It has been confirmed that all analyzed samples from Croatia had the same mitochondrial DNA control region haplotype, identical to the one from the Baltic, Carpathian and reintroduced Swiss populations. Totally 60 Eurasian lynx samples from Croatia had 62 alleles on 20 microsatellites, or on average 3.1 alleles per locus. Allelic richness was 3,049 and the effective number of alleles was 2,113. Observed and expected heterozigosity were 0,435 and 0,490, respectively. Dinaric lynx population showed the lowest genetic diversity out of all researched Eurasian lynx populations.

Poster Communications

The atlas of Moroccan Mammals: a new synthesis.

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In 1986 the "Catalogue des Mammifères sauvages du Maroc" was the first attempt to map the distribution of all terrestrial mammal species living in Morocco on a same grid basis. Twenty five years later, taxonomic changes, population and/or range regression, and knowledge improvement, raised up the need to update this reference. For this second edition we tried to collect the largest set of available data (including Museum collections) thanks to the contribution of Moroccan workers and visitors. The main chapters of the book will deal with identification, distribution, habitat and conservation status of the 105 "historical" species on the basis of texts facing maps that will be issued from a large database (> 10,000 locations) on a 15' x 15' grid (> 5,200 filled grids, 1 for *Gerbillus simoni* up to 239 for *Lepus capensis*). They will be complemented by invited contributions on marine mammals and history of the mammal fauna during the Quaternary, including palaeontological and engraving syntheses. A comprehensive list of references will be added to each chapter. This publication is scheduled for 2012. All additional (published or unpublished) data are urgently welcome.

Interaction bethween common bottlenose dolphin (*Tursiops truncatus*) and marine fish farm in the gulf of Alghero (Sardinia, Italy).

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In this work, we present the results of the first photo-identification study in the Gulf of Alghero (Sardinia, Italy). The objective of this research was to assess, applying mark–recapture technique, the temporal distribution, site fidelity and group dynamics of bottlenose dolphins (*Tursiops truncatus*) in proximity of an offshore fish farm. In this area bottlenose dolphins show an high seasonality with more encounters during Autumn and Winter and no groups sighting during Spring. Prey species movements and interactions with marine fish farm could be potential explanations for the seasonal variation in the presence of bottlenose dolphins. A discovery curve of photographic captures of new permanently marked individuals (n = 22) reach the asymptote. High variability in re-sighting frequencies suggests that some individuals have a high site fidelity while others frequent the study area sporadically. Thus bottlenose dolphins in the Gulf of Alghero appear to be part of a larger, open, coastal population and the North-western Sardinian waters appear to be only a section of a much larger home range for this species. Finally these results can be compared with similar studies carried out along the North eastern coast of Sardinia and confirmed that bottlenose dolphins can frequently capitalize on aquaculture activities in Sardinia Island.

The last of the fallow deer, *Dama dama dama* (L., 1758) of the island of Rhodes, Dodecanese (Greece): an estimate of numbers

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The occurrence of European fallow deer, *Dama dama dama* (L., 1758), on the island of Rhodes, Dodecanese (Greece), is documented since prehistoric times (about 6000 BC). This population can be regarded as the oldest still surviving on any Mediterranean island. Today, it appears to be seriously threatened by poaching and by the continual reduction of the natural areas suitable for its diffusion. The aim of the present paper is to provide a numeric estimate of the extant deer population of the island yielded by empiric methodologies implemented in liaison with the Forestry Service of Rhodes over the course of the last year.

Golden jackal (*Canis aureus*) distribution in Croatia

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During the last 50 years significant fluctuations in golden jackal (*Canis aureus*) population size and distribution was noted in Eastern and Central Europe. First records of jackals in Croatia date from 15th century, but scientific data about their distribution was not systematically collected. In order to determine the current state and provide bases for further distribution monitoring, we analyzed data about jackal hunting management in Croatia from 2007 until 2010. Yearly reports from all hunting units were provided by Hunting Department, Ministry of Regional Development, Forestry and Water Management. They were used to create maps of areas where jackals were recorded and hunted. Jackals were recorded in 297 (27.9%) and shot in 165 (15.5%) hunting units. Based on the analyzed data we estimate that jackals in Croatia are present on at least 17 300 km^2 (31% of total hunting area, national parks not included). In total 70% of all jackals were shot in Mediterranean region (Pelješac Penninsula, Ravni kotari, Dalmatinska zagora), indicating that area has the largest jackal population density. In the continental, north-east part of Croatia we recorded 25% of shot jackals, while other hunting areas with records of hunting were dispersed and indicated low jackal densities. Increase in number of shot animals per year from 2007 (132) till 2010 (790), can be interpreted as a sign of population growth. Grey wolf (*Canis lupus*) and jackal distribution in Croatia significantly overlap in Dalmatinska Zagora and Ravni kotari region, while in the core areas of wolf distribution (Gorski kotar and Lika) jackals were not hunted.

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Session 11 - Aspects of biology, ecology and evolution of *Laonastes aenigmamus* (Rodentia, Diatomyidae)

Invited & Oral Communication

Population Genetics and Distribution of *Laonastes aenigmamus*. Implications for taxonomy, biogeography and conservation.

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Laonastes aenigmamus is the last survivor of a morphologically distinctive Rodent family. It is endemic to the Limestones of the Khammuan Province (Lao PDR) and ecologically strongly specialized. Patterns of genetic structure and signatures of population history (cytochrome b gene) were assessed from the survey of more than one hundred individuals, collected from about 30 localities. Using maximum parsimony, maximum likelihood, Bayesian, network and genetic structure analyses, we inferred intraspecific relationships and tested hypotheses for historical patterns of gene flow within *L. aenigmamus* populations. Phylogenetic analyses reveal a strong phylogeographical structure. Several major geographical clades are identified, each one corresponding to a distinct karst block. Our study gives evidences for strongly isolated populations, between which genetic exchanges have been limited. Genetic distances suggest that *L. aenigmamus* may represent a complex of species and / or sub-species. It represents an exceptional example of micro-endemism for mammals. *L. aenigmamus* is endemic to the Limestones of the Khammuan Province and is ecologically strongly specialized. The common ancestor of all *Laonastes* may have been widely distributed within the limestone formation of the Khammuan Province at the end of the Miocene or beginning of the Pliocene. Most events of karst fragmentation and parallel isolation of populations would have occurred during the Pleistocene or at the end of the Pliocene. The limited gene flow detected between populations from different karst blocks increases the necessity of a strict protection of this rare animal and its habitat.

Laonastes aenigmamus: one species or more ? A cytogenetic study

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For the first time, the karyotype of *Laonastes aenigmamus* has been realized using classical cytogenetic techniques. A karyotypic comparison of six different individuals have been done using classical and molecular (Zoo-FISH) approaches. Surprisingly, three different cytotypes have been identified among these six L. aenigmamus captured in the same area: cytotype 1 and cytotype 2 with 2n = 42 and cytotype 3 with 2n = 40. We show that three or four autosomes are accounting for the differences between the three cytotypes. The involved rearrangements are one Robertsonian fission/fusion and a complex translocation, between cytotypes 1 and 2, one complex translocation and one fission/fusion event, between cytotypes 2 and 3, one Robertsonian fission/fusion, between cytotypes 1 and 3. The probability to be in presence of more than one species is discussed. In addition, the chromosomal homologies between human and *L. aenigmamus* – cytotype 2 have been identified using Zoo-FISH, showing that the twenty two human autosomes are fissioned in forty six chromosomal segments. We find that, while few chromosomal associations are conserved from their eutherian ancestor, a lot of chromosomal associations are specific to *Laonastes*. Our results indicate that *L. aenigmamus* belongs to species with a high rate of chromosomal evolution from the eutherian ancestor.

Pneumocystis (Fungi: Ascomycota) in *Laonastes aenigmamus* (Mammalia: Rodentia): how a pulmonary fungus could help to clarify both host taxonomy and phylogeography

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Pneumocystis spp are airborne transmitted fungal pathogens, well adapted to live inside the lungs of a wide spectrum of mammal hosts, with which they are typically host-species specific. Recent phylogenetic studies on *Pneumocystis* infection in non-human Primates suggest that the high diversity among *Pneumocystis* species probably results from a prolonged process of coevolution with mammal hosts, associated with cospeciation. Thanks to these particular features, *Pneumocystis* species and genotypes could be useful tools to understand taxonomy and phylogeny of their mammal hosts. In this work, we were interested in exploring *Pneumocystis* in *Laonastes aenigmamus*, a rodent which taxonomy is still controversed. For this purpose, lung samples of 85 individuals trapped among 21 localities (karstic zones) of the Khammouan Province (Lao PDR) were obtained. After a molecular detection of the fungus, *Pneumocystis* genotyping was performed by amplifying and sequencing portions of the mitochondrial large and small subunit rRNA genes. Phylogenetic analyses were then conducted with MrBayes and PhyML programs. *Pneumocystis* DNA was found in 73 out of 85 lung samples (85.9%). New and specific DNA *Pneumocystis* sequences were found in these rodents. The phylogenetic analysis conducted with *Pneumocystis* organisms recovered from *L. aenigmamus* and other close rodents seems to confirm that *Laonastes* is the sister clade of the family Ctenodactylidae. Moreover, DNA sequences from *Pneumocystis* organisms harbored within *L. aenigmamus* showed a high intra-specific diversity. Interestingly, the phylogenetic analysis of these *L. aenigmamus*-specific *Pneumocystis* organisms revealed a strong geographical structuring, highlighting the relevance to use *Pneumocystis* genetic diversity as a phylogeographical tool.

Skull Geometric Morphometrics of *Laonastes aenigmamus*

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We present the first populational study using landmark-based geometric morphometrics to analyze the skull variability of *Laonastes aenigmamus*. This exploratory study was carried out on 60 individuals captured from different localities from the Khammouan province (Lao PDR). The study analyses qualitative and quantitative differences on the skull in relation to growth, gender and area localization. The results suggest that there is no sexual dimorphism on skulls. Conversely, differences in shapes are visible between juveniles *versus* adults and senescent specimens. Finally, morphometric analyses suggest that there are two populations corresponding with the North and the South of the distribution area of the species. This last result is congruent with the preliminary molecular phylogenetic analyses.

Anatomy of the gastrointestinal tract and dental ecomorphology of the Laotian rock rat (*Laonastes aenigmamus*)

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While screening the gastrointestinal tract of this intriguing species for helminths, our attention was drawn to the peculiar compartmentalized stomach of this species. Macroscopic examination of several fixed stomachs showed that the stomach has four elongated compartments. The first three compartments are partly folded on themselves making them appear more rounded than the last, pyloric part. The folding partly results from the constriction caused by the strong peritoneal folds originating in the lesser curvature. The texture of the fodder was coarser in the first part of the stomach than in the subsequent three parts. In the fixed specimens, the transition from the stratified squamous epithelium of the esophagus to the glandular epithelium of the stomach was not macroscopically visible. Further histological examination is needed to determine which parts of the stomach are glandular. The unremarkable small intestine terminated into undifferentiated cecum which had no spiraling or taenia. The width of ileocecal end of the cecum was more than twice than that of the cecocolonic end. The ascending colon was looped. In small herbivorous mammals, a high degree of differentiation of the foregut is known to result in the relatively small and undifferentiated hindgut as seen in *L. aenigmamus*.

The masticatory system in *Laonastes aenigmamus*: function and development

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Laonastes aenigmamus presents a unique combination of musculo-skeletal features that represent a mixture of sciurognathous and hystricognathous characters. A recent study on the masticatory muscles in *L. aenigmamus* has demonstrated that this species is the sole member of Ctenohystrica that has retained a sciuromorph type of digastric muscle [1]. Moreover, the pars reflexa of the superficial masseter is present in *L. aenigmamus* despite its sciurognathous condition. Yet, the functional consequences of the differences in jaw muscle architecture and lower jaw morphology remain unclear. As it has recently been suggested that an ontogenetic approach may provide new insights into the relations between the jaw adductor muscles and cranial shape [2], we analyze the development of the skull and jaw musculature in L. aenigmamus using dissections and µCT scans. Moreover, we use simple mechanical models to quantify the functional implications of the different types of jaw adductor organization in representative species within the Ctenohystrica (Rattus, Cavia and Laonastes). Finally we analyze cranial and mandibular shape variation and quantitatively link it to functional diversity to test the hypothesis that the observed muscle architecture evolved in response to functional demands on the jaw system.

References:Hautier L, Saksiri S. 2009. Masticatory muscles architecture in the Laotian rock rat Laonastes aenigmamus (Rodentia, Diatomyidae): new insights into the evolution of hystricognathy. Journal of Anatomy, 215: 401-410.
2. Hautier L *et al*. 2011.- Hystricognathy vs sciurognathy in the rodent jaw: a new morphometric assessment of hystricognathy applied to living fossil Laonastes (Rodentia, Diatomyidae). PLoS ONE, 6(4): e18698. doi:10.1371/journal.pone.0018698.

Placentation in *Laonastes aenigmamus* (Rodentia: Diatomyidae)

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Placenta and fetal membranes of L. aenigmamus were examined by standard histology and immunohistochemistry for comparison with other hystricomorph rodents. The placental disk comprised a labyrinth and spongy zone. It was attached to the mesometrial side of the uterus by a stalk about one-fifth of the diameter of the disk. Immunostaining for cytokeratin (a trophoblast marker) showed that maternal tissue was confined to the stalk plus a small area above it. The yolk sac was attached to the disk but without a fibrovascular ring. The villous part of the yolk sac was folded into the space between the disk and uterine wall on either side of the placental stalk. As a consequence most of the villi faced the placental surface rather than the uterine wall. Unlike in hystricognaths, the labyrinth was neither folded nor lobulated and there was no sign of a subplacenta. These two characters have been related to the reproductive strategy of hystricognaths. Therefore it is noteworthy that Laonastes normally carries a single fetus and likely it is born in a precocial state. In the lack of a fibrovascular ring, folded labyrinth and subplacenta, Laonastes resembles Ctenodactylus, suggesting that these three features are apomorphies of Hystricognathi.

Phylogenetic relationships and taxonomy of cestodes of *Laonastes aenigmamus*

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The morphology and sequences for partial NADH dehydrogenase subunit-1 (Nad1) gene of cestodes from *Laonastes aenigmamus* captured in various localities were studied. All cestodes examined belong to the genus *Raillietina sensu lato* (Davaineidae, Cyclophyllidea). A phylogentic analysis (Bayesian inference) was performed for davaineid sequences obtained from: *Laonastes*, SE Asian murid rodents *(Leopoldamys sabanus, Apodemus agrarius),* an endemic Madagascan nesomyid rodent *(Nesomys rufus)* and a North American cricetid rodent *(Neotoma cinerea).* Several GenBank sequences from bird cestodes were used as outgroups. The phylogenetic analysis revealed two main clades: *Skrjabinia cesticillus* from birds vs. other davaineids. *Raillietina* from *Laonastes*, *Leopoldamys* and *Nesomys* were grouped into a monophyletic lineage, the sister clade of which included other davaineids from birds (genera *Raillietina* and *Paroniella*), together with cestodes from *Apodemus* (*Raillietina*) and *Neotoma* (*Paroniella*). Within the rodent clade, cestodes from *Laonastes* include at least 4 previously unknown species comprising a monophyletic group; one of these species appears to be widely distributed, while the other three occured in one locality only. These results suggest that the davaineid cestodes of *Laonastes* originated from a single host switch from S-E Asian murid rodents. Later, fragmentation and isolation of *Laonastes* populations may have enhanced diversification of the parasites into several species. The davaineids from *Laonastes* and *Leopoldamys* comprised a monophyletic assemblage, also sharing important morphological features: presence of hooks and accessory spines on rostellum and surrounding tissues, but not on suckers. The davaineid cestodes of *Laonastes* are thought to represent an independent and new genus within the *Raillietina* sensu lato.

Laoxyuris laonastii, a new pinworm genus and species parasite of *Laonastes aenigmamus* (Rodentia, Diatomyidae).

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Laoxyuris laonastii n. gen, n. sp. (Nematoda, Oxyuridae: Syphaciinae) is described based on specimens collected from several individuals of the Laotian rock rat, *Laonastes aenigmamus*. If the new species certainly belongs to the subfamily Syphaciinae, which includes a great part of the pinworm parasites of Rodents, the very original characteristics of the male genitalia allows to describe this species in a new genus: *Laoxyuris*. The new species is compared with the pinworm parasites described from the hosts most closely related to *Laonastes*: Rodents of the Family Ctenodactylidae.

Poster Communications

On phylogenetic relationships of the genus *Laonastes* based on studies of the middle ear morphology

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The species *Laonastes aenigmamus* was described as a member of a new rodent family Laonastidae (Jenkins et al., 2005) but later it was identified as a surviving representative of the extinct family Diatomyidae (Dawson, 2006). Using molecular data it was shown that among modern forms *Laonastes* is most closely related to the African family Ctenodactylidae, differing from it morphologically in a large extent. Thus, in the given case visible discrepancy of morphological and molecular-genetic evolution takes place. A study of the middle ear structure is widely used in the phylogenetics. A comparative analysis of the auditory capsule morphology in *Laonastes aenigmamus*, *Ctenodactylus gundi*, and representatives of five families of hystricomorphous rodents has been performed. In *Laonastes*, the auditory capsule has a generalized structure with features indicating a certain morphological specificity. Its construction pattern is the same as in the generalized hystricomorphous rodents (e. g., *Proechimys* or *Octodon*). This similarity has a synplesiomorphic nature and hardly indicates an affinity of the forms compared. In *Ctenodactylus*, the auditory capsule is characterized by a high level of morphological specialization and, at first glance, has nothing in common with that in *Laonastes*. However, some characteristics of capsule specialization are similar in these forms. Therefore the data obtained do not contradict the idea of possible phylogenetic relatedness *Laonastes* and Ctenodactylidae. This study was supported by the RFBR 09-04-01303a.

Morphology of the digestive tract of *Laonastes aenigmamus*

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The rodent has the most voluminous stomach in comparison with all other rodents. The stomach contains up to 70% of the digesta and performs the main role in storing and digesting of plant foods. The stomach consists of sac-like compartments that is enlarged forestomach. The main food of this rodent is the leaves, stems and underground parts of plants, so *Laonastes* is the world's smallest folivorous mammal with foregut digestive system. Its high degree of herbivory is confirmed by various anatomical features: enlarged *ampulla duodeni,* small dimensions of *pars pylorica*, the absence of the gallbladder, the presence of spiral colon, a well-developed gut-associated lymphoid tissue, and the gut mass making up to 25-27% of the entire body mass. Probably, the complexity and enlargement of the stomach are adaptations of the digestive system designed to use the leaves of tropical plants, many of which contain significant concentrations of toxic compounds. Similar patterns take place in the group of marsupials, ungulates, sloths, primates. The high convergence of the digestive system of *Laonastes* was identified with herbivorous marsupials viz. species of Potoridae and Macropodidae families.

Facial musculature and skin in *Laonastes aenigmamus*: new traits to the portrait of the relict form

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An integrated study of facial muscles and skin of *Laonastes aenigmamus* was carried out. In the comparative analysis of the musculature the representatives of Hystricomorpha, Sciuromorpha and Myomorpha were also included. The characters of skin in *Laonastes* are primarily the same as in many other rodents. His skin and epidermis are thin. Hair is mainly integrated in groups, in which the relationship among down-hair and guard hair varies. The sebaceous glands associated with hair follicles and the smooth muscles are found. In the facial muscles of *Laonastes* there are some unique features differentiating him from all other rodents: the intimate connection between mm. platysma myoides et cervicale; the unusual structure of the m. sphincter colli; the weak stratification of mm. cervico-auricularis and their insertion on the occipital crest but not on the dorsal middle line; the absence of typical muscles complex providing the nose mobility. These data are the evidence in favour to the ancient organization of *Laonastes* and can serve as a basis for reconstruction of early stages of morphogenesis of the facial muscles. Our results are in harmony with that of other investigators: this relict rodent belongs to one of the groups which were placed near the source of the wide adaptive radiation of Hystricomorpha and probably not only of their.

Session 12 - Phylogeography

Invited & Oral Communication

Phylogeography of *B. primigenius* during the holocene based on ancient mitochondrial DNA data

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The wild ancestor of the cattle, the aurochs *B. primigenius*, lived in Eurasia during the last 250,000 years, as testified through the fossil record. The animal being cold-sensitive and water-dependent, its populations have probably reacted with retractions and expansions to the cold-warm cycles of the Middle and Upper Pleistocene. In particular, the last two cold maxima might have severely affected the aurochs populations in Eurasia leaving specific signatures in the mitochondrial genomes of extant cattle lineages. In the framework of a close collaboration with archaeozoologists we performed a palaeogenetic study of remains of aurochsen and domesticated cattle from Europe and Southwest Asia (SWA) spanning the last 10,000 years. This study is based on considerable methodological development to overcome the severe problems linked to reagent contamination with bovine DNA. Our recent results question current views of the population structure of the European aurochsen during the Holocene. Moreover, they shed light on some aspects of the domestication process of cattle that can also explain some features of the population structure of extant cattle in Eurasia.

Reticulate evolution and recurrent mitochondrial DNA introgression in hares (*Lepus* spp)

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Non reciprocal monophyly of species for mitochondrial DNA can result from introgression, and hares (*Lepus* spp.) appear to be remarkably affected by this phenomenon. The mitochondrial lineage of the mountain hare, *Lepus timidus*, is shared by several other species, including Eurasian temperate species (e.g. *L. europaeus*, *L. granatensis, L. corsicanus* and *L. castroviejoi*) and North American arctic/boreal ones (e.g. *L. othus*, *L. arcticus*, and *L. townsendii*), suggesting that mtDNA introgression might be generalized. However, whether haplotype sharing among species is due to introgression or incomplete lineage sorting requires a detailed knowledge of the history of divergence of the involved taxa. We address this issue by analysing sequences of 14 nuclear DNA fragments (8,196 bp) and two mtDNA fragments (1,113 bp) from 50 specimens that represent 11 hare species from Eurasia, North America and Africa. Using a combination of coalescent-based methods we could not reject incomplete mtDNA lineage sorting among *L. timidus*, *L. arcticus*, *L. othus* and *L. townsendii.* We could however demonstrate mtDNA introgression from *L. timidus* into four southern European species (*L. europaeus*, *L. granatensis*, *L. castroviejoi*, and *L. corsicanus*). In the case of the two sister species *L. castroviejoi* and *L. corsicanus*, this resulted in the complete replacement of the aboriginal mtDNA lineage, presumably after an ancient hybridization event affecting their common ancestor during the Pleistocene. By analyzing over 700 samples from all over the Iberian Peninsula, we show that *L. timidus* mtDNA is frequent and sometimes even fixed in northern populations of the three hare species occurring there. It is noteworthy that mtDNA introgression is frequent, extensive and seems to occur always from the same donor arctic species, *L. timidus*. Taking apart the selective and accidental demographic causes for this seemingly deterministic phenomenon is a challenge that new sequencing technologies will help meeting.

When an island matches a glacial refugium: the case of Sicilian mammals

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The traditional outlook, until 20 years ago, considered current Mammal diversity of Mediterranean islands as the result of turnover occurred in the Holocene, caused by man who extinguished the old endemic Pleistocene fauna and replaced it with modern species. This scenario stemmed mostly from paleontological research in Corsica and was generalized to all other Mediterranean islands which, accordingly, would share: i) a low endemism rate; ii) some feral and game species; and iii) many commensal small mammals. The outstanding role of man would have produced a monotonous and supersaturated mammal fauna, under the Equilibrium Model of Island Biogeography assumptions. Sicily, although rarely cited, was implicitly assumed to conform this view, because is the largest among Mediterranean islands and very close to Italy. Albeit this scenario is still useful to explain the presence of mammals in the Balearics, Corsica and other islands and, at a first glance, the Sicilian mammals match well too; current phylogeographic research revealed some unexpected patterns. For this reason, we reviewed the existing molecular studies concerning the mammals listed in Sicily; excluded the 7 alien and reintroduced species; molecular research involved 10 out of the remaining 14 species, revealing the striking role of glacial refugia in this area and an earlier than Holocene divergence from continental populations. Such a low-latitude island, located at the end of a long and narrow peninsula, would have stressed the effects of isolation despite its large area and proximity to the continent. An historical hypothesis, i.e. the genetic differentiation in isolation during geological events would thus fit better to species richness and composition of the Sicilian mammals. These new findings focus on the necessity of conservation and taxonomical reconsideration of those genetically distinct insular populations.

Lineage sorting in Eurasian field voles (*Microtus agrestis sensu lato*): a multilocus approach

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Recent studies of mitochondrial and sex-linked nuclear DNA clearly demonstrated the existence of northern and southern lineages of the field vole, sufficiently divergent that they may represent two cryptic species. In addition, within the southern lineage, two mtDNA sublineages were identified in the Iberian Peninsula, suggesting the existence of two glacial refugia in that area. Available data suggests that one of these lineages has a limited distribution restricted to central Portugal. Here we extend these findings through a multilocus approach. We have expanded the sampling to include 133 individuals from 32 localities, mainly in the Iberian Peninsula, and sequenced mtDNA (cytochrome *b,* 1140bp), sex-linked nDNA (two X introns, 654bp; two Y introns, 1138bp) and autosomal nDNA (two exons, 2547bp). Our analysis shows that the mtDNA sublineage identified in Iberia is in fact a distinct third lineage. All seven markers substantiate the presence of three field vole lineages in Europe: northern, southern and “Portuguese”. In addition, we show that the latter has a wider distribution within Iberia than was previously identified. These data provide us with an exciting opportunity to examine lineage sorting around the population-species transition.

Phylogeography of red deer *Cervus elaphus* in central and eastern Europe

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We analysed a fragment of mtDNA control region using over 500 samples of red deer *Cervus elaphus* collected in Belarus, Denmark, Germany, Lithuania, Poland, Ukraine and western Russia and compared our sequences with data from earlier studies on red deer available in GenBank. According to the results of earlier studies, there are three mtDNA lineages of red deer in Europe: western, eastern and North African/Sardinian. The western lineage includes red deer from the largest part of the continent: from Iberian Peninsula and southern France to the British Isles, Scandinavia and some regions of central Europe. The eastern lineage covers southeast-central Europe, the Carpathians and the Balkans. However, until now there were no genetic data on red deer most of central, east and northeast parts of the continent. The results of our analyses filled this gap and showed that the western lineage is dominant also in the central and eastern Europe. However, in the Polish Carpathians, in Ukraine and Russia only the eastern linage was found. We recorded 28 haplotypes of mtDNA including 23 new ones. Most of them belonged to the western lineage. We suppose that the presence of the western haplotypes of red deer in eastern Europe could be a result of past translocations and reintroductions of red deer into the areas where the species became extinct in the 18th-19th centuries.

Identification of the barrier to gene flow between phylogeographic lineages of the common hamster, *Cricetus cricetus*

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In the anthropogenically disturbed habitats, the natural barriers still exist and have to be recognized, as they are important for conservation actions. The areas of phylogeographic breaks within the species are often stabilized in inhospitable regions, which act as natural barriers. Here we describe the area of contact of two phylogeographic lineages of the common hamster (*Cricetus cricetus*) in the Malopolska Upland in Poland. A total of 142 common hamsters were captured during 2005 – 2010. All hamsters were genotyped in 17 microsatellite loci and partial sequences of the mtDNA control region were obtained. No mixed populations with mtDNA haplotypes of both lineages were found. The distance between marginal populations was about 20 km and in the area between no hamsters were found. The PCA analysis was performed on microsatellite data and the greatest change in PC1 scores was found between marginal samples. No gene flow through the barrier was found. The barrier is formed most probably by the presence of unfavourable soils with rocky layers shallow under the surface. This area serves as a sink, as the hamsters cannot survive winter in such conditions. The distance is too large to be crossed within dispersal abilities of single individual, ie there is an estimate of treshold distance of unsuitable habitats which serves as an efficient barrier.

Ancient and recent hybridization between *Myodes glareolus* and *M. Rutilus* (Rodentia)

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Myodes glareolus and *M. rutilus* are small forest Holarctic rodents having a wide sympatric zone (northern Europe, Siberia). Individuals of *M. glareolus* with mitochondrial (mt) genome of *M. rutilus* found in this zone are genetically different from *M. rutilus.* The aim of our study is to reconstruct the history of the sympatric zone formation.
We analyzed 199 cytochrome *b* gene sequences of *M. glareolus* and 110 sequences of *M. rutilus* collected in the sympatric zone. To find modern hybrids 841 individuals of *M. glareolus* have been studied using mt and nuclear DNA markers. Demographic analyses supported the hypothesis of a recent population expansion for *M. glareolus*, *M. rutilus* and individuals of hybrid origin. Estimates of time since expansion were earlier in *M. rutilus* at 13.4 Ka and more recent in the pure *M. glareolus* at 5.9 Ka and *M. glareolus* with mt genome of *M. rutilus* at 8.1 Ka. It is likely that *M. glareolus* had multiple colonization waves to this region. Hybridization between species may have occurred in the South Urals refugium with subsequent migration of *M. glareolus* individuals of hybrid origin northwards in the Holocene. Populations of *M. glareolus* with own mitotype colonized these regions in the second wave of dispersion.
Although we can detect only first generation hybrids our results suggested that the modern hybridization is represented by occasional events within the wide area of sympatry. We succeeded in finding the F1 hybrid which is the only one among the studied voles.

Colonisation history of the Azores archipelago by the house mouse (*Mus musculus*): clues from mtDNA and microsatellites

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The Azores islands constitute the most remote archipelago in the North Atlantic, comprising nine volcanic islands spread along a length of 600 km. The presence of the vast majority of Azorean mammals currently inhabiting the islands was the result of human-mediated introductions. The arrival and settlement of the first human colonists in the 15th century is commonly accepted as the most likely occasion for the introduction of most invasive mammals. The house mouse (*Mus musculus*) is no exception as it successfully colonized all nine islands, quickly becoming one of the most common and widespread mammals in the archipelago. Following a 'phylogeographic' approach, the colonisation history of Azorean house mice was assessed by comparing a total of 239 mitochondrial sequences (D-loop) of mice from all nine islands with mice from potential source areas. The pattern of mitochondrial DNA variation was obtained through a Bayesian analysis that revealed an unexpectedly complex colonisation history. Different islands seemed to have been colonised from different origins and most islands presented evidence of high resistance to reinvasion. The historical link with mainland Portugal was reflected in the pattern of D-loop variation of some islands but not all. For example, there was an unexpected association with a distant Northern European source area on three of the islands. Additionally, 18 polymorphic microsatellite markers were screened to assess the level of population admixture within the archipelago (amount of gene flow) and to detect any demographic bottlenecks.

Pseudocongruece in phylogeographical patterns in Mediterranean North Africa

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The Mediterranean Basin is an acknowledged hotspot for biodiversity yet historical processes that shaped this biodiversity in North Africa remain poorly understood. This study aims to elucidate phylogeographic patterns in the Mediterranean areas of North Africa and to evaluate the relative roles of climatic change, habitat patchiness and geological barriers in structuring patterns of diversity in the Mediterranean ecoregion in North Africa, using new data on an endemic species, the Greater Egyptian Jerboa Jaculus orientalis, and a comprehensive review of data published so far in the region. The Greater Egyptian Jerboa displays a phylogeographic structure into three areas along a west-east axis, corresponding to Morocco and western Algeria; eastern Algeria, Tunisia and western Libya; and eastern Libya and Egypt. Data published for 43 species or species complexes including plants and animals are generally congruent with the west-east pattern of differentiation roughly corresponding to the major mountain ranges (Rif- Atlas, Aures and Cyrenaica), yet the timing of genetic divergence events (inferred from genetic data) appeared highly variable, ranging from 0.1 to 20 My. Several major historical events, which occurred at different times since late Tertiary, like the disconnection of the Betic arch, the Messinian crisis and the Quaternary climatic fluctuations, have likely initiated and maintained the currently observed patterns of biodiversity organization. Collectively these results emphasize the potential of the southern Mediterranean areas to generate and maintain biological diversity since the last Tertiary, which explains its belonging to a major biodiversity hotspot today. Finally we address several points, including uncertainty in time estimates, uncompleteness in geographic sampling coverage and relationships with other biogeographic areas, towards which future studies should be directed.

Continental islands – The biogeography of the East African forest-dwelling mountain rodent *Praomys delectorum*

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Mountain forests in Eastern Africa form archipelagos of specific habitats with particular flora and fauna. Fragmented distribution of specialized taxa has important consequences for their genetic structure with the most important effects on the reproductive isolation of populations and allopatric speciation. In present study, we employed morphological and genetic (nuclear microsatellites and the mitochondrial cytochrome *b* sequences) data to review the status of fragmented populations of endemic forest-dwelling rodent *Praomys delectorum* (family Muridae). This species occurs in a long narrow zone of the mountain chains and isolated massifs, from southern Kenya (Taita Hills), northern (Mt. Kilimanjaro) and eastern (Eastern Arc Mountains) Tanzania as far as southern Malawi (Mulanje Massif). Considering the character of distribution of this species it is possible to employ *P. delectorum* as a model for studying interesting biogeographical tasks, e.g. for the reconstruction of the evolution of mountain biota of East Africa or for the testing of the relationship between genetic variation and the population size (i.e. the size of the "forest island"). Genetic data showed significant genetic differentiation of individual populations. The phylogenetic analyses of mtDNA imply the successive splitting of lineages from the south towards north (especially the southernmost populations are very distinct). Microsatellites show slightly different pattern for some populations and suggest the important role of genetic drift during habitat fragmentation. Classical and geometric morphometry again indicate remarkable variation among populations, which is now analysed in relation with predictions of island biogeography.

Phylogeography of the cosmopolitan genus *Myotis* (Chiroptera) using model-based reconstructions

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The genus *Myotis* (family Vespertilionidae, order Chiroptera) constitutes an attractive model to understand mammalian evolution: a worldwide distribution and high specific richness (more than 100 species which makes it the second mammalian genus in terms of diversity). Because mouse-eared bats show recurrent ecomorphological convergences, it is essential to use molecular characters to infer their phylogenetic relationships. This study aims to infer the phylogeographic history of nearly all current *Myotis* species, using nuclear and mitochondrial DNA information. We produced a dataset of ~130 specimens representing over 90 species and sequenced about 1148 base pairs of the nuclear RAG2 gene and

1140 base pairs of mitochondrial gene CYTB gene. The phylogenetic tree of *Myotis* obtained with probabilistic methods of inference (maximum-likelihood and Bayesian inference), was used as a framework to investigate diversification rates and biogeographic evolution of that genus. The main results include highly different diversification rates in the African and Australian regions, compared to other biogeographic regions, and surprisingly low intercontinental faunal interchanges in this otherwise highly vagile and widespread taxon. Model-based reconstructions of ancestral biogeographic areas suggest that the Oriental region is most probably the cradle of the spectacular *Myotis* radiation.

Evidence of complex phylogeographic structure for the threatened Rodent *Leopoldamys neilli* endemic to limestone karsts of Thailand

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Limestone karsts are highly threatened biodiversity hotspots supporting huge levels of endemic species. Karsts are patchy distributed within Southeast Asia and their isolation from one another give them the features of “islands on the continent”. We have studied the phylogeography of Neill’s Rat *Leopoldamys neilli*, a threatened murine rodent species endemic to limestone karsts of Thailand, in order to assess the influence of its endemicity to karst habitat on its phylogeographic pattern. Two hundred twenty-two individuals of *L. neilli* were collected in 26 limestone karsts throughout the geographical range of this species and were used in this study. Phylogeographic structure and population genetics of *L. neilli* were investigated on the basis of two mitochondrial markers, the cytochrome *b* gene and the cytochrome c oxydase subunit I gene, two nuclear fragments, the β-fibrinogen intron 7 and the intron 1 of the X-linked gene G6pd, and 12 microsatellite loci. Our study gave evidence of a complex and strong geographic structure of the genetic diversity for *L. neilli.* Several highly differentiated genetic lineages were observed throughout Thailand. These results suggest a severe fragmentation of *L. neilli*’s populations, correlated to the fragmented distribution of its habitat and highlight its high endemicity to limestone karsts. In conclusion, this study revealed an unexpected high level of intraspecific diversity within *L. neilli*. These results consolidate the importance to strengthen the protection of limestone habitats and to preserve not only their huge interspecific but also intraspecific diversity.

Mitochondrial DNA variation in weasels (*Mustela nivalis*) from Poland: implications for postglacial colonization of Europe

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There is mounting evidence that some European species did not respond to the Last Glacial Maximum by simply shifting their distributions to Mediterranean regions. These species also survived at higher latitudes, previously considered inhospitable. The majority of phylogeographic studies to date have understandably adopted an approach to sample from as large of a geographic area as possible to infer refugia and postglacial colonization routes. However, recent studies have begun to focus on more localized regions to understand the role of more northern refugia in Europe. In this study, we utilized ~50 archived, museum specimens of weasels (*Mustela nivalis*), which were collected in Poland over the last 50 years. The entire cytochrome *b* gene of the mitochondrial genome (mtDNA) was amplified in four overlapping fragments and these were compared with previously published sequences from European specimens. We identified four distinct lineages in Polish weasels, corresponding to previously identified lineages found on a wider European scale. Therefore, our results strongly indicate that the current distribution of mtDNA haplotypes in Poland stems from multiple glacial refugia. Three of these lineages were widespread throughout Poland, and these lineages had western, eastern and (what we propose to be) Carpathian distributions in a wider European context. Interestingly, we also found a Balkan lineage in southern Poland, indicating that a more southern refugium had a pronounced influence on the postglacial colonization of Europe. This study highlights the importance of localized sampling when inferring postglacial colonization processes and shows the value of utilizing museum collections for phylogeographic studies.

Phylogeography of the asiatic wild ass

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DNA data from ancient skeletal remains are very useful in the reconstruction of phylogenies since they help to avoid certain biases that are intrinsic to the approaches based on genetic data from extant animals. During the Pleistocene and the early Holocene the Asiatic wild asses populated a vast territory reaching from Northern Africa to Eurasia before becoming threatened by extinction. Little is known about their phylogeography. We undertook a palaeogenetic study of the genetic diversity of the Asiatic wild ass during the Middle-Upper Pleistocene and the Holocene by analysing the mitochondrial and the Y chromosomal DNA in ancient and modern bone and teeth remains and modern samples originating from Europe and Southwest Asia. At present, the mitochondrial data that we obtained from ancient bone and teeth samples outnumber the mitochondrial data from extant species in Genbank. Our data resolve the population structure of the Asiatic wild asses and show the existence of seven significantly distinct populations, a result that could assist in devising conservation strategies.

Comparative estimation of genetic originality of the sable in the East and the West parts of distribution area

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The Kamchatka sable - *Martes zibellina kamtschadalica* - was described in 1918 by A.A.Bjalynitsky-Birula and since then is regarded as a separate subspecies. The complete morphological studies on the Kamchatka sable have been done by some researchers (Kuznetsov 1941; Timofeev and Nadeev 1955; Belov and Monakhov 1970). Analasys of the cytochrome *b* gene restriction polymorphism revealed monomorphy (homogenity) of the sable population on Kamchatka, and the originality of Kamchatka population versus Sakhalin, Khabarovsk and Magadan populations - so, the genetic data agreed with the Kamchatka sable subspecies status (Balmysheva et al. 2002). Separation of the Ural sable into the subspecies *M. z. zibellina* Linnaeus, 1758 is also undoubtedly for researchers. Although taxonomic status of the Kamchatka and Ural sable is certain enough, the history of existence of these populations differs and can define their genetic originality. The present study was undertaken in order to reveal and estimate the probable genetic differentiation between these two subspecies. We obtained data on mtDNA control region sequences (495 b.p.) and allele frequencies of 11 microsatellite loci for sable samples from Kamchatka and Northern Urals. A total of 13 control region haplotypes (H=0.91) was identified among 23 Kamchatka specimens, and 35 haplotypes (H=0.96) were found within 67 individuals from Northern Urals. At the same time, a level of nucleotide diversity (π) of Kamchatka sampling was 0.54 %, and (π) of Ural sampling was 2.14 %, i.e. 4 times higher. There were no shared haplotypes among two populations, and pairwise Φ-st value was 0.26 (p=0.000). For 11 microsatellite loci for sample set of 37 Kamchatka sables~~,~~ an average value of expected heterozygosity was 0.706, an average number of alleles for a locus - 7.7. For 71 sables from Northern Urals average expected heterozygosity (0.733), an average number of alleles for a locus (9.4) was evidently higher. Differences between populations were highly significant (Fst=0.14639, p=0.000). Thus, performed analysis confirms not only a high level of genetic differences between the sable populations on Kamchatka and Northern Urals, but also considerably lower genetic variation level of the Kamchatka population. That can be explained by consequences of introduction in Urals of East-Siberian sables in the beginning of 1950th, by high level of natural isolation of a sable on Kamchatka, and, presumably (Balmysheva et al. 2002), by low number of founder individuals, initially inhabited the peninsula. Most probably, all of mentioned factors function simultaneously.

Variability of mitochondrial DNA in beech marten (*Martes foina*) from central Croatia

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Beech (stone) marten (*Martes foina*, Erx. 1777) is found throughout Europe and Central Asia. This mustelid species prefers open landscape, being less dependent on forested habitats and is often found near human settlements. Although beech martens play a role in controlling rodent populations, in urban areas they are often treated as pests. Probably due to stabile and still growing population size throughout its habitat, studies on population genetic of beech marten are quite rare. Most of the data about sequence variation of beech marten mitochondrial DNA comes from research on molecular evolution and research on species-specific primers used for species identification, mostly based on cytochrome b, less often on control region sequence variation. We have analyzed 22 beech marten liver/kidney samples, collected in urban areas of central Croatia. In total, 28 polymorphic sites have been found on 302 base pair mitochondrial DNA control region sequence, representing 8 haplotypes. Two polymorphic sites were a result of insertion/deletion, while other resulted from substitution. The 8 haplotypes showed 2 - 26 pairwise differences resulting in sequence divergences of 0.7%-8.6%. Haplotype diversity (H) was 1.000 ± 0.0137, while the nucleotide diversity (Π) was 0.0343 ± 0.0182. Clear geographical pattern in the distribution of haplotypes in central Croatia was not found. Comparison of 8 Croatian mtDNA haplotypes found in this study with 3 control region sequences deposited in the GenBank (2 from Iberian Peninsula and 1 from undefined European country) revealed no potential matches between haplotypes.

Poster Communications

Where Did They Come From – The Origin Of Sika Deer Population In The Czech Republic

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The sika deer (*Cervus nippon* Temminck, 1838) was introduced to the Czech Republic at the end of 19th and beginning of 20th century. Since its introduction to the enclosure Kluk in 1891 sika deer has established two free-living populations and continued to increase in numbers. However, the exact places of origins as well as the subspecies status of the introduced animals are unknown. The scarce historical sources suggest the introduction from mainland as well as island populations. The origins of the Czech population was studied using two mitochondrial markers – cytochrome *b* and control region. The phylogenetic reconstruction, using neighbour-joining algorithm, maximum-likelihood criterion and Bayesian estimation, was performed on a data set containing Czech samples as well as samples from sika's native areas in Japan and Russia. The results of the analyses of 449 cyt *b* and 447 D-loop sequences yielded phylogenetic trees with nearly identical topology, containing three main haplogroups, *nippon*1, *nippon*2 and *hortul*. The *nippon* haplogroups contained samples from the Czech Republic and Japan, while the haplogroup *hortul* contained samples from the Czech Republic and Far East Russia. The animals belonging to the *hortul* group are related to the mainland subspecies *C. n. hortulorum*, while those from haplogroup *nippon*1 belong to the larger subspecies *C. n. yesoensis* from northern Japanese islands and those from haplogroup *nippon*2 originate from the smaller subspecies *C. n. nippon* living in Southern Japan.

Population genetics of the Egyptian mongoose (*Herpestes ichneumon*) in Portugal

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The Egyptian mongoose (*Herpestes ichneumon*) is one of the most abundant carnivores in Portugal. It was established that it was introduced in the Iberian Peninsula in historical times. However, recent genetic studies concluded that this carnivore suffered a scenario of sweepstake dispersal during the Late Pleistocene sea-level fluctuations. The range of the Egyptian mongoose was restricted to the southern part of Portugal. Nevertheless, some studies concluded that the species was successfully expanding to the north of the country, a phenomenon still ongoing. The Egyptian mongoose's conservation status is "Least Concern" and it is listed in the Portuguese hunting species checklist. Since the species is in expansion and knowing that population dynamics can be shaped by the genetic characteristics and population demography of the species, this study focuses on understanding the micro-evolutionary processes - population structure and landscape genetics - of the Egyptian mongoose. By an analysis combining mitochondrial DNA, Y-linked genes and microsatellites that will reveal the genetic variability of the Egyptian mongoose in Portugal, the main objectives of this study are: comparing the genetic structuring among Portuguese regions with higher mongoose densities and those with lower densities, determining migration mechanisms in relation to the sex and age of the colonizing individuals and contributing to a better knowledge of the species' population dynamics relative to landscape in Portugal. The recent range expansion of this carnivore will be unraveled through this first study focusing the population genetics of the Egyptian mongoose in Portugal.

Intra-species molecular-genetic variability in *Marmota bobak* (Marmotinae, Sciuridae, Rodentia)

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Steppe marmot (*Marmota bobak*) is a single marmot species having a distribution both in Europe and Asia. Changes of M.bobak area had occurred due to nature and anthropogenic influences. At the recent time the area is partly fragmented. Though steppe marmot is an object of intensive studies as a commercial species, some diseases carrier and a component of biodiversity, its intra-species genetic variability is not clear yet. Subspecies systematic and borders between subspecies are disputable. A study of nDNA variability by inter-SINE-PCR method showed an absence of ordering genetic structure in *M.bobak* (Brandler *et al*., 2010). We used nucleotide sequencing of mtDNA control region (about 1000 bp) for an elaboration of this question. A sample of M.bobak includes 43 specimens from 9 European and Asian localities. Specimens of M.baibacina and M.sibirica were used as outgroup. A cluster analysis (NJ, MP, UPGMA) showed separation of M.bobak specimens into 5 clusters. Marmots from Kazakhstan are distinct from others. This sample is separated into two groups. One of them is the basal cluster in M.bobak tree and another is clustered with other specimens as separate branch. This result may be explained or by multiple fluctuation of the area with fragmentation of its different parts or by an anthropogenic re-introduction of steppe marmots from other Western localities. Separate clusters are formed by Ukrainian, Eastern Orenburg region and Trans-Volga marmots with segregation to right- and left-riverside clusters. This work is supported by RFBR and the Program of RAS "Biodiversity and Dynamics of Gene Pools".

Early diversification of African pouched mice of the genus *Saccostomus* (Cricetomyinae) in Africa – detailed pattern based on mitochondrial sequences and morphology

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Pouched mice (*Saccostomus* sp.) are common species of rodents from an antique genus distributed in savannah and cultivated areas from Southern to Eastern Africa. In spite they are intensively studied in several aspects of their biology, the taxonomy of the genus still remains obscure. Until now, two species are recognized, *S. campestris* and *S. mearnsi.* Nevertheless, it seems that they might represent two species complexes based on karyology and available DNA sequences (Corti et al. 2004). In our study, we performed a large scale intensive sampling covering most of the geographic range of the genus and used the sequences of mitochondrial marker (cytochrome *b*) to analyse its phylogeographical history. The results reveal three main very divergent clades (divergence dated to late Miocene) corresponding to two known species complexes '*mearnsi*' and '*campestris*', and a new sister lineage to '*mearnsi*' from northern Kenya. The '*campestris*' group is composed of three mitochondrial clades that have probably differentiated during Plio-Pleistocene. The south-African clade is separated from the east-African clade by the Zambezi River, while the third lineage is represented by population east of Lake Malawi in southern Malawi (and probably also in northern Mozambique). Morphological analyses (in progress) and detailed genetic data from nuclear markers (e.g. microsatellites) from the areas of possible secondary contacts between lineages are necessary to prove the presence of different species of *Saccostomus* and reproductive barriers among them.

Development of non invasive genetic identification methods for the pyrenean desman (*Galemys pyrenaicus*) and first study of its genetic structure

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The Pyrenean desman (*Galemys pyrenaicus*) is probably one of the most threatened European mammal species. This small insectivorous and semi-aquatic species is endemic to the Pyrenean Mountains and of the north of the Iberic Peninsula. Many biologic aspects of this species are currently suffering from a major lack of information, particularly those concerning its genetics. Therefore the implementation of conservative efforts for the Pyrenean desman remains extremely difficult. In order to improve the knowledge of this vulnerable species and notably, to better understand its distribution area, the first aim of our research was to develop non invasive genetic identification methods based on faeces. The second aim was to have a first look at the phylogeographic structure of the Pyrenean desman. The identification methods were developed on the basis of the sequencing of a small mitochondrial DNA (cyt b) fragment as well as a RFLP method. These approaches led to the identification of the Pyrenean desman and to the differentiation of the latter from two other species living in the same type of habitat, the white-throated dipper (*Cinclus cinclus*) and the water shrew (*Neomys fodiens*). Two haplotypes were found in the studied Pyrenean populations but no phylogeographic structure could be established. A dozen of microsatellites markers were also developed during this work and 5 of these were found to be polymorphic. The results of this preliminary work tend to show a low genetic diversity for the Pyrenean desman but this result needs to be confirmed in the future with a more extended and complete study.

Colonisation of the baltic region by field voles since the late Vistulian (Weichselian) stadial

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Entire mitochondrial cytochrome *b* gene sequences have been obtained from field voles *Microtus agrestis* in the countries surrounding the Baltic Sea, particularly Poland and southern Scandinavia. Bayesian genealogy sampling was used to analyse the new data together with a larger group of sequences from the whole range of this Eurasian rodent. The geophysical manifestations of climatic events, such as the timing of glacial retreat and post-glacial changes in sea level, are well documented in the area around the Baltic. They are used here to refine the calibration of the range-wide field vole cyochrome *b* genealogy that was derived from similar events in the British Isles (Herman and Searle, *Proc R Soc B*, in press).

Unexpected genetic diversity among the *Crocidura obscurior* west african pygmy shrew complex (Soricomorpha, Soricidae): phylogeny and phylogeography

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The aim of this study is to provide a better understanding of the taxonomy, genetic relationships and biogeography of the West African Pygmy Shrew (*Crocidura obscurior* group) which inhabits tropical rain forests of West Africa (Liberia, Guinea, Ivory Coast, Ghana and Sierra Leone). Recent studies based on molecular data have confirmed the monophyly of the genus *Crocidura* and have brought precisions about phylogenetic relationships between species. Nevertheless, a lot of taxonomic problems remain unresolved, leading to the existence of several species complexes. The West African Pygmy Shrew is one of the most abundant shrew species in West African rain forests. The description of the genetic structure of this complex will provide a better understanding of shrew biodiversity, speciation processes and biogeographic patterns in this area. Our study includes 153 specimens of *Crocidura obscurior* from Guinea, Ivory Coast and Liberia. We use an alignment of 3027 base pairs of both mitochondrial (16S, cytochrome oxidase I and cytochrome *b*) and nuclear (STAT) genes. Our results show the existence of four main clades, with some of them coexisting in sympatry in the same habitat. Calculations of genetic distances show values much higher than those allowing discrimination between species. Phylogenetic relationships between clades and genetic structuration within each of them allow us to infer biogeographic patterns.

Phylogenetic status and genetic diversity of raccoon dogs in Eurasia.

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In the raccoon dog (*Nyctereutes procyonoides*), six endemic subspecies are distributed longitudinally in the various parts of East Asia including the Korean peninsula. Although the previous study using the chromosomal number and comparative skull morphology suggested that all Japanese populations are distinct from others, the phylogenetic status of this species has not been established. Here, we determined the sequences of mitochondrial DNA genes (2,779 bp) including cytochrome oxidase I (COI), cytochrome *b* (cyt *b*), and control region of the raccoon dogs from Korea, Japan (Honshu and Shikoku in Hokkaido), Russia, China, Vietnam, and Finland to examine the phylogenetic intraspecific relationships. The phylogenetic trees drawn by mtDNA haplotypes were grouped into two major clades that consisted of the Japanese population and other continental populations. This sugests that Japanese raccoon dogs are relatively more differentiated from other raccoon dog subspecies, and the mean sequence divergence between the two clades was 2.4% for cyt *b*. In addition, it is inferred that Japanese raccoon dogs probably migrated from the continental populations during the Middle Pleistocene, following the roughly estimated divergence time (0.59 ~ 0.67 MYS). Although, the Korean raccoon dog is a common species, it has low genetic diversity (cyt *b* = 0.08%), which might be influenced not only by climatic oscillations but also by anthropological activities. To understand the detailed phylogenetic patterns and evolutionary history of raccoon dogs, analyses of other genetic markers such as microsatellites and nuclear DNA sequences will be necessary.

Genetic structure of moose *Alces alces* population in Europe

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We studied over 500 tissue samples of moose *Alces alces* from 10 European countries: Belarus, Estonia, Finland, Lithuania, Latvia, Norway, Poland, Russia and Ukraine. Based on analyses of 548 bp fragment of mtDNA control region, we found 18 haplotypes. All except one clustered with other European moose sequences found in GenBank. Results of genetic structure analyses showed that there are four mtDNA subpopulations of moose in Europe: two in Sweden and Norway, one in central Poland, and one (the largest) in eastern Poland, Belarus, Estonia, Finland, Lithuania, Latvia, Norway, European part of Russia and Ukraine. We also performed preliminary analyses using 14 microsatellite loci and 98 moose samples from four regions, where refugia of moose probably existed at the end of 19th century (NE Poland, Belarus, Latvia, Estonia). Genetic distances (Fst) among moose from these areas were small and the largest values of Fst were found among moose from NE Poland, Belarus and Estonia. There were two or three microsatellite subpopulations in these four regions. The first one consisted of moose from NE Poland, the second included individuals from Polesie (E Poland and W Ukraine), Vitebsk region (Belarus), Estonia and Latvia. The third one (the smallest) consisted of several moose from Belarus. Analyses of more samples are needed to confirm the existence of that last subpopulation.

Analysis of mitochondrial DNA from ancient bovine remains to elucidate holocene phylogeography of *B. primigenius*

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Bos primigenius, the wild ancestor of the cattle called aurochs, populated Eurasia during the Upper Pleistocene before being domesticated in the course of the Neolithic revolution at the beginning of the Holocene, roughly 10,000 years ago. The aurochs being a cold-intolerant and water-dependent animal, its populations were affected by the Late Pleistocene ice-age cycles. This should have shaped the population structure. Therefore, we performed a palaeogenetic study of remains of aurochsen and domesticated cattle from Europe and Southwest Asia (SWA) spanning the last 10,000 years. This study required considerable methodological developments to overcome the severe problem of reagent contamination with bovine DNA that distorts ancient DNA analyses from bovine remains. Our recent results shed light on the population structure of the European aurochsen during the Holocene that can also explain some features of the population structure of extant cattle in Eurasia and on the domestication process of cattle and question current views.

Evidence of two highly divergent genetic lineages on the African buffalo (*Syncerus caffer*): implications for its conservation

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Until this day, a small number of studies concentrated on the phylogeography of the big African mammals at a continental scale, most reduced to a weak sampling. Thus, the consequences of the past fragmentations on the genetic diversity remain weakly studied. Nevertheless, the available data tend to indicate the existence of a general phylogeographic pattern applicable to the big mammals. There would be three different genetic lineages, structured geographically between West, East and South Africa (ex. kob (*Kobus kob*), giraffe (*Giraffa camelopardalis*), warthog (*Phacochoerus africanus*)). We thus tried to determine in which measure the phylogeographic pattern of the African buffalo corresponds to that of the other species of African mammals studied until now. A total of 773 samples distributed on the whole distribution area of the buffalo, including samples of the four recognized subspecies defined on morphological characteristics, were used and sequenced for the D-Loop (mDNA). An important phylogeographic structure has been revealed, showing a clear separation between the individuals of the Southeast and Centralwest Africa. This separation seems to be directly correlated to the presence of the Rift valley. Furthermore, our analyses indicate that these two lineages would have differed during the Pleistocene, which is coherent with previous studies of other African species. In conclusion, these results would support the existence of only two subspecies: *S.c.caffer* and *S.c.nanus* (including *S.c.brachyceros* and *S.c.aequinoctialis*), which have important consequences on the conservation strategy to employ.

Mitochondrial diversity in red deer, *Cervus elaphus* in Poland

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We analyzed DNA sequences of 750 bp long fragment of the mitochondrial control region (CR mtDNA) of 327 red deer samples from 30 sampling sites in Poland. 35 CR mtDNA haplotypes were found. Phylogenetic trees constructed by nieghbour-joining and maximum likelihood methods revealed two main, highly supported clades: the Western (26 haplotypes) and the Eastern (9 haplotypes). 16 out of total haplotypes were singletons and they were found in 12 sampling sites. Haplotype diversity ranged from 0.00 to 0.87 and nucleotide diversity ranged from 0.00 to 1.77. Both measures of mtDNA diversity did not show a significant increase with longitudinal position of populations (nucleotide diversity: $R^2 = 0.05$, $p = 0.25$; haplotype diversity: $R^2 = 0.03$, $p = 0.33$). The correlations with latitude were not significant, either (haplotype diversity: $R^2 = 0.01$, $p = 0.74$) or close to significant (nucleotide diversity: $R^2 = 0.13$, $p = 0.05$). There were only two sampling sites where haplotypes from both lineages were present. We conclude that numerous translocations did not influence on the phylogeographic pattern of the red deer in Poland.

Session 13 - Systematics and Barcoding

Invited & Oral Communication

Cryptic lineages or cryptic species in European barcoded bats (Chiroptera)?

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Bats are the second most speciose order of mammals, and species are often difficult to discriminate by their morphology. Other independent characters such as DNA nucleotides are valuable in resolving identification problems of cryptic species. In an initial survey of mtDNA COI barcodes of nearly all bat species known to occur in Europe, multiple major cryptic lineages were discovered in several species. Some of these lineages diverged by over 10% K2P genetic distance within what is currently treated as a single species. However, as mitochondrial lineages in general are transmitted clonally by females only and are prone to horizontal transfer in hybridizing taxa, it is unclear whether these cryptic lineages represent genetic variants in an otherwise panmictic population, or whether they flag the existence of cryptic species within the European bat fauna. To test this important issue for biodiversity conservation, we used 17 loci of biparentally-inherited, nuclear markers to estimate the amount of potential gene flow between individuals bearing different barcodes in a European species of *Myotis*. We genotyped 344 individuals from 21 populations sampled across Western Europe, and inferred the amount of genetic admixture with Bayesian assignment of individual nuclear genotypes. Results suggest that most groups of individuals identified by different barcodes, even when found in sympatry, do segregate in distinct nuclear gene pools, supporting the existence of several cryptic, biologically isolated species within the European bat fauna.

North palearctic serotines, molecular study

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There are a number of poorly studied forms and difficulties in morphological identification of serotines (*Vespertilionidae*,*Eptesicus).* Molecular methods are efficient in revealing cryptic diversity and recovering species-level phylogenetic structure. We tried to assess molecular diversity of serotines from the former USSR, making emphasis on *E. serotinus* / *E.nilssonii* introgression problem and *E. serotinus* subspecies structure, using *Cytochrome b* mitochondrial gene as a main marker. Cyt*b* data confidently discriminate two haplogroups in *E. serotinus*. The first is usual for the European part of species distribution eastwards to Ukraine and westernmost Russian districts. This haplogroup originates apparently from *E. nilssonii* haplotype introgressed about 2 MYA. The second haplogroup, in our opinion native to *E. serotinus*, is typical for the rest of the species distribution. We used additionally 3 nuclear genes (*THY* and *SPTB* autosomal, *UTY* Y-linked). All three genes did not point to any ongoing hybridization, and cluster in groups according to species. Also no genetic isolation between population, carrying haplotypes from European and south-eastern groups was observed. For a long time *E. serotinus* populations with sand-colored pelage and less pigmented skin were considered as very distinct subspecies or even species. *Cytochrome b* did not reveal any distinction, corresponding to these forms. Nuclear genes data also indicates no barrier to gene flow, but pronounced phylogeographic structure points to past such barriers. In this work, we also assessed the position of the poorly studied species *E. bobrinskii* and *E. gobiensis* on the species tree and genetic distance between them. Surprisingly, differences between these species fall into intraspecific range.

DNA barcoding of African fruit bats (Mammalia, Pteropodidae). The mitochondrial genome does not provide a reliable discrimination between *Epomophorus gambianus* and *Micropteropus pusillus*

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Sequences of the mitochondrial *COI* gene have been shown to be useful for species identification in various groups of animals. However, the DNA barcoding approach has never been tested on African fruit bats of the family Pteropodidae. In our study, the *COI* gene was sequenced from 120 bats collected in the Central African Republic and belonging to either *Epomophorus gambianus* or *Micropteropus pusillus*, two species easily diagnosed on the basis of morphological characters. Two additional molecular markers were used for comparisons: the complete mitochondrial Cyt*b* gene and the intron 7 of the *FGB* gene. Our results reveal an unexpected discordance between mitochondrial and nuclear genes. The nuclear *FGB* signal agrees with our morphological identifications, as the alleles detected for *E. gambianus* are divergent from the alleles found for *M. pusillus*. By contrast, this taxonomic distinction is not recovered with the analyses of mitochondrial genes, which support rather a polyphyletic pattern for both species. The conflict between molecular markers is explained by multiple mtDNA introgression events from *M. pusillus* into *E. gambianus* or, alternatively, by incomplete lineage sorting of mtDNA haplotypes associated with positive selection on *FGB* alleles of *M. pusillus.* Our work shows the failure of DNA barcoding to discriminate between two morphologically distinct fruit bat species and highlights the importance of using both mitochondrial and nuclear markers for taxonomic identification.

Phylogenetic structure of superspecies *Sorex araneus* with special emphasis to *S. satunini* haplotypic diversity

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Maximal parsimony network was constructed to investigate phylogeographic patterns in the superspecies *Sorex araneus* L. It is shown that the superspecies *S. araneus* includes closely related sister species diverged from common ancestor. Hypothetical equally distanced common ancestral point can be indicated. Within *S. aranaus*, a number of phylogenetic lineages were traced, with an apparent scarcity of recent "core" haplotypes. In most cases coincidence with any racial or geographical subdivision is lacking. Only one apparent phylogenetic lineage can be determined within *S. araneus*, comprising the haplotypes distributed in European parts North of Russia. The branch originates from haplotypes distributed in Eastern Europe and is almost equally divergent as *S. antinorii* and *S. satunini*. Two different Cytochrome *b* groups of haplotypes (A and B) were discovered within *S. satunini* populations both in Ciscaucasia and Transcaucasia, with distance between them higher than any distance in superspecies. It may suggest that type A is original and evolved during the whole superspecies history whereas the other was acquired by introgression or intraspecific allopatric hybridization. This event might have taken place outside of the recent specific range, for example in the Balkans. *S. araneus* races "Pelister" and "Istranca" inhabit the Balkans and share the metacentric *ik* with *S.*

satunini. The highest number of autosomal rearrangements in *S. satunini* (10) suggest that *S. satunini*, was the first to radiate from the common ancestor. In spite of significant divergence between A and B mtDNA haplotypes in *S. satunini* karyotypes from different haplotypes were identical.

Reticulate evolution and recurrent mitochondrial DNA introgression in hares (*Lepus spp.*)

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Non reciprocal monophyly of species for mitochondrial DNA can result from introgression, and hares (*Lepus* spp.) appear to be remarkably affected by this phenomenon. The mitochondrial lineage of the mountain hare, *Lepus timidus*, is shared by several other species, including Eurasian temperate species (e.g. *L. europaeus*, *L. granatensis, L. corsicanus* and *L. castroviejoi*) and North American arctic/boreal ones (e.g. *L. othus*, *L. arcticus*, and *L. townsendii*), suggesting that mtDNA introgression might be generalized. However, whether haplotype sharing among species is due to introgression or incomplete lineage sorting requires a detailed knowledge of the history of divergence of the involved taxa. We address this issue by analysing sequences of 14 nuclear DNA fragments (8,196 bp) and two mtDNA fragments (1,113 bp) from 50 specimens that represent 11 hare species from Eurasia, North America and Africa. Using a combination of coalescent-based methods we could not reject incomplete mtDNA lineage sorting among *L. timidus*, *L. arcticus*, *L. othus* and *L. townsendii.* We could however demonstrate mtDNA introgression from *L. timidus* into four southern European species (*L. europaeus*, *L. granatensis*, *L. castroviejoi*, and *L. corsicanus*). In the case of the two sister species *L. castroviejoi* and *L. corsicanus*, this resulted in the complete replacement of the aboriginal mtDNA lineage, presumably after an ancient hybridisation event affecting their common ancestor during the Pleistocene. By analysing over 700 samples from all over the Iberian Peninsula, we show that *L. timidus* mtDNA is frequent and sometimes even fixed in northern populations of the three hare species occurring there. It is noteworthy that mtDNA introgression is frequent, extensive and seems to occur always from the same donor arctic species, *L. timidus*. Taking apart the selective and accidental demographic causes for this seemingly deterministic phenomenon is a challenge that new sequencing technologies will help meeting.

Barcoding of shrews (Soricomorpha, Soricidae) of Mont Nimba (Guinea, Liberia and Ivory Coast)

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The aim of this study is to assess the accuracy of DNA Barcoding in discriminating and identifying shrew (Soricomorpha, Soricidae) species occurring on Mont Nimba (Guinea, Liberia and Ivory Coast). Shrew biodiversity of Mont Nimba has already been well documented. This mountain is 1752 meters high, holds several endemic species and is covered up to 1200 meters by an original altitudinal forest. The 11 shrew species inhabiting this mountain have only been described on the basis of morphological characters. So there is a need to test their molecular validity. Barcoding is currently being developed as a taxonomic tool to assign specimens to already characterised species, thanks to a 658 base pairs fragment of the 5' half of the COI (cytochrome oxidase I) gene. In this study we test the efficiency of Barcoding by including 148 shrew specimens from Mont Nimba, representing 10 of the 11 species described on this mountain. These specimens were first identified thanks to morphological identification keys. We then built a robust phylogeny using an alignment of 1847 base pairs of both mitochondrial (16S and Cytochrome *b*) and nuclear (BRCA) genes, to assess the identification of each individual thanks to molecular data. To test Barcoding, we use an alignment of 702 base pairs of the 5' half of the COI gene. We conclude that both phenetic and phylogenetic Barcoding methods are accurate to discriminate and identify shrew species occurring on Mont Nimba.

How many species in the black rat complex (*Rattus rattus sensu lato*) in Southeast Asia?

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Black rats are among the major invasive vertebrates with severe ecological, economic and health impacts. Remarkably, the evolutionary history of black rats has received little attention and there is no firm agreement as how many species should be recognized within the *Rattus rattus* complex. Members of the species complex are native from India and Southeast Asia. Current taxonomy suggests that four taxa live in sympatry in several places of Thailand and Cambodia where the present study was conducted: three accepted species *(R. tanezumi, R. losea, R. argentiventer*) and an additional lineage of unclear taxonomic status sometimes referred as *Rattus R3*. We used an extensive sampling, morphological data and diverse genetic markers of different evolutionary rates and parental inheritance (two *mt*DNA genes, one nuclear gene and eight microsatellite loci) to assess the genetic structure among the four taxa. Genetic analyses revealed discordant patterns between the *mt* and the nuclear data. The *mt* phylogeny identified three reciprocally monophyletic clades corresponding to the four putative taxa while the nuclear phylogeny failed to separate *tanezumi* and *R3*. Within geographic localities, microsatellites revealed free gene flow between *tanezumi* and *R3* but no gene flow between those two taxa and *losea or argentiventer*. Altogether theses analyses do not support the taxon *R3* as a valid species and advocate for synonymy with *tanezumi*. As a consequence, *R. tanezumi* becomes paraphyletic with respect to *losea*. Simulation analyses are now ongoing to determine whether a recent speciation event between *tanezumi* and *losea*, or an incomplete lineage sorting within *tanezumi* could explain this uncommon pattern.

Biosystematics of mouse-like hamsters genus *Calomyscus* (Calomyscidae, Rodentia), Iran

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Mouse-like hamsters of genus *Calomyscus* is one of the most interesting groups of rodents presented in Iranian plateau. This group can be regarded as an example for integrative researches. It is distributed in rocky habitats in foothills and mountains region of Iranian plateau as isolated populations. Although karyological analysis is providing important information for their evaluation as different species, the taxonomy of genus *Calomyscus* remains somehow controversial and demands a revision of the taxonomic value of new isolated populations found in Iran. Up to now 5 species have been reported in Iran, *C. bailwardi* from south and west, *C.*

hotsoni from south east ; *C. elburzensis* from north east; *C. grandis* from north and *C.urartensis* in Azerbaijan region. For this study 76 specimens were collected from 11 localities and taxonomic determination performed by molecular methods including PCR-RFLP and sequencing of a mitochondrial gene (CO1). The multivariate and landmark analyses of mandibles were done to obtain the taxonomic characteristics of each species. The molecular study confirms two major clades: 1- *C. hotsoni* and *C. bailwardi*, in South–west and 2- *C. elburzensis* and *C. grandis* in central and North-east Iran. *C. elburzensis* is composed of different isolated populations, one of which as new records was recently found in Yazd, central Iran. So this species should be regarded as a complex species. This study also confirms that south-east of the Iranian plateau should be the center of origin of actual mouse-like hamsters of Iranian plateau, which is in accordance with previous paleontological data. Finally the landmark analysis of mandible total shape space showed significant morphological differences and proved taxonomic character states that can be used for determination of each species of genus *Calomyscus* in applied studies like archaeozoology, paleontology and neontology.

Ancient hyridization in the Genus *Marmotta* (Rodentia, Sciuridae) and position of *M. Olympus* in the molecular phylogenetic tree

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Phylogeny of the Holarctic genus Marmota was examined using molecular genetic markers. Comparing studies of the phylogeny by gene cyt b (Kruckenhauser et al. 1999, Steppan et al. 1999) revealed nearly identical results with the exception of the M. olympus position. Kruckenhauser et al. showed that M. olympus is a sister species of M. vancouverensis. In contrast Steppan et al. found M.olympus to be a basal member of the North American clade Marmota. The genus Marmota is subdivided into the Palearctic and Nearctic clades. But American M.broweri was attributed to the first clade. Very different morphological species, M.caudata and M.menzbieri, appeared to be very close genetically. We got the new Marmota phylogenetic tree based on sequencing of cyt b (1140 bp) and 13 intron BCR gene nDNA for 61 specimens of all 15 species with new material of 2 M.olympus from the Burke Museum. Phylogeny of Marmota was examined using inter-SINE-PCR nDNA test (Brandler & Lyapunova, 2009; Brandler et al., 2010). We used also the data presented by Steppan et al. (in press), sequencing of 1223 bp mtDNA and 2147 bp RAG1 nuclear gene. Joint data show basal position of M.olympus to M.vancouveransis and M.caligata and mistaken data of Kruckenhauser et al. (1999) due to a contamination by M.vancouverensis DNA. M.broweri is placed in a cluster of American marmots at all 'nuclear' trees, and in Eurasian at 'mitochondrial' ones. M.caudata and M.menzbieri are close by mtDNA but distant by nDNA. Both cases can be explained by ancient hybridization.

Poster Communications

Molecular identification on Iberian rodents

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Species identification using morphological characters can be misleading, namely in cryptic species or when using non-invasive samples like faeces and hairs. In this work we developed a straightforward genetic technique for the identification of the 20 rodent species in Iberia using mitochondrial (Cytochrome *b*) and nuclear (IRBP) genes. Using the IRBP gene, this test can be applied to non-invasive samples through the amplification of short highly diagnostic regions. The cyt*b* gene identified all species but was excluded from the non-invasive samples analysis due to preferential amplification of pseudogenes in the genus *Apodemus*. The IRBP gene successfully distinguished all rodent species, with the exception of *Microtus lusitanicus* and *M. duodecimcostatus*. Amplification success rates on non-invasive samples ranged from ~94% in fresh scats (n=16) to ~35% in aged scats (n=17). These rates are consistent with amplification success on non-invasive samples from other mammal species as reported in previous studies. Additionally we observed that misidentification is a common problem within species of the same genus. The major concern is the case of non-invasive samples, for which we detected a misassignment rate of ~19%. Overall, we believe that we have developed a method that will improve the possibility to assess ecological, demographic, and genetic data from Iberian rodent species, including rare and elusive species like the Cabrera and the Southwestern Water voles. DNA analysis of non-invasive samples will facilitate the estimation of population connectivity levels in these species, helping determine matrix permeability and the capacity for species persistence.

Chromosomal variability and molecular phylogeny in the genus *Sicista* (Rodentia: Dipodoidea): Preliminary data.

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The chromosomal (routine, G-, C-, AgNOR-banding) and molecular-genetic (cytb, LCAT) data for 5 species of *Sicista,* representatives of the groups betulina (*S. betulina, S. strandi*) and subtilis (*S. subtilis, S. severtzovi*) collected in different localities of Russian plain and for *S. caucasica* (used as an outgroup) from the West Caucasus are represented. The chromosomal study (including 40 specimens from 13 localities in general) not only showed a high level of differentiation between sibling-species within groups betulina and subtilis, but also found karyological originality of some populations. Some examples of such karyologically original populations in *S. subtilis, S. severtzovi* and *S. strandi,* distinguished at the territory of Russian plain are given and considered. In molecular-genetic studies, we carried out sequencing of the fragment (1102 bp) of mitochondrial (cytb) and a fragment (488 bp) of nuclear (LCAT) gene in 13 samples of *Sicista*. Analysis of the phylogenetic tree constructed using UPGMA algorithm shows significant differentiation between the birch mouse groups betulina and subtilis, identifying the close relationships of *S. caucasica* to representatives of the group betulina, rather than to the group subtilis. The next level of clustering of the relevant branch falls within the groups *betulina* (*S. betulina - S. strandi*) and *subtilis* (*S. subtilis - S. severtzovi*). Interpopulational structure of birch mice in molecular genetic markers was not found. The congruence between chromosomal and molecular data for *Sicista* under study is discussed.

Lepus Mc1r genetic variation in mediterranean refugia

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The variation of *MC1R* gene within *Lepus* species inhabiting the Mediterranean basin (*L. granatansis*, *L. europaeus*, *L. corsicanus L. castroviejoi* and *L. mediterraneus*) and their closely related species in Europe (*L. timidus)* and Africa *(L. saxatilis, L. capensis)* was analysed in order to infer evolutionary relationships and assess the concordance of nuclear and mitochondrial molecular markers. Twelve different sequences, involving changes in five amino acids were isolated. *Lepus corsicanus* and *L. castroviejoi* had identical alleles. All other species harboured their own alleles. Three species (*L. europaeus*, *L. capensis* and *L. mediterraneus*) harboured each one or two different alleles. MC1R supported conspecificity between *L. corsicanus* and *L. castroviejoi* and bidirectional introgressive hybridization between *L. europaeus* and *L. timidus* in Switzerland. MC1R and mtDNA phylogenetic trees showed lack of concordance, indicative of a selection pressure acting on key functional genes such as those regulating coat colour. The MC1R diversity observed in the Mediterranean area is in agreement with the species' recent evolutionary history. This region served as refugia during the last glaciation and only part of the polymorphism observed in these regions is found in populations from North and Central Europe, as a consequence of repetitive founder effects. Within *L. europaeus*, a group of Israeli hares was distinguished from others in Europe and Anatolia by a different MC1R functional allele. Differences in coat colour markers in this group together with differences in other genetic markers (Y DNA, mtDNA) raise doubts about its taxonomic status.

Towards systematic revision of rock rats (*Aethomys*)

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Rock rats of genus *Aethomys* are African murids related to the genera *Arvicanthis*, *Grammomys* and *Lemniscomys*. Another related genus *Micaelamys* has been considered congeneric with *Aethomys,* but several recent genetic studies demonstrated that they are not even in sister relationship. At present, nine *Aethomys* species are recognized. However, delimitation of some of them is still provisional because information on discriminating traits is incomplete and the limits of their geographical distribution are unresolved. Phylogeny of the genus has never been studied using molecular-genetic methods. Our preliminary morphometric analysis together with published morphological data suggest three clades in this genus: *chrysophilus*-like (*chrysophilus*, *ineptus*), *hindei*-like (*bocagei*, *hindei*, *stannarius*) and *kaiseri*-like (*kaiseri*, *nyikae*, *silindensis*, *thomasi*). Analysis of available Cytochrome *b* sequences supports monophyly of *chrysophilus*-like and *kaiseri*-like clades, but the position of *hindei*-like species and *A. thomasi* have to be tested. Within the *kaiseri*-like clade, we further analyzed three East African species. Genetic as well as geometric and traditional morphometric analyses suggest that they are distinct and that *A. nyikae* and *A.* cf. *silindensis* are sister lineages divergent from *A. kaiseri*.

Geographical variation and its taxonomic implications in *Meriones Meridianus* (Rodentia)

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Gerbils belonging to *Meriones meridianus* species complex are widely distributed across the arid zone of Eurasia. High among-population morphological variability and lack of data on affiliated taxa of uncertain status (such as *M. dahli* and *M. chengi*) warrant revision of *M. meridianus* sensu lato. We examined geographical variation of midday gerbil based on craniometric data and compared it to the pattern of mtDNA variation as revealed in recent publications. 635 skulls of *M. meridianus* from Russia, Kazakhstan, Uzbekistan, Turkmenistan, Tajikistan, Mongolia, China and 30 skulls of *M. dahli* were examined. Model-based clustering analysis, as implemented in Mclust, was used to identify the number and content of morphological clusters. The pattern of craniometric variation perfectly agrees with the one suggested by mtDNA. Three clearly defined morphological groups corresponding to mtDNA clades are evident. We believe that these three taxa (*M. meridianus, M. penicilliger, M. psammophilus*) should be elevated to full species rank*. M. psammophilus* occurs in the Mongolian part of the range except for the western Mongolian Dzhungaria which inhabited by *M. meridianus*. The range of the latter extends westwards to NW Kazakhstan and Kalmykia. *M. penicilliger* occupies the southern part of the range from Tian Shan to Turkmenistan. *M. chengi* is most probably a synonym to *M. psammophilus. M. dahli* is craniometrically rather close to *M. meridianus* and, hence its species status appears questionable. RFBR 10-04-01788 supported this work.

Terrestrial vertebrate species from Iberian peninsula: A reference collection of DNA-barcode sequences

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The biodiversity of each country is a vulnerable and valuable natural source, and the identification and study of species are among the first steps for their protection and benefit. The Iberian Peninsula is recognized as a region of very high biodiversity and it was one of the most important Pleistocene glacial refugia in Europe. The region harbours about 50% of European plant and terrestrial vertebrate species and more than 30% of European endemic species. The Cytochrome c oxidase subunit I has been successfully used as a genetic marker for species identification in animals. However, one of the core tenets of DNA-barcoding initiative is that sequences should be linked to voucher specimens, which serves as a basis of study and are retained as references. Natural History Museums have been playing a key role on this process, both as guardians of newly DNA-Barcode voucher specimens and as source of valuable voucher specimens present in their collections. Despite the worldwide application of the concept, the use of DNA-barcodes as an identification tool requires the prior construction of a carefully validated reference database matching DNA-barcodes to professionally curated specimens identified through traditional taxonomic work. Here we present a Reference Collection of DNA-Barcode sequence of terrestrial vertebrate species from Iberian Peninsula. The dataset is based on the mammal, bird, reptile and amphibian's collections of the Natural History Museum of Lisbon, Portugal. Such collection aims to contribute to a better understand of the Iberian biodiversity and allow the endorsement of species identification made through DNA barcodes.

A combined analysis approach to the phylogeny of the Talpidae

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The family Talpidae, consisting of 17 extant genera, exhibits some of the most pronounced apomorphies amongst mammals. Although best known for their fossorial specialisations, a number of genera exhibit semiaquatic adaptations (*Desmana, Galemys, Condylura*) or possess a more generalized body plan (*Urotrichus, Neurotrichus, Uropsilus* and *Dymecodon*). In 2006 Sanchez-Villagra et al. carried out a detailed morphological study of the Talpidae with the aim of elucidating the evolution of talpid fossoriality. They produced of a genus-level phylogeny based on 157 morphological characters. This topology is tested herein by combining 8 loci from both mitochondrial and nuclear DNA to produce the most comprehensive molecular phylogeny of the Talpidae to date. Bayesian analysis is used to compare the concatenated supermatrix approach, analysed in Mr Bayes, to the coalescent model for species trees, implemented by *BEAST. Finally the molecular and morphological datasets are combined into a single analysis in an attempt to accurately reconstruct both character evolution and dating in this fascinating mammalian family.

Session 14 - Urban Ecology

Invited & Oral Communication

Use of conflict maps and collision data to model collisions involving small and large mammals

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With the growth of road networks in most countries the conflict between wildlife, roads and traffic is getting more severe. Since collisions are the most serious direct effects of roads, they must be reduced at the first place. Conflicts can be reduced with proper technical solutions, provided that hot spots are located first. In most cases, an examination of the whole road-line is impossible for lack of time and financial resources. Modelled conflict maps which consider attributes of species, like habitat preference, ecological needs, behaviour, natural value, sensitivity to disturbance, and also the environmental parameters of high importance (habitat type, landscape, water regime, etc.) can provide an adequate solution. Our goal was to create conflict maps of this kind, and to test them with actual collision data. The two groups of animals studied – small and large mammals – ply ecologically different strategies. Therefore, we are not certain if modelled maps could be applied for both groups the same way. Our results show that, probably because of their high abundance, large mammals can not be linked to certain locations. On the other hand, these conflict maps show those road segments problematic for small mammals, especially for rare species, quite accurately. These road segments are usually related to junctions having built in the vicinity of natural or close-to-natural habitats. For increasing data accuracy of this research, more environmental parameters should be considered. Using higher resolution vegetation and relief maps, we could be able to take into account the micro-habitat preferences of different species.

Small mammal communities in forest site habitats transformed by urban environment

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A model for studying of urban effect was the great industrial city of the Middle Urals (Ekaterinburg). Undergrowth and subordinated layers of forest phytocenosis was established to be most transformed in the park-forests of city. Coniferous undergrowth (species-edificator), as a rule, is small or absent; and formation of deciduous undergrowth occurs frequently by invasion species. However domination in underbrush remains behind local species. Unusual for coniferous forest species invaded into herb-suffruticous layer. They are especially numerous in the Central park. In studied places recreational influence appears powerful enough that peripheral park-forest sites separated from the native part of park-forests by their geobotanical and edaphic characteristics. The basic distinctive feature of inviolate forest (control – outside of the urban influence) is presence of viable undergrowth submitted by plants of different ages and height and absence in undergrowth and underbrush synanthropic species. Communities of small mammals were estimated according to their dynamics of number and specific structure, and also by Diversity (*Shannon*) and Domination indices. On the basis of Cluster analysis (results of six-year catches) there were divided two great separate cluster groups: the control and the urbanized localities. In the cluster of urbanized habitats intercity sites form separate group from the park-forest communities. Comparison of the dendrograms of phytocenosis and small mammal communities has displayed that specificity of small mammal communities in urban environment is determined not only edapho-vegetative conditions, but also other site parameters, such as isolation of territory and recreation what in some cases can plays a decisive role. *Researches are maintained by the integration project of the Ural Branch of RAS № 09-И-4-2002*

The genetic structure of two *Apodemus* species inhabiting city parks in Warsaw, Poland.

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The aim of the study was to compare the genetic variability of local populations of *Apodemus agrarius* and *Apodemus flavicollis* living in the area of Warsaw conurbation. *A. agrarius* has been frequent since 1920 and now it is a dominating component of rodent community living in the wild in downtown, reaching very high concentrations there, while *A. flavicolis* has been invading the city very recently. Molecular analyses were successfully performed for nearly 100 individuals of *A. flavicolis* and more than 200 individuals of *A. agrarius* captured in 7 parks located in different parts of the city. Genetic variability and genetic differentiation among parks were estimated using microsatellite markers. The results indicated the presence of distinct genetic structure in urban populations of both species, but the differences between local populations in *A. flavicolis* were more pronounced than in *A. agrarius*. Significant heterozygote deficiency and high F_{IS} values found in *A. flavicolis* seem to be the results of "founder effect" which is still clear in newly-established local populations of this species in city parks of Warsaw. The pattern of genetic differentiation among local populations within the city indicates that banks of the Wisła river form an ecological corridor for both species entering the city from its suburbs. *The study was financed by the Polish Ministry of Science and Higher Education (grant no: N N304 169539)*

Marten in the city – dietary plasticity in stone marten (M*artes foina*) in a city environment

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Stone marten (*Martes foina*) is an urban adapter, which is able to use human-subsidised food resources as well as natural resources. Often they reach their highest densities in low to moderate levels of urbanisation, but about densities and food composition in a large city knowledge is limited. The diet of stone marten along an urban gradient in the city of Vienna (1.67 million inhabitants), Austria, was examined based on 337 scats. A total of 811 food items was determined and analysed. Two different consumption-intensity indexes and trophic niche-width showed a high dietary plasticity. Altogether 26 animal and plant species were recorded. Fruits occurred in 52% of scats, additionally earthworms (22%) mice and voles (17%) and passerines (6%) are the groups most frequently consumed. Although anthropogenic food (garbage) was used year-round, it was surprisingly of less importance (3%), as due to pest control this resource is only difficult to access. Based on scat numbers per study area, density of stone marten was up to 10-times higher at city periphery in comparison to densely populated city centre. Areas at periphery were used year round, whereas the centre was visited only irregularly during summer months presumably due to food shortage and lack of suitable dens.

Poster Communications

The contamination with organochloric compounds of small mammals inhabiting city parks of Warsaw, Poland.

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Qualitative and quantitative analyses of organochloric pesticides and quantitative analyses of polychlorinated biphenyls were performed for tissues of two Apodemus species – striped field mouse (*A. agrarius*) and yellow-necked mouse (*A. flavicollis*) caught in parks located in different parts of Warsaw. The levels of PCBs in *A. agrarius* differed markedly between parks and well reflected the levels of local contamination of the environment. The levels of DDT and its metabolites were very low in all analysed samples, while the PCBs levels were much higher in *A.agrarius* - the species present in Warsaw since 1920. than in *A. flavicollis* – the species which has been invading the city very recently. *The study was financed by the Polish Ministry of Science and Higher Education (grant no: N N304 169539)*

Abundance and diversity of small mammals under industrial pollution

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We studied abundance and diversity of small mammals (SM) – rodents and shrews near copper/nickel smelters in Russia (Revda, Karabash, Monchegorsk) and in Finland (Harjavalta). Ten sampling plot were established along 1-30 km distance from each smelter, consisting of 3 lines with 25 snap-traps per line and exposed during three nights each, in total 879 SM were caught. As the distance from the pollution source we observed significant increase (min-max): density (from 0.7-1.3 to 4.6-10.0 ind./100 trap-nights) and biomass (from 11-35 to 76-211 g/100 trap-nights) of SM populations; species richness of SM community (from 0.2–1.7 to 3.2–3.4 species/plot). Distinct trophic/taxonomic groups demonstrated a different response on industrial pollution. The most vulnerable to heavy metal pollution and/or habitat disturbance are insectivorous mammals.

Session 15 - Postglacial recolonization patterns and mechanisms

Invited & Oral Communication

Postglacial recolonisation: continental large-sized mammals in the circum-Mediterranean region

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The concept of post-glacial recolonisation implies the existence of glacial refugia from where the different species begun to recolonise their original range of distribution. This is a phenomenon well known for micromammals. Up to not many years ago, the populations of the species today dispersed in the temperate zone of central and northern Europe were regarded as derived from those survived, in the course of the last late-glacial episod and/or at the beginning of the Postglacial, in few Mediterranean refugia. Other mammalian species survived, drastically reducing, however, their range of diffusion. In general, this seems, however, not to be the case of large-sized mammals. In fact, in recent historical times large predator and herbivore populations have declined in Western Europe and the circum-Mediterranean region due to progressive habitat disruption and to direct persecution by man. As a consequence, different species approached extinction, i.e. *Ursus arctos* L., 1758, *Canis lupus* L., 1758, and *Lynx lynx* (L., 1758), whereas some other mammal became extinct in the wild, surviving only as domesticated animal (i.e., *Bos primigenius*, Bojanus, 1827). Furthermore, several species, such as the European fallow deer, *Dama dama dama* (L., 1758), did not recuperate the former ranges of distribution, lost during the last glacial episode. Since prehistoric times, several other mammals of cynegetic interest have been reintroduced by man in their former homelands or first introduced in new territories. On the contrary, due to a general improvement of environmental conditions and legal protection, very few other large-sized mammals, such as the wolf, *Canis lupus* L., 1758, shows a recent expansion. Finally, it is convenient to recall that some species, such as the Asian jackal, *Canis aureus* L., 1758, and/or the stone marten, *Martes foina* (Erxleben, 1777), have colonised Europe naturally entering from the Near East in the course of the Holocene.

Mammals and the 'irish question': neolithic introductions of small and large mammals onto Ireland

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There is great uncertainty about how and when Ireland attained its current mammalian fauna, with intense debate about the presence/absence and relative role of *in situ* glacial refugia, land bridges and human introductions ('The Irish Question'). In order to understand the complexities surrounding 'The Irish Question', we investigated the colonization history of two very different mammals in Ireland; the pygmy shrew (*Sorex minutus*) and red deer (*Cervus elaphus*). For the pygmy shrew, we used a suite of molecular markers [mitochondrial (mtDNA), Y chromosomal and microsatellite DNA] on approximately 800 individuals from Ireland and Europe to decipher the timing and origins of the Irish population. Based on evidence from our molecular data, along with biological and distributional data, we argue that Irish pygmy shrews arrived from Britain. Molecular dating analysis is congruent with fossil data, placing the arrival of pygmy shrews in Ireland about 5000 years before present (BP). For red deer, we utilized mtDNA sequence data from almost 1400 modern individuals from Ireland and Europe. We also sequenced 9 ancient Irish specimens ranging in age from ~2,000–30,000 years BP from previously and newly dated fossils. Modern Irish red deer have a strong association with Scottish individuals, reflecting known historical introductions. However, one modern population in the southwest of Ireland has links to both Scotland and the ancient specimens, indicating a presence in Ireland dating back to the Neolithic. These two studies highlight the important role that humans have played in the constitution of Ireland's current mammalian fauna.

Evolutionary history of the genus *Erinaceus*

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Western Palearctic hedgehogs from the genus Erinaceus are important model organisms for revealing recolonisation routes after the last glaciation. Recently, the distribution of this group involves major part of Europe. There were introduction events in several islands including New Zealand. In this study, we have focused to a broad zone of sympatric occurrence of *Erinaceus europaeus* and *E. roumanicus* in the Czech Republic. We used the mitochondrial control region and nine nuclear microsatellites to assess the distribution patterns, population structure, demography and landscape genetics. E. roumanicus was less frequent in the study area and restricted to regions with lower altitudes. Demographic analyses suggested recent population growth in this species. A comparison of patterns in the spatial variability of mitochondrial and nuclear DNA indicated less sex-biased dispersal and higher levels of gene flow in *E. roumanicus*. No evidence of recent hybridisation or introgression was detected. We propose that Central Europe was colonised by *E. roumanicus* by the beginning of the Neolithic period and that there was a subsequent reinforcement stage as well as the formation of a zone of sympatry after the complete reproductive isolation of both species. The effect of ecological factors on spatial genetic structuring was studied in recently introduced population in New Zealand. The project was supported by Ministry of Education, Youth and Sports of the Czech Republic (MSMT 0021620828). Main author is supported by scholarship of Ostrava City.

Ancient DNA reveals the glacial history of Norwegian lemmings and their re-colonisation of Fennoscandia

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The Norwegian Lemming (*Lemmus lemmus*) is a cold-adapted rodent found in the alpine and subarctic parts of Fennoscandia. Compared to other lemmings it has a very restricted range, and its peculiar endemism to these previously glaciated regions has caused speculations about the species' geographic origin. Numerous paleontological findings have shown that the genus *Lemmus* had an expanded distribution during the Late Pleistocene, inhabiting large parts of the mid-European tundra-steppe zone south of the Weichselian ice sheet. However, it has not yet been established whether these fossil remains come from the ancestors of modern *L. lemmus*, or if they in fact represent lineages that went extinct during the Pleistocene-Holocene transition. Here, we address that question by analysing ancient DNA variation retrieved directly from late glacial *Lemmus sp*. remains sampled throughout the genus' formerly large range. By comparing these results with sequence data from modern individuals we evaluate whether the Norwegian lemming descends from late glacial mid-European populations that managed to track their shifting tundra habitat north during Holocene warming, or if the species' geographic origin is to be found elsewhere.

Detailed morphometrics reveals fine history of Holocene colonization of central Europe by four rodent taxa

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The present paper summarizes result of comparative morphometric study on four rodent taxa dominant in the Late Vistualian and Holocene communities obtained from a series of continuous sedimentary sequences of that age from Czech and Slovak Republics. The respective material (*Microtus arvalis*: 1877 M/1, *Microtus gregalis*: 2396 M/1, *Myodes glareolus*: 1579 M/1 and *Apodemus* spp.: M1/ and M/1) were analyzed with aid of a series of morphometric and non-metric variables and compared both in the regional and temporal respects. Considerable interregional difference in dental morphometric characteristics were found both in M.arvalis and M.gregalis. The regional specificities persisted throughout Vistualian and Holocene and were stronger than the phenotypic differences between the syntopic Vistualian and Holocene populations. In contrast, only faint and instable interregional difference were found in Apodemus spp. and Myodes glareolus, i.e. the index elements of the Holocene woodland communities even in the Carpathians where the latter species survived throughout whole the Vistulian glacial. In both the species we observed abrupt enlargements of phenotypic variation at early Boreal followed by its decrease by the end of Boreal (with increasing curtosis suggesting a pronounced stabilizing selection) and again considerable enlargement at Atlantic. In Myodes the Atlantic rearrangements turned the Early Holocene phenotypic trends more or less continous throughout the Early Holocene (supposedly due to introgression of an alien population probably associated with expansion of Fagus at that time). The synchronous phenotypic shift in Apodemus flavicollis is tentativelly interpretted as character displacement after a spread of A. sylvaticus, the species until then quite a rare in Central Europe.

Holocene small mammal communities at the north-western margin of Continental Europe: some zooarchaeological considerations about the timing of post-glacial re-colonisation.

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The maritime area located between Brittany, Cornwall and southern Ireland corresponds to the western margin of the Eurasian continental shelf. Constituted of shallow seas this zone was partially emerged before the start of the Holocene. Sea level was far below current level, and its rise during the last 18 000 years led to the dismantling of this vast land, of which nowadays only subsist the highest points. All islands of the western Channel from Jersey to Molène archipelago, Ushant and the isles of Scilly, as well as the islands stretching along the southern coast of Brittany, from the Glénan archipelago to Belle-Ile, Houat and Hoëdic constitute the relics of this lost territory. All these insular entities today support original vertebrate communities, constituted of a combination of introduced and native taxa, as demonstrated by zooarchaeological data. Native species have been trapped on these small territories by the post-glacial sea-level rise. Estimating the time of their cut-off from the continental populations according to known sea-level rise curves allows setting a *terminus ante quem* to their arrival in north-western Europe. The comparisons of these chronological milestones with the late glacial and early Holocene data contained in the I2AF databases hosted at the National Museum of Natural History (Paris) allows considerations about the timing of post-glacial re-colonisation in this part of the continent and in some cases about the likelihood of the existence of “cryptic” glacial refuges.

Tempo and mode of the Holocene community rearrangements in Central Europe: sources of regional differences

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A rich fossil record obtained from continuous Late Pleistocene-Holocene sedimentary in Czech Republic and Slovakia was analyzed and compared with that in the neighbouring countries of Central Europe. Despite of the common trends in the Late Pleistocene-Holocene faunal development (disappearance of glacial elements, arrival of core elements of the Holocene communities, dramatic changes following the Neolithic deforestration etc.) we found considerable interregional differences in tempo and mode of particular faunal events. The multiple evidence suggests (a) continuous survival of several woodland elements *(Clethrionomys glareolus, Sorex araneus, Micotus subterraneus, Microtus agrestis)* throughout Weichselian (including LGM) in the Carpathians, (b) prolonged survival of the glacial elements *Ochotona pusilla* and *Microtus gregalis* until middle Holocene in the Pannonian basin and (c) *Dicrostonyx gulielmi* in the Carpathian foredeep, contrasting to (d) the early disappearance of these elements in S-Germany and Bohemia. At the same time (e) some of the apochoric elements of the Holocene interglacial, such as *Crocidura suaveolens, Pipistrellus pipistrellus* first appeared as early as at the Late Pleistocene while a number of other (e.g. *Myotis myotis, Plecotus austriacus*) are obviously of the historical time only. The corresponding regional differences were found also in other cenologic traits. While the glacial communities were nearly homogenous in their structure throughout whole the region, the Holocene development produced a considerable faunal provincialism, which was the most pronounced during Boreal.

Session 16 - Introduced and invasive mammals in Europe :pattern and processes

Invited & Oral Communication

Investigating the introduction of house mice to Madeira: examining mitochondrial and nuclear genomes

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The Atlantic island of Madeira, a Portuguese dependency, is inhabited by several chromosome races of *Mus musculus domesticus*. The introduction of house mice to Madeira, past and present, is undoubtedly human-mediated (e.g. accidental introduction with agricultural produce). We investigated the colonization of Madeira by house mice using mitochondrial DNA (mtDNA) sequences and mapped nuclear microsatellite loci. MtDNA sequence identity to mice from northern Europe (e.g. Denmark, Sweden, Germany) rather than mainland Portugal indicates a north European source area for the introduction, possibly prior to the Portuguese settlement of Madeira in the 15th century. In contrast to the mtDNA data, results for the nuclear microsatellites suggest a significantly stronger link to mainland Portugal than northern Europe. We found no evidence for the introduction of a metacentric chromosome (metacentric 3.8) from a putative source area in northern Europe (Denmark). Overall, our results support a scenario involving an initial colonization from a north European source, followed by more recent and possibly on-going introductions from mainland Portugal. Recent or current gene flow from mainland Portugal to Madeira appears to be predominantly male-mediated, for which mtDNA sequences are not informative.

Do rabbits eat voles? The spatial dynamics of an indirect interaction in a native/invasive upland system

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Species invasion can profoundly alter ecosystem processes, although the direct and indirect interspecific interactions that ultimately determine the outcomes remain hard to predict. Habitat heterogeneity is expected to influence the persistence of multispecies assemblages, however, the spatial scale of indirect interactions has rarely been considered. Here we examine how the persistence of a native prey (water vole, *Arvicola terrestris*) is determined by the spatial distribution of an invasive prey (rabbit, *Oryctolagus cuniculus*) and directly infer how this is defined by the mobility of a shared invasive generalist predator (American mink, *Neovison vison*). Connectivity to rabbit habitat had a clear and dominant negative effect on water vole patch occupancy when mink were present, but not when mink were absent. Parameterisation by profile likelihood indicated an effective level of mink mobility that strongly biologically couples water vole and rabbit habitat separated by as much as 10 km. This study uniquely quantifies the spatial dynamics of important indirect interactions resulting from species invasion.

Habitat selection patterns of native and exotic ungulates in a Mediterranean environment

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Numerous ungulate species have been introduced with hunting purposes in ecosystems outside their native range. Native sympatric species have coevolved and, therefore, tend to show resource partitioning; however, when exotic species are present in a community, resource competition might be expected. The Iberian red deer (*Cervus elaphus hispanicus*) is among the six native ungulate species living in the Iberian Peninsula. In addition, the European mouflon (*Ovis orientalis musimon*) and the aoudad (*Ammotragus lervia*), both of exotic origin, have been introduced in Spain. Yet, practically no studies have been carried out to establish whether these species compete for resources with native ones. We examined and compared the habitat selection by red deer, mouflon and aoudad living in sympatry in a Mediterranean area of central Spain. Our aim was to infer whether resource partitioning or resource competition takes place between them. Habitat selection was assessed comparing animal locations with randomly distributed points. Habitat types, distance to feeding troughs and waterholes, and reproductive period were used as predictors in logistic regression models to identify which variables best predicted habitat selection by each species. Habitat selection pattern in red deer was mostly influenced by their reproductive period, whereas in mouflon and aoudad habitat selection was more homogeneous throughout the year. Under summer constrained conditions, potential resource competition may be high in one-year fallow land and at feeding troughs between the three species, and in scrubland close to waterholes between mouflon and red deer. A series of implications for native *vs*. exotic coexistence are discussed.

Adaptation of an alien species to a new environment: variation in the diet composition and body size of american mink over temporal and spatial scales

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Introduced species must adapt their ecology, behaviour and morphological traits to new conditions. The successful introduction and invasiveness potential of a species are related to its rate of adaptation. We analysed changes in body mass and length of American mink (*Neovison vison*) since its introduction into a new area in relation to its feeding habits and progress in colonising the area at local and geographic scales. The body size of the mink decreased significantly during the period of population establishment within the study area, with an average decrease from 1.36 to 1.18 kg in males and from 0.83 to 0.70 kg in females. Diet composition varied seasonally and between consecutive years. The main prey consumed were mammals and fish in the cold season, and birds and fish in the warm season. The proportion of mammals and fish preyed upon increased, whereas birds decreased, over the study period. Following their introduction, the proportion of large prey (large birds, muskrats and water voles) decreased. The average yearly proportion of large prey and average-sized prey in the mink diet was significantly correlated with the mean body masses of males and females. Biogeographic variation in the body mass and length of mink was best explained by the percentage of large prey in the mink diet in both sexes, and by latitude for females. American mink rapidly adapted their body size to local conditions, which suggests phenotypic plasticity resulting from natural selection rather than direct genetic evolution.

Changing distributions, management and disease; the impact of alien grey squirrels on native red squirrels in Britain, 1990-2010

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Many invasive, non-native species cause environmental and/or economic damage. One such species is the North American grey squirrel *Sciurus carolinensis* in the British Isles, first introduced 140 years ago. As it has spread throughout the countryside, it has replaced the native red squirrel *S. vulgaris* and caused economic damage to timber crops. For many years there have been concerns that the red squirrel may disappear completely from the British mainland, perhaps within the next 20-30 years. Using presence-only data collected by volunteers, we focus on the changing distributions of red and grey squirrels within different landscapes in the north of England and Scotland between 1990 and 2010. We consider the rate of spread of grey squirrels over this period, attempt to understand whether grey squirrel control and a virus infection, fatal only to red squirrels but carried by grey squirrels, are influencing the changing distributions, and what the future may bring.

Is the introduced siberian chipmunk (*Tamias sibiricus barberi*) an amplifying host of the lyme disease risk in a french periurban forest?

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How introduced species may act as a new host for native infectious agents and modify the epidemiology of a local disease has received little attention. In the Sénart forest, near Paris, we studied the consequences of the introduction of a potentially new reservoir host, the Siberian chipmunk (*Tamias sibiricus barberi*), on the ecology of Lyme disease. This disease is caused by pathogenic bacteria of the *Borrelia burgdorferi* sensu lato complex and is transmitted in Europe by *Ixodes ricinus* ticks. We studied the relative importance of chipmunks on the circulation of *B. burgdorferi* sl in comparison to native reservoir hosts, bank voles (*Myodes glareolus*) and wood mice (*Apodemus sylvaticus*). First, we determined if chipmunks are competent reservoir hosts for *B. burgdorferi* sl. We demonstrated that, in the Sénart forest, chipmunks could carry and maintain *B. burgdorferi* sl. Then, we tested if the presence of the chipmunk modifies the "acarological risk" for human (density of infected questing nymphs) by comparing sites with and without chipmunks at the period of high questing tick density in May-July 2008. Then we calculated the contribution of each reservoir host to the Lyme borreliosis risk for human. A statistical model was developed to estimate the number of infected nymphs produced per host, which take into account the temporal variability of the parameters. If chipmunks are competent reservoir hosts for *B. burgdorferi* sl, they may spillback *B. burgdorferi* sl to native communities and increase the risk of Lyme disease transmission to humans.

Hidden impacts and cumulative effects of invasive small mammals

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Myodes glarelous, a cricetid, arrived in Ireland some 80 years ago. *Crocidura russala*, a soricid, arrived more recently within the invasive range of *M. glareolus*. It was believed that neither species would impact 'early Irish' species, the murid *Apodemus sylvaticus* and *Sorex minutus*. The current distribution of these species facilitates examination of the impacts of invasive species which are not closely related to the recipient small mammal community and cumulative effects of two invasive species. Two studies were conducted to ascertain the distribution and impact of the invasive species on early Irish species in field boundaries which comprise the most common small mammal habitat on the island. The first study covered 165 x 10km^2 squares and established the current range of the invasive species. The second study focussed on estimating species abundance in three zones of invasion: early Irish species only, early Irish plus long established *M. glareolus*, and early Irish plus two invasive species. These studies show unsuspected negative relationships between species, in particular, the complete absence of *S. minutus* where *C. russala* is present and marked declines in abundance of *A. sylvaticus* where *M. glareolus* have been present many years. We present further data on resource utilisation and suggest mechanisms whereby species replacement is occurring.

Invasive European rats in Britain and New Zealand: same species, different outcomes.

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Two species of European commensal murids, the Norway rat (*Rattus norvegicus*) and the ship rat (*R. rattus*), have colonised two island archipelagos of comparable size and temperate climate but in opposite hemispheres and with opposite outcomes. Ship rats were common commensals in Britain until replaced by Norway rats; Norway rats were hugely abundant in native forests throughout New Zealand until widely replaced by ship rats. Ship rats are smaller than Norway rats and vulnerable to interference competition from them, so that explains the first case, but not the second. We investigated exploitation competition between these two species by observing the climbing behaviour and 'giving-up time' of wild-caught captive rats searching for food at different heights above the ground, and at the unsupported ends of tree branches. Both could climb, but *rattus* were faster and more agile; *norvegicus* climbed awkwardly and fell more often. Our data confirmed that the smaller size and greater agility of *R. rattus* give it a competitive advantage in exploiting scattered small arboreal food items. We propose that (1) the outcomes of the interactions between the two rat species in any given place depend on the distribution of structurally complex habitat, moderated by winter temperatures, and hence (2) the different outcomes of invasions by the two species can be explained in Britain by interference competition, and in New Zealand by optimal foraging theory and by the absence of specialist arboreal rodents (squirrels).

Alien mammals in Europe: an assessment of the effects on biodiversity, and of the mechanisms of impact

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Europe is the region in the world with the longest history of introduction of alien mammals. The effects of mammals invasions have been in this area particularly severe, causing the extinction of many native species, as in the case of the islands of the Mediterranean. Invasive mammals are in fact known to cause particularly severe impacts when compared to other alien taxonomic groups. Although mammals have been introduced in Europe for a very long time, the trend of invasions is now growing at an unprecedented rate, making particularly urgent to identify the main mechanism of arrival and of impact, in order to develop more effective conservation measures to mitigate the threats posed by introduced species. In order to provide an updated overview of this phenomenon, we carried out an analysis of the available information on mammals introductions, the different mechanisms of impact on biodiversity, and the effects on threatened species in Europe. For this aim we used the information stored in DAISIE (database on alien species in Europe), the IUCN ISSG Global Invasive Species Database, and in the IUCN Red list of threatened species. The results of the analysis provide an updated overview of mammals invasions in Europe, of the species responsible for the most severe impacts, and of the native species most at risk because of this specific threat.

The origin of introduced populations of the siberian chipmunk (*Tamias sibiricus*) on Ile-de-France

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Last taxonomical research of Siberian chipmunks diversity based on external morphology, morphometrics and cytochrome b, reveal three taxa within this species: *Tamias sibiricus sibiricus* (Laxmann, 1769) — inhabiting the northern part of the range: Russia, extreme northeast Korea, Mongolia, Japan and northeast China; *T.s. barberi* (Johnson and Jones, 1955) — present on the Korean Peninsula except extreme northeast region and *T.s. senescens* (Miller, 1898) — central China, to the south from Liaoning Province. Noticeable differences between these three taxa allow distinguishing their representatives. Siberian chipmunks are known from several introduced populations in Western Russia and Europe. The main task of this presentation is to investigate the place of origin of introduced populations of *T. sibiricus* in Ile-de-France. As a basis for comparison, 823 skulls, sequences of complete mitochondrial cytochrome b gene from 144 individuals of *T.s. sibiricus* and *T.s. barberi* and records of 198 alarm calls from 35 *T.s. sibiricus* were taken from individuals on the whole native range. Also, individuals were collected from 4 populations introduced to suburban areas near Paris, and 21 skulls were prepared, 20 partial sequences of cytochrome b (between 399–1140 positions) obtained, and 5 long-time calls series recorded. Cluster between-sample analysis of craniometrical features and phylogenetic analysis of cytochrome b point to the proximity of Parisian chipmunks to the Korean race. Peculiarities of alarm calls structure and acoustic repertoire display strong differences from the same of *T.s. sibiricus*. Alarm calls are the first to be analyzed for *T.s. barberi*, as it is not known in native Korean populations.

Poster Communications

The potential spread of the grey squirrel (*Sciurus carolinensis*) in central Italy: a GIS cost-distance analysis

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The grey squirrel (*Sciurus carolinensis*) represents one of the most damaging invasive alien species that threaten biodiversity. Its spread in the British Isles and in northern Italy is causing the progressive decline of the native red squirrel (*Sciurus vulgaris*), through ecological and disease – mediated competition. It also causes damage to forests and tree plantations. Currently, there are established populations of grey squirrels in Piedmont, Lombardy and Liguria; a local population has also been reported in central Italy, near Perugia (Umbria). Considering the extensive forest cover in the Apennines, the expansion of the species in a near future is very likely. In this work we 1)analyze the potential distribution of the grey squirrel in Umbria through an expert – basedecological model, and 2) evaluate the functional connectivity through a GIS cost-distance analysis,illustrating scenarios of expansion risk to adjacent regions.In the potential distribution model we included only land – cover categories, whose suitability for the species was evaluated by a score ranging from 0 to 3. The resulting map indicated that 97% of the region is suitable, and that 34% is highly suitable. In the connectivity analysis a cost map was built, assigning a resistance-to-movement value to each patch, according to its suitability. Two major rivers, Tevere and Nera, were treated as barriers. The cost-distance analysis was carried out starting from Perugia to eight provinces that surround Umbria. According to our results, the province of Arezzo is the most exposed to a potential spread of the grey squirrel from Perugia.

The breeding behavior of a mediterranean mammal subspecies introduced on an atlantic island: the wild rabbit (*Oryctolagus cuniculus algirus*) in Azores (Portugal)

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The wild rabbit (*Oryctolagus cuniculus*) is endemic from the Iberian Peninsula, where two subspecies (*cuniculus* and *algirus*) are distributed along segregated (NE and SW, respectively) but partially overlapped ranges. Domestication and most colonization events outside Iberia were performed using the *cuniculus* subspecies, being the Azores one of the few known cases where *algirus* subspecies was introduced. Due to its importance as a game species, rabbit sustainable hunting requires knowledge of local breeding cycles. However, little is known about *algirus* breeding behavior outside Iberia. Since climate in Azores is Atlantic we hypothesized that rabbit breeding cycles would be different in relation to Mediterranean populations from SW Iberia. To test this hypothesis we adjusted a predictive model, previously validated for this species, to environmental data from Azores. Additionally, a total of 563 adult rabbits were collected monthly from November 2006 to October 2008, on Flores Island (largest of western group) to record the following parameters: testis (position) and epididymis weights; ovaries and uterus weights, number of embryos, and mammary glands development. Despite the climatic differences between the Atlantic and Mediterranean regions, both model predictions and observational data on reproduction suggest similar breeding cycles in Azores and SW Iberia, with annual peaks in March-April, a reproductive pause during summer (July-October), and mean litter sizes of 3.65±0.21. The main limiting environmental factor seems to be high temperatures, since green pastures are available throughout the year. This study is ongoing as part of a project aimed at improving game species management in Azores.

Characterising the historic and future spread of an invasive mammal for the purposes of management and control

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Biological invasion is a major threat to biodiversity and ecosystem function and the negative impacts of invasive mammals on native species can be devastating. The American mink (*Neovison vison*) was introduced to the UK for fur farming and consequently feral populations have established. Mink are generalist predators and although they appear to have spread steadily throughout Scotland since the 1950s, various recent surveys have implied that the north-west of Scotland is mink-free, and is, therefore, a haven for native wildlife. However, since the last survey in 2008 there have been repeat sightings of mink suggesting that the range is further north than currently documented. Is it only a matter of time before the Highlands of Scotland are invaded? The ultimate aim of this project is to develop management plans for mink control in Scotland, based on research findings. The methods by which this research is being conducted are presented here. These include species distribution modelling on historical sightings data to analyse patterns and rate of spread. In addition, stable isotope analysis and landscape genetic analysis will be used to establish habitat use and dispersal patterns. The combination of these methods aims to characterise the spread of mink in Scotland to facilitate effective control of the species.

Adaptation to cold and predation – shelter use by invasive raccoon dogs in Białowieża forest (Poland)

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Based on radio-tracking of raccoon dogs *Nyctereutes procyonoides* in Białowieża Primeval Forest, we addressed the hypothesis that pattern of shelter use by this invasive carnivore is an adaptation to both, climatic conditions and predation. Raccoon dogs used various types of shelters but were invariably concealed in dense vegetation or in the shelters created by trunks, branches or roots of fallen trees (58% of days). Burrows (mainly badger setts) were selected on 27% of days. In crucial periods of their annual cycle, raccoon dogs used shelter offering better protection: burrows and hollow trees (use of which increased with decreasing ambient temperature) in winter, and hollow trees and dense vegetation during breeding and raising pups. In winter, 88% of badger setts were occupied by raccoon dogs. Duration of occupation of badger setts by raccoon dogs ranged from 53 to 206 days. The pattern of shelter use by raccoon dogs was modified by forest structure. Raccoon dogs living in the pristine old-growth stands (with large amounts of dead wood) utilised mainly natural shelters created by fallen trees, and sedge tussocks, while individuals inhabiting the managed forests used mainly burrows and thicket. We conclude that hiding behaviour and plasticity in shelter use is a response to high mortality due to predation and to unfavourable climatic conditions. High adaptability to various environmental conditions and facilitation by badgers (through habitat amelioration and refuge from cold and predation) were probably important factors underlying successful range expansion of raccoon dogs in Europe.

The neverending story: archaeozoological evidence for the dispersal of the beech marten (M*artes foina erxleben, 1777)* into Europe

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The historical biogeography of the beech marten (*Martes foina*) is still sparsely known. Its current European distribution is supposed to be the consequence of a colonization from central/southwest Asia in the Holocene, but evidence for this process remains poorly documented. This issue is further complicated by the fact that (i) the postcranial bones of the beech marten are easily misidentified with those of the autoctonous pine marten (*Martes martes*), and (ii) the available genetic data for the beech marten does not allow any potential distribution scenarios in the recent past to be tested. In this paper we thus review the presence of beech martens in the light of the chronology of archaeozoological finds since the late Pleistocene, for the Mediterranean Basin and Europe. In addition, we discuss whether this dispersal process throughout the continent was in any way connected with the entrance of Neolithic people. We conclude that the clarification of the beech marten's distribution scenario in Europe will benefit from analyses dealing both with bones and genes.

The population dynamics and density control of American mink in four National Parks in Poland

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American mink (*Neovison vison*) is a semi-aquatic species, endemic to North America, which was introduced in the wild in Europe in the 1930s. In many introduced areas, the American mink has an excessive predation impact on waterfowl and riparian mammals, leading to a marked decrease in their density. The aim of this study is to analyze adaptation of mink in their introduced range and to determine factors affecting population dynamics and colonization rate after eradication in the 4 National Parks of Poland (Biebrza, Narew, Warta Mouth and Drawa National Park). Fieldwork was conducted in 2 series of trapping (March and November 2009, 2010 and 2011). Trapping took place in two sites: experimental area [EA] (on which the mink were removed) and control area [CA] in which mink were marked and released. During the spring and summer 20 rafts were deployed for population monitoring. In total 248 mink were caught. The preliminary results show large differences in morphological traits and population parameters between the various national parks. The average body weight of males and females from the West of Poland was 1.35 kg and 0.6 kg respectively, and from the East of Poland mink 2.0 kg and 0.8 kg. The lowest density of mink was in the Drawno (2.5 inds./10 km watercourse), and the highest was in the Narew NP (9 inds./10 km watercourse).The rate of recolonisation was related to the time since eradication and density of the mink in the NP. The number of signs found in the EA after 6 months of mink eradication was similar to the number of signs found in the CA, suggesting a fast recolonisation of the eradication area in all parks.

Overcoming compensation through dispersal in the eradication of the invasive american mink

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Invasive species are a major threat to biodiversity at a global scale. Programmes that aim to eradicate invasive species to protect native biodiversity face considerable logistic and financial challenges. A particular issue in the eradication of well-established, widely spread invasive species, is overcoming compensation through dispersal from adjacent uncontrolled areas. The development of feasible and effective eradication strategies can therefore be greatly enhanced by incorporating information about dispersal rates, distances and dynamics. Here we use genetic data to construct pedigree relationships between American mink removed during a large scale (>10000 km^2) eradication project in the Cairngorms National Park, NE Scotland. This data is used to demonstrate: 1) large scale connectedness through mink dispersal between different geographically distinct management units (river catchments); 2) differential rates of mink reinvasion from areas with different intensities of control; 3) 'hotspots' that contribute disproportionately high levels of emigrants and represent particularly significant management targets. These findings have been used to define the appropriate spatial scale of control and allocation of resources required to achieve specific goals for the conservation of native biodiversity, and have also been instrumental in securing extended funding to geographically expand the range of the mink-free area in Scotland.

Session 17 - Movement Ecology

Invited & Oral Communication

Decoding animal behavior from movement

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The main challenge of movement ecology today is decoding movement paths to characterize and understand the spatial behavior of animals. Depending on scale, four types of behaviors can be inferred from movement data. At the coarsest scale are landscape-dependent movement-related behaviors (e.g. home-range dynamics, dispersal) which have been studied intensively using low resolution VHF data. Using high-resolution GPS platforms finer scale behaviors can be studied starting with the finest scale of the Fundamental Movement Element (e.g. running, trotting, walking), followed by the Canonical Activity Mode (e.g. feeding, directional walking, resting) which may combine several FMEs, and finally the strategic aspect of movement (i.e. foraging strategy) that combines several CAMs. We present two new methods, one to identify CAMs and one to discern foraging strategy from movement data. Both methods are developments of the First Passage Time. Using a first-passage radial-scaling-of-time (FiRST) function and its time derivatives, we successfully classified CAMs from GPS data obtained from elephants and zebra in Etosha National Park, Namibia. We successfully discerned foraging strategy from simulated movement data based on: (1) The animal's response to resource distribution in space, which we evaluate using variance-scale patterns derived from the First Passage Time index, and (2) The animal's response to the resources' temporal dynamics, evaluated using site revisiting patterns. These methods can be used to confront empirical data with predictions derived from the two spatially-oriented theories of foraging: search and patch-use. As such, the methods allow and encourage the use of movement data in more general, behavior-related fields of ecology.

Natal dispersal in european hare (*Lepus europaeus*)

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Identifying the factors that shape dispersal and its costs is crucial in the understanding of the dynamics and evolutionary processes of local populations. For game species, little is known about the influence of hunting on each dispersal stage (emigration, transcience, settlement). We studied natal dispersal in respectively 84 and 87 juvenile radio-collared juvenile hares (Lepus europaeus) in two harvested populations of France differing by the type of landscape (mixed farming or intensive agriculture) and hare density. The objectives were to describe movement patterns, to assess dispersal and survival rates, in relation to population density and hunting. We developed multi-state capture recapture models to investigate survival and movements at each dispersal stage. In both populations, dispersal mainly occurred before the age of 6 months, and it was male-biased: Males dispersed twice more than females but females moved over longer distances. When considering the concurrent survival probability, we showed that dispersing juveniles suffer from a higher mortality rate during transience compared to philopatric juveniles, due to both hunting and predation. We did not detect any clear effect of population density on dispersal departure rate. Further studies are needed to identify the factors (for example local hare density) that influence settlement in a new area.

Natal dispersal in roe deer: heavier animals disperse more frequently and further

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Natal dispersal is defined as the net movement between the natal site to the first breeding site and is one of the most important processes in population dynamics. The choice an individual makes between dispersal or philopatry may be influenced by its phenotype or by the habitat. The European roe deer *Capreolus capreolus*, a medium-sized species widely spread across Europe, has shown a marked expansion of its range since the 1960s. We investigated the ranging behaviour of 63 juvenile roe deer monitored with GPS collars over one year prior to their first reproduction from 2003 to 2010 in South-West France. We assessed the influence of sex, body mass and the degree of habitat fragmentation on dispersal propensities. The population's overall dispersal rate was 37%, with a mean linear distance between natal and post-dispersal home ranges of 12.3 ± 10.5km. We found no sex-bias in dispersal, but a lower dispersal rate for forester animals. Body mass was positively correlated to a continuous index of dispersal based on the distance between the natal and the post-dispersal home ranges. A minimum threshold weight of 15kg seems to be necessary for an individual to disperse on our study site. Thus, we show that the natal dispersal behavior of roe deer is both phenotype- and habitat-dependent. A better understanding of the mechanisms involved in natal dispersal, such as phenotype-dependence, will help us to understand the evolution of this behavior as well as providing a basis for better prediction of the geographic expansion of this large herbivore.

Bats 'sit-and-wait' and learn to lévy triat: resource variability effects foraging movements

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Optimal Foraging Theory (OFT) is a central concept of animal behaviour exploring aspects of animal movements with respect to foraging patches and efficient resource acquisition. We examine if optimal foraging movements of the insectivorous bat, *Myotis mystacinus* are modified in response to temporal resource availability. This is explored using the frequency distribution of foraging movement step-lengths and ambient temperature as a proxy of resource availability. A change in with the distribution of movement step lengths from a Gaussian distribution to a Pareto distribution, with a truncated tail, was observed from low to high temperatures. The Pareto distribution is associated with Lévy search behaviour an important characteristic of which is superdiffusive movement. However, this feature was not apparent within the foraging behaviour of *M. mystacinus*, as long movements ended significantly closer to core foraging areas. We argue that the observed pattern arises from optimised behaviour and knowledge of resource availability. This may be indicative of a 'sit-and-wait' strategy when food is abundant, with bats making long flights to optimal areas and short flights within these areas. At lower ambient temperatures, and lower prey availability, *M. mystacinus* have to move further to encounter sufficient prey. Using techniques which utilise changes in movement step-length distributions may allow the triggers of behavioural changes to be explored in a wide range of species and examine the processes which lead to these patterns. Insights from adaptive search behaviour, optimised for environmental conditions, may provide a framework for efficient strategies to be developed in other disciplines.

Studying of amur tiger space use with GPS-Argos system

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Within the framework of the long term Program of the Amur Tiger Research in the Russian Far East studying of space use of these carnivores was conducted using the GPS-Argos system. During the first 2 years (September 2008 through October 2010) we collared 11 tigers (6 males and 5 females) using transmitters from Sitrack, New Zealand (8 units), Telonics, USA (1 unit) and Pulsar ES-PAS, Russia (3 units). Best results was gathered by both Sirtrack (16,8 locations/month uplinked) and ES-PAS transmitters, specially the last ones (104,4 locations/month). Telonics transmitter failed to reach Argos Satellites so it operated as on-board GPS transmitter attached to a female tiger that was recaptured and retagged. A total of 2598 locations were uplinked by all collars, ranging from 11 to 1222 per tigers. Minimum convex polygon home ranges for each individual range from 197,5 km^2 to 869,8 km^2 for adult females (n=3) and 689,4 km^2 to 2688 km^2 for adult males. Males home ranges overlap much more than females' do. Tigers on the transborder regions (n=2) rarely trespassed state border. This project was financed by "Konstantinovskiy" International found, petrol transportation enterprise "Transneft", "Tekhsnabexport" and Russian Geographic Society.

The home range sizes and movements of Eurasian lynx in Finland

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Despite being the most common large carnivore in Finland, current minimum population estimate around 2300 to 2500 individuals, the ecology of Eurasian lynx *Lynx lynx* has been relatively unknown, particularly the size of home ranges and movement distances. With using GPS-GSM-collars, the movements and home range use of 21 radio-collared Eurasian lynx was studied in three areas in Southern and Central Finland during years 2008-2011. Landscape in the study areas consists of mosaic of urban and semiurban fabric, agricultural areas and forests and semi-natural areas. The observed variation in the home ranges sizes was high (MCP home range sizes varied from about 100 to 1300 km2), males having slightly larger average home ranges than females. The daily movement distances varied between few hundred meters to over ten kilometers. The reasons behind the large variation of home ranges sizes and movement distances will be further discussed

On the importance of lemmings and sea ice: long-distance movement and genetic structure in the circumpolar Arctic fox

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The spatial and temporal distribution of genetic variation reflects the interplay between the organism and its environment. Movement is in general considered as the most prominent process forming the genetic population structure. The factors promoting movement however differs between habitats and is often connected to resource availability. The Arctic fox (*Vulpes lagopus*) is a climate change flagship species with circumpolar distribution throughout the Arctic. It is distinguished into two distinct ecotypes ("lemming foxes" and "coastal foxes") adapted to habitats with different resource abundance and stability. The Arctic fox has extremely high capacity for long-distance movement and through microsatellite analysis, we concluded that the global genetic structure was mainly determined by the presence of sea ice connecting areas during winter and facilitating long-distance movement. Sea ice is accordingly an important Arctic fox winter habitat and based on genetic and demographic data, we demonstrated that such long-distance movement across the sea ice is induced by resource fluctuations caused by the lemming cycle in inland habitats. As a consequence of lemming crashes, "lemming foxes" immigrate into coastal areas where food resources are temporally stable, suggesting that switching to marine resources is a strategy for surviving lemming crashes. The rate of the ongoing climate change is considered to be of higher magnitude in the Arctic ecosystem compared to other ecosystems and with this in mind, we discuss how the Arctic fox will be influenced by a warmer climate.

Monitoring and GIS-based range of sympatric species otter *Lutra lutra* and mink *Mustela vison* in the Russian far East

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The monitoring program on otter and mink is conducted in the Lazovsky Reserve (43° 05' N, 134° 55' E) since 1958. The otter is an aboriginal species. The mink was introduced in 1947 and occupied the reserve very slowly. Collected information about visual sighting and tracks during 52 years was transferred into GIS database (otter – 450 records, mink – 352). We were constructing 6 maps representing decades from 1960 to 2010 for each species. In 1960s the otter range along water-currents was linear and continuous. The coast of Sea of Japan is occupied incompletely the range is reduced. The otter live both in small rivers and in the sea. The otter range in 1970s has undergone essential changes in reserve because of two strong typhoons 1971 and 1972 and the drought that have followed of them. The mink range in 1970s became fragmentary, has lost linear outlines. In 1980s there was a strong depression of number of otter and mink. Because of catastrophic high waters of the end of 20 century the populations of both species still are in decline though last 7 years there was a partial restoration of number of otter and mink. Ranges of both species on water-currents remain broken off, and their linear character is lost.

Fisher movement patterns and corridor use across an urban gradient

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Fisher (*Martes pennanti*) have traditionally been considered a wilderness species. While their populations in western North America are classified as rare and endangered, their populations in the northeast United States are robust, and recently have started colonizing urban and suburban woodlots New York State. Detailed studies on fisher movement paths, habitat-behavior associations, and corridor use do not yet exist, hindering our understanding of their adaptability to human development. We are using remote cameras and tracking collars to study the ecological and behavioral adaptations that have allowed fisher survive within these human dominated landscapes around Albany, New York. Our raw data suggest that fisher show a strong preference for forested habitat, avoiding developed areas and open fields, and often make multiple moves between multiple urban forest fragments during their nightly activities. We will use our high spatial and temporal-resolution (≥2 minutes) location data to identify functional movement corridors and to pinpoint locations where animals cross roads. Preliminary winter field-investigations of these road crossing sites suggest a high use of under-road drainage tunnels. Data from the tri-axial accelerometers (recorded at 3 minute intervals) will be used to identify potential behaviors along movement paths, with the purpose of distinguishing corridor use versus foraging, resting, etc. Our study will provide valuable information on how threatened species can adapt to encroaching human development over the scale of just a few decades, helping us help other species that are threatened by similar forces.

Poster Communications

Home range size, movement pattern and testosterone level in an immigrant and resident males of the root vole (*Microtus oeconomus*)

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Male dispersal from the natal place is common for the majority of rodents' species; additionally males engage in secondary or breeding dispersal following natal emigration. However, the patterns and causes of secondary dispersal are poorly understood due to the difficulty in following emigrants. Especially, still there is no answer for the key question – do immigrant males differ in their quality from the residents? This paper describes detail differences between immigrants and residents of the root vole (*Microtus oeconomus*) males studied in July 2009 in Biebrza National Park, Poland. We managed to distinguished immigrant and resident males based on intensive live trapping. Among 21studied males, 5 were classified as an immigrants and 16 as a residents. Males were quantified in relation to their behavior (locomotory activity and daily range size), body mass and plasma testosterone level. Generally, we found evidence that immigrant males have higher plasma testosterone level, higher locomotory activity and bigger daily range size than resident males. These results show that adult males of the root vole which immigrate are more aggressive and active compared to resident males. It suggests differences in fitness (measured as a number of offspring) between resident and immigrant males.

Network analysis of density dependent dispersal of small mammals between reforestation and closed forest habitat patches

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Dispersal has an important role in fragmented habitats and it depends from the quality of the patches and the local densities of populations. Small mammals were captured in two 1-ha grids using CMR method in South-Hungary along the upper Drava River in a strictly protected closed gallery forest and in its neighbouring reforestation habitat. We divided the sampling area into nine patches by right of the quality of vegetation, the size of the interior and exterior sites of the closed and reforestation habitats and its bordering edges. We used the capture data of the low and high density years of the three most abundant species *Apodemus agrarius, Apodemus flavicollis* and *Myodes glareolus*. We prepared the dispersal networks of the species from the recapture data. These showed toward which patches are centralized the movements and we examined the differences between these networks. The bank vole uses closed forest mostly, but it occurred with higher density in the reforestation habitat through 2007. This substantial change caused the decentralization of the movement networks between patches on both sites by 2007 autumn. Root causes of decentralization were those individuals that moved from the interior site of closed forest to the reforestation patches. After dispersal of the bank vole the striped field mouse were crowded out from the patches of the reforestation habitat that they had occupied stably previously. The habitat use of bank vole affected the yellow-necked mouse less; the relative abundance of the mouse did not decrease substantially in the high density year.

Wild boar (*Sus scrofa* l.) dispersal in four contrasting Belgian forests

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We were investigating the natal dispersal patterns of the wild boar (*Sus scrofa* L.) population in Wallonia (Belgium) according to the fragmentation level of four forested areas. The study areas selection was based on a decreasing gradient of fragmentation from A (high) to D (low fencing network). Since 2005, 1627 wild boars were captured, sexed, aged, weighed and ear-tagged in order to measure the euclidian distance between capture and recovery. The recovery data reach 42 %. Some adult females (20) were also monitored by telemetry to compute their home range size. We defined dispersal as the confidence interval of the length of the mean home range (4,8 km). Dispersal patterns were generally similar for piglets and females. The distances covered were generally higher for male yearlings. Forests having a higher level of free-range showed the highest dispersal distances (for piglets: Mood's test KHI² = 11,6; df=3;p<0.01 - median distance varies from 1,32 km to 4,19 km). The proportion of piglets and females staying in a radius < 5 km is , *A*: 100% ; *B: 89%* ; *C*: 93% & *D*: 84%). The proportion of male yearlings staying in a radius < 5 km is , *A*: 74% ; *B: 79%* ; *C*: 65% & *D*: 60%). The mean dispersal rate reach 43% for yearlings males and around 19% for piglets and females. It varies according to the study area. The fencing network seemed to affect the dispersal distances but still allows natal dispersal.

Large-scale navigational map in a mammal

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The ability to navigate is crucial for animals, yet navigational mechanisms are poorly understood, especially in mammals. Here we report the first GPS-tracking of bats. Egyptian fruit bats commuted from their cave to a remote fruit-tree in high, fast and very straight flights, and returned to the same individual feeding-tree night after night. Bats that were displaced 44 km south homed to one of two goal locations – cave or feeding-tree – which allowed ruling out navigation based on beaconing, route-following, or path-integration mechanisms, and suggested instead map-based navigation. Bats released within a deep natural crater exhibited severe disorientation, while bats released atop crater-edge homed well – indicating navigation by the geometric configuration of distal visual landmarks. These results provide the first evidence for large-scale navigational map in mammals.

Biological signal field of wolves (C*anis lupus*) in experimental conditions

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The concept of "biological signal field" is expanded to information field of biotope, considering as attractors not only signs of vital activity of animals, but also other objects in biotope space that organize the activity of animals. The work was done in 2008-2009. We observed a group of 4 wolf cubs in the fenced area of 600 m^2 of natural forest. Odorous marks, such as urine and excrements, in high concentration left by wolves along each of runs (the most significant elements of the biological signal field actively formed by animals its selves and mainly used for movement in enclosure) raise a signal importance of these pathways and serve as peculiar orientation road signs for wolves. The observed changes during the time in spatial activity of wolves, depending of spatial distribution of attractors differently interesting animals, is associated with changes in biological signal field and system of attractors. The most effective attractors, organizing behavior of both the individuals and group as a whole, are the objects of environment that noticeably stand out for general background, for example log piles, where heightened activity of animals and, as a result, maximal accumulation of signs of vital activity (thickening of the biological signal field), are observed around. First of all, complex of such attractors determine the spatial structure of the biological signal field – system of attractors of the second order being formed by population itself.

Session 18 - Biodiversity erosion and Conservation in Europe

Invited & Oral Communication

Modelling potential distribution of the western population of the endangered european mink (*Mustela lutreola*)

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The European mink (*Mustela lutreola*) is one of the most threatened carnivores in Europe, with three major populations remaining in the eastern and western parts of the continent. Recent studies highlighted that the western population, whilst disappeared from the north of France in the last years, is slowly expanding his range southwards in Northern Spain. In order to contribute to efficient conservation policies, we aimed at identify those areas suitable for re-colonization or expansion by the western population using Species Distribution Models (SDMs). As the species suffered a severe reduction of his range, we proposed the following hierarchical modelling approach to deal with the species-environment equilibrium assumption violation: **a**. Specie's bioclimatic range at European-scale was defined using different methods of SDMs with historical presence data and climate predictors (resolution 10 km); **b**. Regional-scale models were built for France and the Iberian Peninsula using different methods of SDMs with species current distribution and environmental predictors (resolution 1 km); **c.** Final potential distribution model was built combining the prediction from the ensemble regional model with the prediction from the ensemble bioclimatic model. Our study provides useful information about the areas potentially suitable for the recovery and the most likely direction of spread of the population, which should be considered in future management actions. The proposed modelling approach stresses the importance of integrate regional models with models considering the whole extent of distribution in order not to underestimate the true potential range for a species in non-equilibrium with his environment.

Contribution of Natura 2000 to mammal conservation in Europe.

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The Natura 2000 network is the most important conservation effort being implemented in Europe. However, no comprehensive and systematic evaluation of the effectiveness of the network has been conducted at the European level. We used habitat suitability models and extent of occurrence of 288 species of terrestrial mammals to evaluate the contribution of the Natura 2000 network to biodiversity conservation considering also the existing national networks of protected areas. We performed a gap analysis and we identified regions, species, and strategies that can be important for consolidating and expanding the existing network. First results outline that if Natura 2000 is taken to represent the final point of all the EU conservation policies it will inevitably fail. Its role in conservation could be enhanced by integrating the Natura 2000 system into a more general strategy that considers natural processes and the ecological and evolutionary mechanisms acting behind.

The importance of community level interactions in designing conservation strategies based upon species distribution modelling: a focus on future threats to the persistence of the arctic fox in fennoscandia

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While species distribution modelling is frequently used to assess the impact of future climate change on species distributions, biotic factors are rarely taken into account. The Fennoscandian population of the arctic fox (*Alopex lagopus*) is currently assessed as critically endangered, which is mainly due to low availability of its main prey, the Norway lemming (*Lemmus lemmus*), and competition from the red fox (*Vulpes vulpes*). Future climate change might form a further threat to its persistance in the region. We used this species-community to investigate whether changing biotic interactions play a significant role in species distribution modelling in the face of climate change. Our results show that whilst the range of the arctic fox is predicted to have decreased in 2080, due to temperature related variables, both the predicted lower prey availability, and predicted increased competition pressure further reduced its potential future range. The results illustrate the importance of accounting for community level interactions in species distribution modelling, when designing (future) conservation strategies. Our results further have large implications for the design and implementation of conservation strategies for the arctic fox in Fennoscandia, potentially necessitating control of red fox abundance as well as feeding arctic fox during unfavourable periods.

Local threats for a globally common large carnivore – the Eurasian lynx

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The status of Eurasian lynx (*Lynx lynx*) population in Europe is dramatically variable. Whereas it expands despite of hunting harvest in some areas, it shrinks despite of protection in the other. This has triggered numerous researches aiming at developing sustainable management of the population on the one hand or understanding limiting factors on the other. Studies have revealed a number of aspects contributing to the observed variability in the population state. Enormous variation in home range size and densities has been associated with their main prey (roe deer) abundance. Prey depletion had an immediate effect on lynx spatial organization and movements resulting from increased foraging efforts, particularly in females. The prey availability was found to affect also females' body size, which was likely linked to their hunting success related to climatic conditions. This, in turn, as one of the factors, lead to high genetic differentiation among populations. The populations differ also by the level of genetic variability with low variation recorded in its most severely fragmented parts. The habitat characteristics (structure of the forest) have been shown to be a key factor for lynx hunting efficiency and resting site selection. Diversity and complexity of the habitat structure may thus determine carrying capacity of the habitat for lynx, which in concert with environmental discontinuity and prey scarcity can result in lowering the viability of the population. The studies showed that local lynx populations in Europe can be threatened despite of currently secure global situation of the species.

Brown bear in the European Russia at the beginning of the 21st century: current status, protection and use of resources

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The species area was formed in the region in the early- mid Holocene. Decrease of the area and digress of its southern boundary towards the north started at the end of the 16th century, accelerated by the end of 19th century and lasted until late sixties. The reasons included felling, plowing of wild lands, hunting. Since early 1970-ies until mid 1990-ies the population was increasing. Later it started to decrease again due to problems in the economy, agriculture and use of resources during "market reforms" (1990-ies). However since the beginning of the 21st century the bear population started increasing again. Population growth was followed by the species expansion to the south and inhabiting abandoned agricultural lands overgrown with forest; while northern boundary was practically unchanged. Studies in 33 regions showed that population growth and expansion towards south is going on. According to the official data of 1999 there were 44340 bears in the region (not including the Caucasus population), in 2004 – 45850, in 2010 – 54400 bears (total in Russia – 181940 bears). Legal crop was respectively 1414, 1867, 1779 (4215) bears. Illegal take was probably twice as much. Currently the number of bears is the biggest (33340) in the taiga forests of the north and north-west parts of the region. Problems of the species wellbeing are related mostly to the anthropogenic factors rather than to the natural factors (climate warming effect on the bear physiology is beyond doubt and being studied though). Major factors include ecosystem transformation, especially due to felling, poaching in the spring and squat periods, selectivity of take (preference to trophy specimens), poaching for obtaining derivates (bile, feet).

The french national otter action plan

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A National Action Plan for the Eurasian otter was written in 2009 by the French Mammal Society (SFEPM) and will be implemented from 2010 until 2015. This project is part of the action plan policy of the French Ministry of Ecology (MEDDTL). The first part of the plan is a status report on otter in France and the second part presents the conservation strategy for the next five years. The main issues of the plan are the strengthening of the stakeholder network and the development of cooperation to improve research and conservation, a better circulation of knowledge about otter biology and conservation issues, the implementation of actions to reduce otter mortality, protect and restore otter habitat and increase prey availability and the improvement of cohabitation between otter and aquaculture.

A french conservation action plan for the pyrenean desman, *Galemys pyrenaicus*.

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In 2008, the French Ministry of the Environment asked for the production of a Conservation Action Plan for the Pyrenean Desman in France. This decision relies on Desman's population status, its restricted and declining geographic distribution, the numerous threats and the lack of knowledge on its biology and its ecology. The French Mammal Society (SFEPM) and about 40 partners drew up this plan and identified 25 priority actions corresponding to three main objectives : (1) To improve knowledge of the Desman's biology and ecology and of the threats (12 actions), (2) To protect Desman populations and its habitats (3 actions) and (3) To structure a network of profesional and volunteer partners involved in Desman conservation and to increase public awareness on the Desman and river protection (10 actions). The « Conservatoire régional des espaces Naturels de Midi-Pyrénées » coordinates this plan with a steering commitee (≈ 30 partners) and a scientific commitee (≈ 15 researchers). Launched in September 2009, the plan will last until 2015. It is supported by the European Commission and 9 other financial partners. In 2010 17 actions have been initiated. This presentation will propose a synthesis of these results such as the genetic study led to challenge the species' and the individual identification from faeces or the elaboration of a protocole to update the distribution map or the publication of a booklet on the Desman.
This plan is the first initiative of its kind for this species in France. It seems highly successful, stimulating and promising…

Current trends in French bats population higlihgted by ancient banding data

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Bats are an important component of biodiversity but most European species have a bad conservation status due to various threats such as agriculture intensification, urbanization, and forest management. Some qualitative reports from the last fifty years indicate that most, if not all, French cave dwelling bats suffered then a dramatic decline. Conversely, during the last 10 years in France, hibernacula counts indicate that many species of conservation concern are stabilizing or, for some of them, increasing. But how can we interpret these trends without a precise knowledge of those past declines ? This is why we used banding data uncovered from ancient registers to analyze the evolution of past populations. From 1939 to the late 70's, hibernating bats have been banded by volunteer bat workers right in roost. Poor handling and injuries arising from band itself were certainly responsible for some lethality but cannot account for the overall decline. Moreover, by comparing species distribution, roost community composition, decline rates per species and threats between these two periods, we stress that the recent increase in populations is very far to compensate for the previous drop. Thus, using recent populations trends in Europe as an evaluation criteria (Natura 2000, IUCN) for bats, have to be done with caution.

Poster Communications

The national action plan for the pyrenean desman (*Galemys pyrenaicus*)-(PNAD): ecology, distribution and conservation issues: methodological approach

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The National Action Plan for the Pyrenean Desman (PNAD) was launched in September 2009 for a period of 5 years. Three axes (Study, Conservation and Communication) composed of 25 actions have been proposed to enhance the conservation status of the species. The recommendations for management are difficult to implement duet to the very poor knowledge about the biology, ecology and distribution of Pyrenean Desman. The priority is to coordinate a survey of Desman to update the distribution map of the species via a standardized reproducible survey over time. For this, consider what protocols should be considered to ensure reliable and robust results (procedures, frequency over time, the representative sample size, etc) in response to the conservation issues? The objective of this poster is to present the adopted methods which enable to update the distribution map of the Pyrenean Desman (1), to characterize the preferred habitats of the species (2), the genetic characteristics of the species (gender, diversity, fragmentation of populations ...) by faecal sampling (3), to study the impact of human activities including hydro-electric power plants (4). The application of the method, approved by the scientific committee of PNAD, will be implemented in July 2011 throughout the French Pyrenees and on experimental study sites.

How landscape and predation shape eurasian lynx distribution: modeling potential redeployment of lowland western europe by a large carnivore

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Tolerance of anthropic environment has allowed large carnivores to recolonize and to be reintroduced within Europe in the last forty years. This indicates that, even in areas where the return of large carnivores seems unlikely, their presence and establishment is possible, even in highly modified environments. In the current context of the return of large carnivores in Europe, there is a need for scientific conservation tools to assess the full potential and consequences of the return of large carnivores in Europe, and in particular to evaluate potential impact on game and livestock. Today, the return of the Eurasian Lynx (*Lynx lynx*) in areas where it has been absent for long periods is becoming increasingly probable, and this requires further investigations. Three main lines of research will be particularly important: the use of habitat by Eurasian Lynx, the effect of habitat on predation behavior, and potential sources of conflict with human populations. The research project will address fine scale habitat use, the effect of prey's spatial variation on Lynx predation behavior, the use of different statistical methods to estimate Lynx's viability in various habitats and landscape, and a review of current conflicts throughout Europe. Results should allow better understanding of the Lynx redeployment potentials in lowland Western Europe.

The most endangered rodents in Europe? - Taxonomy, distribution and protection status of the mole-rats of the carpathian-basin

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The subfamily of mole-rats (Rodentia: Spalacinae) is one of those mammal groups in Europe whose taxonomy could not have been regarded as clearly established. Out of the taxa representing the group in Europe, mole-rats of the Carpathian Basin have been the least known and understood from a taxonomical point of view. During our research we were the first to run cytogenetic investigations on the Hungarian populations followed by molecular biological study extended to all populations of the entire Carpathian Basin. Our results have proven the existence of five karyologically different chromosomal forms, all endemic to Carpathian Basin. When investigating DNA from mitochondrial genes we found such differences between different froms that arise the necessity of species-level differentiation between some forms. Distribution areas of each form signifcantly differ in climatic terms as well. In the same time while we mapping the distribution of the mole-rat populations of the Carpathian Basin, we also had to face the fact that these unique taxa are extremely endangered. We created an inventory of the factors endangering their habitats. Based on this data we made the IUCN risk assessment of these forms. It has proven that each form has to be treated as a separate conservational unit as they significantly differ in terms of population size and the degree of endangerment. Their protection is a task with prominent importance for nature conservation as with their extinction, rodents that are unique and separated in evolution for a long time would disappear from the planet forever.

Change of small mammal community and subspecies (*Microtus oeconomus mehelyi*) conservation problems in a central-european marshland

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The change in environment will cause a rapid alteration in community composition of small mammals, this may result to the local extinction of specialist species. To avoid this, we need to obtain information from this species such as glacial relict subspecies root vole (*Microtus oeconomus mehelyi*), which only occurs in some relict marshland habitats in Hungary (Fertő-Hanság, Szigetköz, Kis-Balaton). Our investigation was conducted in a marshland area on Kis-Balaton, where data are available for community of small mammals from 12 years. On the basis of anthropogenic effects (firing, mowing) and natural disturbance (drier, wetter weather-period) the 12 study years can be divided into five periods. As a result of habitat degradation, the abundance of several species decreased and some of them (*Microtus agrestis, Microtus oeconomus mehelyi*) became locally extinct. Due to the human perturbance and environmental disturbance significant differences were found in the composition of small mammal community and diversity changes. Due to improving habitat quality and the planned human habitat management such as land-use regulation and mowing, the specially protected root vole recolonized on this marshland area. The multi-season occupancy models showed that the detection probabilities of the two protected vole species was significantly different. The regeneration of habitat quality (2004-2005) was indicated firstly by the field vole. The root vole's estimated probability of occupation of the 4th period (2007-2009: 42%) did not reach the original value (1999-2000: 98%) observed in the homogeneous sedgy habitat.

Abundance and diversity of small mammals under industrial pollution

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We studied abundance and diversity of small mammals – rodents and shrews near copper/nickel smelters in Russia (Revda, Karabash, Monchegorsk) and in Finland (Harjavalta). Ten sampling plots were established along 1-30 km distance from each smelter, consisting of 3 lines with 25 snap-traps per line and exposed during three nights each. In total 879 small mammals were caught. As the distance from the pollution source increased we observed a significant increase (min-max) in: density (0.7-1.3 to 4.6-10.0 ind./100 trap-nights), biomass (11-35 to 76-211 g/100 trap-nights) and species richness of small mammal populations (0.2–1.7 to 3.2–3.4 species/plot). Distinct trophic/taxonomic groups demonstrated a different response on industrial pollution. The most vulnerable to heavy metal pollution and/or habitat disturbance were insectivorous mammals.

Recent extinction of two european mammals – the probable extinction of two mole-rat taxa

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Large scale species extinctions are mainly associated with the biodiversity rich Third World, particularly so with the tropics. Contrary to this, the temperate regions commonly face local and regional extirpations while global extinctions are exceptional. The majority of mammalian extinctions were of smaller-bodied species and more than half of all mammals that went extinct over the last 500 years were rodents. Also the majority of mammals which are supposed to die out in the next few decades, are of small size. Poor taxonomic knowledge hampers the conservation status of many rodents, the situation however is nowhere so hopeless as the one related to the Eurasian mole-rats (subfamily Spalacinae). Frequently claimed that while morphological species of mole rats are possibly not yet threatened within their wide geographical ranges, some of the chromosomal forms are raising conservation concern as being distinct evoilutionary significant units which are worth to maintain. We report subsequently on a probable extinction of two among latter described units. The first is taxonomicaly clumped in the European lesser blind mole-rat *Nannospalax leucodon* from the very margin of the Carpathian basin. It was originaly described as a subspecies *syrmiensis*, but defined subsequently by its unique karyotype with diploid number 2n=54, and number of fundamental arms NF=90. The second was known as a subspecies of the Balkan mole-rat *Spalax graecus*, namely the *istricus* from Romania. During the peak activity of mole-rats the authors visited all the known localities described in the literature of both taxa. But were unable to certify the presence of mole-rats in any of them.

Species and sex identification of otter (*Lutra lutra*) spraints using real-time polymerase chain reaction assays.

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Monitoring and conserving biodiversity is increasingly being recognized as critical for sustainable development. Developing strategies to maintain biodiversity requires baseline information on the current status of each individual species. DNA identification of non-invasively collected samples is an important tool in surveying mammal species. This study demonstrates two assays which utilize real-time polymerase chain reaction technology in the species and sex identification of otter (*Lutra lutra*) spraints. These species-specific assays are based on primers and fluorogenic probes designed to amplify fragments of either the mitochondrial control region (species identification) or zinc finger gene sequences on the X (ZFX) and Y (ZFY) chromosomes (sex identification). The assays are currently being implemented in non-invasive genetic monitoring of otter populations in Ireland and the U.K, and are shown to work efficiently with tissue and spraint DNA. When used together with genotyping assays to identify individuals, the aim is to obtain a more comprehensive estimation of size and structure in otter populations.

Effect of tourist pressure and reproductive period on physiological stress responses in wildcats

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The effects of human activities can have a significant impact on animal populations. The analysis of faecal glucocorticoid levels is a non-invasive method of measuring physiological stress responses of wildlife to human disturbances. The aim of this study was to examine the effects of tourist pressure and reproduction on physiological stress responses in wildcats. The study was conducted from May 2005 to June 2009 at Montes do Invernadeiro Natural Park (NW Spain). Natural Park is divided into three areas depending on the level of protection: restricted public-use, restricted area and integral reservation. To locate fresh scats of wildcats, transects were surveyed on foot along forest roads in the three areas of the park. The number of visitors per day was recorded. Sex steroid hormone and cortisol concentrations were determined from faecal extracts by an enzyme immunoassay. A total of 110 fresh faecal samples were collected. The results indicated that park area and progesterone concentration were the factors that explained the observed variation in the faecal glucocorticoid levels. Cortisol levels were higher in restricted public-use area, where tourism pressure was more intense. Faecal cortisol levels were also higher when progesterone concentrations were high (spring) and during the females gestation and the dispersion of the young (autumn). The results demonstrate negative effects of tourism on wildcats at the physiological level. Therefore, we recommend that some areas be maintained free of visitor impact and that visitor number be controlled during the animals' sensitive periods (gestation and young dispersion).

Session 19 - Conservation and population genetics/genomics of ungulates

Invited & Oral Communication

Performance of different genetic markers in revealing the genetic make-up of a perturbated wild boar population

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Population genetics and phylogeography of game species are challenging. Humans can affect the genetic make-up of wild populations in a number of ways (by harvesting, culling, releasing, translocating, or crossbreeding individuals). The genetic effects of this practices are poorly understood, and the performance of different markers in detecting them should be considered. We investigated wild boar (*Sus scrofa*) populations in Sardinia where the species presence dates back to the Early Neolithic. The genetic divergence of this isolated population justifies its classification as a distinct subspecies (*Sus scrofa meridionalis*). In the last centuries, however, the Sardinian wild boar was likely affected by the introduction of farmed boars from the mainland and the admixture with commercial domestic pig breeds. We sampled wild boars from throughout the island and analysed them with three different classes of molecular markers: 1) the D-loop region of the mitochondrial DNA; 2) 16 autosomal microsatellites; and 3) 60,000 SNPs (Illumina Porcine Beadchip). Sardinian wild boars were examined within a phylogeographic context at a trans-European scale, and compared to commercial and local free-ranging pigs to evaluate possible genetic introgression from the domestic form. All markers revealed a high proportion of endemic diversity in the Sardinian population. Microsatellites emphasized the effect of genetic introgression from non-Sardinian wild boars and from local domestic pigs. Both microsatellites and SNPs detected a cryptic genetic structure, with two pure and geographically separated subpopulations. The relative performance of SNPs and microsatellites was also assessed in relation to the number of markers used.

Microsatellite diversity and population structure of the wild boar in Croatia

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Over the last decades the wild boar (*Sus scrofa*, L.) population experienced a true biological expansion that followed the trend prevalent in all of Europe. Here we analyzed the genetic structure and microsatellite biodiversity of the population of wild boars (260 animals) collected from 16 different locations during organized legal drive hunts. We have also analyzed the genetic structure of 25 domestic pigs as an out-group cluster. Individuals were genotyped for 14 microsatellite loci (S0002, S0005, S0026, S0090, S0097, S0155, S0226, SW122, SW240, SW632, SW857, SW911, SW936, and SW951). At the first level, the Bayesian methods implemented in STRUCTURE program were discriminated into three clusters, one with domestic pigs and two wild boar clusters (Northern versus Southern). At the second level, both, Northern and Southern clusters were further separated into two clusters each. The mean pair-wise F_{ST} values were much lower between the Northern clusters and domestic pig cluster (F_{ST} = 0.161) than between the Southern clusters and domestic pig cluster (F_{ST} = 0.261), while the pair-wise F_{ST} between Northern and Southern clusters was equal to 0.092. The classification and admixture pattern observed was geographically dependent. The phenotypic appearance (white coat color and large number of teethes) of some wild boars indicated hybridization between wild boars and domestic pigs. However, the estimated proportion of domestic pigs based on microsatellite information was negligible (up to a few percent). The results presented will be used in management programs of wild boars in Croatia.

Unexpected population genetic structure of the European roe deer in Poland: an invasion of the mtDNA genome from the siberian roe deer

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Hybridization and genome introgression in animals are more common and have more complex outcomes than it was previously realized. We analyzed the nucleotide sequences of the mtDNA control region (539 bp) and four sex-linked nuclear markers: ZFX (474 bp), SRY gene (621 bp), DBY4 (217 bp), and DBY8 (129 bp) fragments, aiming to infer population genetic structure of the European roe deer (*Capreolus capreolus*) in Poland. The data set consisted of 153 samples of roe deer collected from 17 sites in Poland. We also included samples of eight European roe deer from France and five Siberian roe deer (*C. pygargus*) from Western and Eastern Siberia as references. Unexpectedly, the mtDNA sequences from Polish roe deer were split in two distinct clades corresponding to both *Capreolus* species. The European roe deer in Poland are mainly admixed, as we found 29 *CR* mtDNA haplotypes belonging to Central, West and East Clades. Six mtDNA *C. pygargus* haplotypes found in *C. capreolus* genome were closely related to the Siberian roe deer from Western Siberia. No evidence of introgression were found in sex-linked nuclear markers. MtDNA of *C. pygargus* was noted in 11 out of 17 populations and frequency of hybrids ranged from 17% to 75%. In addition, the number of days with snow cover had an effect on *C. pygargus* mtDNA distribution in the studied area.

The first cross-bred hybrids of wild asses

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Equid remains from Umm el Marra, a northern Syrian elite burial site at the end of the 3rd millenium BC, have been previously proposed on morphological grounds to be hybrids between *E. hemionus* and *E. asinus* (Weber Jill, Archaeozoology of the Near East VIII, 2008). We performed paleogenetic analysis on these as well as remains from other sites as part of a larger-scale palaeogenetic study of the genetic diversity of mitochondrial and Y chromosomal DNA of the small equids *E. hydruntinus*, *E. hemionus*, and *E. asinus* in Eurasia during the middle-late Pleistocene and the Holocene, working in close collaboration with archaeozoologists. Indeed, the genetic diversity of wild asses is poorly known, even at present, and almost nothing was known about their phylogeography. The results of our phylogeographic study allowed us to determine molecularly in an unambigous manner to which species the equids belonged.We will show that some of the genetic results validate the morphological results obtained, i.e., that these equids were indeed hybrids. Moreover, our genetic results also reveal the direction of the hybridization, a detail not possible using only morphological criteria. In conclusion, we present the first genetic proof of the presence of hybrids in an archaeological context, which might have been among the first hybrids in human history.

Identification of illegally introduced deer and their source populations: a European perspective

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Red deer (*Cervus elaphus*) have been subjected to anthropogenic interference for many centuries. Most populations are managed according to hunting schedules, some are kept long-term in enclosures and other extinct, or nearly extinct, populations have been restocked with foreign deer. Moreover, it has been shown previously that farmed red deer have been released illegally in some areas, probably for hunting purposes. Here, we used microsatellites to genotype red deer from 32 different localities across Europe, as well as from one deer farm from northwestern France. Using a geographically explicit genetic assignment method, we show that the farmed deer originated from Scotland, as well as from Eastern Europe. Deer previously excluded from a population in Belgium-Germany-Luxembourg were also assigned to the UK, confirming that it was very likely that they originated from a deer farm. Furthermore, we found evidence of releases of farmed deer in other European populations. We have generated a tool that should allow identification of illegally releases of farmed deer in any European population.

Where did they come from – the origin of sika deer population in the Czech Republic

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The sika deer (*Cervus nippon* Temminck, 1838) was introduced to the Czech Republic at the end of 19th and beginning of 20th century. Since its introduction to the enclosure Kluk in 1891 sika deer has established two free-living populations and continued to increase in numbers. However, the exact places of origins as well as the subspecies status of the introduced animals are unknown. The scarce historical sources suggest the introduction from mainland as well as island populations. The origins of the Czech population was studied using two mitochondrial markers – cytochrome *b* and control region. The phylogenetic reconstruction, using neighbour-joining algorithm, maximum-likelihood criterion and Bayesian estimation, was performed on a data set containing Czech samples as well as samples from sika's native areas in Japan and Russia. The results of the analyses of 449 cyt *b* and 447 D-loop sequences yielded phylogenetic trees with nearly identical topology, containing three main haplogroups, *nippon*1, *nippon*2 and *hortul*. The *nippon* haplogroups contained samples from the Czech Republic and Japan, while the haplogroup *hortul* contained samples from the Czech Republic and Far East Russia. The animals belonging to the *hortul* group are related to the mainland subspecies *C. n. hortulorum*, while those from haplogroup *nippon*1 belong to the larger subspecies *C. n. yesoensis* from northern Japanese islands and those from haplogroup nippon2 originate from the smaller subspecies *C. n. nippon* living in Southern Japan.

Microsatellite based genetic diversity and population structure of chamois (*Rupicapra rupicapra*) in a contact zone between the alps and Northwestern Balkans

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During the 19th century the chamois was reduced to very low numbers in the Alps and was almost exterminated from the Dinaric Mts. of Slovenia. Populations recovered following the implementation of effective conservation management after 1945, but were decimated again in the Alps by a catastrophic sarcoptic mange epidemics in late 1970s. A subsequent recovery increased the chamoix to a currently estimated 104 animals. By scoring sixteen microsatellite loci in 163 individuals in nine populations we analysed genetic variation at the intra- and interpopulation level. Factorial correspondence analysis, Bayesian analyses, and allele sharing distances clustered individuals into tree groups according to their main geographical centres of distribuition (the Alps, the Dinaric Mts. and Mt. Pohorje). Spatial genetic analyses of Dinaric populations retrieved a significant isolation-by-distance pattern. This is explained by a limited gene flow between population isolates in a predominantly forested landscape and severs bottlenecks in the past. The observed demographic history can be explained by low probability of dispersion and small effective size of populations. The effect of the past bottleneck was detected also in a contigoues Alpine population, possibly a legacy of sarcoptic mange epidemics.

Application of bovine SNP chips in conservation genetics of the European bison (B*ison bonasus bonasus*)

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Heavy poaching on the European bison during the World War I lead to its extinction in wild and caused an extremely severe bottleneck. The effects of that bottleneck event had shaped all the genetic aspects of the species and made the European bison one of the least genetically variable species known. High homozygosity caused by almost 50% inbreeding and high homogeneity of the species disable effective applications of standard molecular methods of identity and parentage analyzes. Studies and simulations performed with bovine SNP chip panel showed that application of bovine SNP chips is a credible and reliable equivalent of microsatellites in reproduction success and identity attempts in species with low genetic variation. The simulations showed that customizing of SNP chips and using small SNP panels containing only the most informative loci minimizes the costs without losing the efficiency of SNP application. Bovine SNP chips has been also successfully used in phylogeny studies of the European bison and its relatives, as well as in the analyzes of the genetic purity of some of the European populations with probable hybridization event (events) in its history. Application of high density SNP chips containing 700.000 loci has allowed for advanced and important studies on disease-genome associations in the European bison males affected by postthitis.

A phylogeographic framework for the conservation of Saharan and Arabian Dorcas gazelles

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Many species of gazelles (*Gazella* spp.) are nowadays threatened by hunting, poaching, habitat loss and habitat deterioration. Conservation efforts for this group not only face the problem of maintaining remnant populations, but often natural populations have been extirpated from the wild. In some cases though, captive breeding programs exist that might provide a valuable source for future reintroductions. A major problem in this context is that phylogeographic relationships among different (potentially locally adapted) populations, and even basic phylogenetic relationships between species, are only poorly understood, thus hampering the assignment of management units, breeding groups, or stocks for reintroduction projects. Our present study focused on dorcas gazelles (*G. dorcas* and '*G. saudiya*') from the species' entire distribution range, with samples originating from western Saharan Africa into Saudi Arabia. In stark contrast to previous studies reporting on pronounced genetic structure in taxa like mountain gazelles (*G. gazella*), we detected only low genetic diversity and no evidence for major phylogenetic splits when analyzing two mitochondrial genetic markers. Using a coalescent approach we inferred a steep population decline that started app. 25,000 years before present and is still ongoing, which coincides with pre-historic human activities in Saharan Africa. Our phylogenetic analyses, statistical parsimony network analysis and inferred colonization patterns shed doubt on the validity of various described subspecies of *G. dorcas*.

The impact of Neolithic domestication on the evolution of the genetic structure of cattle populations in Europe and southwest Asia

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The aurochs, the wild ancestor of the cattle, populated Eurasia during the Upper Pleistocene before being domesticated in the course of the Neolithic revolution at the beginning of the Holocene, roughly 10,000 years ago. From archaeological data it is clear that its domestication took place in the Northern Fertile Crescent. The proof on the genetic level of this fact has not been brought about unambiguously yet. It is also unclear whether domestication processes or introgression events took place in Europe.In the framework of a close collaboration with archaeozoologists we performed a palaeogenetic study of remains of wild and domesticated cattle from Europe and Southwest Asia (SWA) spanning the last 10,000 years. This study is based on considerable methodological development to overcome the severe problems linked to reagent contamination with bovine DNA. Our recent results identify SWA as one of the centers of domestication and allow for secondary domestication events to have taken place in Europe. These initial processes followed by migrations and zoonoses seem to be responsible for the population structure of the taurine cattle at present.

Population genetics of the Asiatic wild ass: insights from the past

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Paleogenetics can potentially elucidate past animal population structures and monitor recent human-induced fluctuations of the genetic diversity. The Asiatic wild asses whose geographical distribution in the Pleistocene and the early Holocene stretched from Northern Africa to Eurasia had to be put on the IUCN Red List of threatened species before they were genetically well studied. Indeed, little is known about their population dynamics, population structure and phylogeography. We undertook a palaeogenetic study of the genetic diversity of the Asiatic wild ass during the Middle-Upper Pleistocene and the Holocene by analysing the mitochondrial hypervariable region and Y chromosomal SNPs in ancient and modern bone and teeth remains and modern samples from Western Europe and Asia. The genetic data that we obtained from ancient bone and teeth samples in combination with data from extant individuals reveal seven significantly distinct populations. This structure becomes only apparent through the ancient DNA data. Two of the populations are exclusively composed of extant animals because ancient samples from the corresponding area were not analyzed. Most importantly, however, three of these populations seem to be extinct at present. Two populations are composed of ancient and modern individuals that were thought to belong to two different subspecies, i.e., *E.hemionus kulan* and *E. hemionus hemionus*. These results should assist in devising conservation strategies.

Poster Communications

The Taxonomy and Phylogeography of two Arabian gazelles

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The phylogeny of Arabian gazelles is generally not well understood. The existence of several described species and subspecies with partly unknown relationships led to considerable confusion about taxonomy. Phylogenetic relationships were so far inferred primarily from morphological features. The aim of this project was to characterize several Arabian, African and Asian gazelle species genetically while including those taxa with taxonomically uncertain status. Here we analyzed sequence divergence of mitochondrial DNA markers of the two most widespread gazelles on the Arabian Peninsula, the mountain gazelle (*Gazella gazella*) and the goitred gazelle (*G. subgutturosa*). Our genetic analyses uncovered phylogenetic relationships that are not congruent with previous classifications based on morphological data. In the case of the mountain gazelle (*G. gazella*) two reciprocally monophyletic lineages were found, one of which is restricted to a small area on the Golan Heights. In the case of the goitred gazelle we could demonstrate that '*G. subgutturosa*' is polyphyletic and that Arabian sand gazelles (*G. marica*) – which were previously thought to be a subspecies of goitred gazelle – are more closely related to African gazelles than to Asian *G. subgutturosa*.

Genetic diversity and phylogeny of the western Derby eland (*Taurotragus derbianus derbianus*)

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The Western Derby eland belongs to the animals critically endangered by extinction. The last wild population of approximately 170 individuals (in 2006) was discovered in Niokolo Koba National Park in Senegal. The unique semi-captive breeding programme was established in 2000 in the Bandia Reserve in Senegal. The breeding programme started with 6 wild-caught founders (1 male, 5 females) and currently developed into 76 individuals managed by the programme of Czech-Senegalese cooperation. The kinship relations in the population are determined by means of direct observation of sucking calves and their mothers. We have succeeded in having almost complete pedigree data forming the base of studbook. The aim of this study was to determine genetic diversity in the population using microsatellites and to revise some uncertain pedigree data. Another aim was to identify phylogenetic relationship between Western (*T. d. derbianus*) and Eastern (*T. d. gigas*) subspecies by means of mitochondrial DNA (cytochrome *b*), because their phylogeny has been described only on the basis of morphological characters. We used 13 microsatellite loci for evaluation of genetic diversity. We examined the microsatellites which were originally developed for cattle and goats. Preliminary results showed very low number of alleles per locus, we have found only 5 polymorphic loci with 3 alleles. This indicates low genetic diversity in the population, which relates to low number of founders and their high genetic similarity to each other. The low level of polymorphism complicated the determination of kinship relations and the description of population parameters.

Session 20 - Macroevolution

Invited & Oral Communication

The importance of time and geography to the study of mammal paleocommunities

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The community paleoecology of mammals is one of the cornerstones in our understanding of mammalian evolution. In addition to this, an understanding of mammalian paleocommunities and their responses to changes in climate and environment has the potential to become a key aspect in the study of the effects of the present global climate change crisis on mammals. But what do we then mean by 'community'? In order to develop the potential of community paleoecology, paleontologists and neontologists should, ideally, have a common frame of reference setting the boundary conditions of their work. Neontology and, paleontology share a number of problems when it comes sampling of communities. However, these are more clearly evident in paleontology, where issues such as the scale of the geographic catchment area of a 'paleocommunity' and the time-averaging of most, if not all, paleontological samples mean that paleocommunities rarely if ever are directly comparable to modern mammal communities (which themselves are often poorly defined). Therefore, some form of mutual *rapprochement* is required, so that it becomes possible to integrate modern community studies with paleocommunities. In this contribution I shall explore some issues related to paleocommunities and their significance, with emphasis on how geographic and temporal scale affects the relationship between paleocommunities and modern communities, as an initial step towards such integration.

Opening of habitat and colonization exchanges drive diversification in South American Caviomorpha (Rodentia, Hystricognath)

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With the increase of our knowledge about the tree of life, the recent development of phylogenetic methods has offered an alternative way in assessing evolutionary processes through time. These methods that do not rely on fossil evidence have shed new light on macroevolutionary patterns for many clades such as Mammalia. Within the Rodentia, the South American Caviomorpha constitute a major evolutionary radiation with more than 131 extant species and 46 genera. This astonishing specific diversity is shown most notably in terms of ecology, morphologies, and geographical distributions. Using recent methods of ancestral area reconstruction, macroevolutionary methodologies, morphometric data and a molecular dated tree, we studied the biogeographical and morphological history of the Caviomorpha. Our biogeographical analysis reveals 4 dispersals into and 8 out of Central Amazonian area to adjacent regions. We also detect three shifts in diversification rate linked to shifts between close/open habitat and changes of altitudinal gradients. We show that, during the late Miocene, the Southern South American and Andean lineages significantly increased their taxonomic and morphological diversity compared to their Amazonian counterparts. This increase in diversification rate is correlated with major ecological shifts (e.g. open close vs habitats, nocturnal vs diurnal, different types of diet). In agreement with paleontological studies, our results show that the opening of the habitat have likely played a major role in the diversification dynamic of Caviomorpha.

Time scale in evo-devo and emergence of new phenotypes: The case of vole teeth (Rodentia)

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Recent studies have improved our knowledge of tooth developmental processes and the impact of development on resulting phenotype. Different morphogenetic processes as reiterative signaling cascade of inhibitor and activator balance along the dental row have been described. New methodological advances have also been proposed allowing the inference of developmental processes from adult morphologies (modularity/integration, Klingenberg, 2003) and from molar proportions (Kavanagh et al., 2007). The characterization of the degree of developmental integration/modularity of morphological traits is now approached by studying the patterns of variation within and among individuals. Modularity is defined by the fact that organisms are divided into biological parts which are hierarchically structured and partially integrated to ensure coherence. For instance, most modularity and integration studies on mammals have dealt with skulls and mandibles. For a paleontological perspective, we focused our study on teeth and particularly on the vole lower molar row. Our results have suggested i) quasi-independence of each molar at the developmental level (developmental modules), even slightly stronger for the third molar as demonstrated by genetic and developmental hypotheses, and ii) more pervasive integration processes among molars at the morphological level. On another hand, a model established from murine dental development has recently been proposed to predict evolutionary patterns in lower teeth. Changes in inhibitor or activator produce modifications in molar tooth proportions and lead to different morphotypes. However, some taxa, as voles, do not fit well the model due to their oversized and prismatic first lower molar (Renvoisé et al., 2009). We here tried to understand the emergence of this phenotype and the timing of the occurrence of new prisms through time, from five up to nine, in some vole lineages.

Evolution of mammal tooth patterns: New insights from a developmental prediction model

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Understand how plants and animals have been survived in their past history and how developmental mechanisms constrain phenotypic traits to evolve, can help to predict their change of future survival. The classic adaptive radiation of mammals during the Eocene epoch, 55-35 Ma ago, is punctuated, and thought to be facilitated, by several evolutionary novelties in their dentition. These structural changes range from highly organized enamel microstructure to specific cuspal features increasing chewing efficiency. Development is a key component in the production of endless forms and has a crucial role in constraining biotic diversity and evolutionary trajectories. One example is the developmental model proposed by Kavanagh et al. (2007), which provides a high-level testable model to predict mammalian tooth evolution. It is constructed on an inhibitory cascade model based on a dynamic balance of activators and inhibitors, regulating differences in molar size along the lower dental row. Nevertheless, molar sizes in some mammals differ from this inhibitory cascade model, in particular in voles. The aim of this study was to point out arvicoline and murine differences within this model and to suggest an alternative mathematical model. Here we demonstrate that the inhibitory cascade is not followed, due to the arvicoline's greatly elongated first lower molar. We demonstrate that arvicoline evolution is rather characterized by a large gap from the oldest vole to more recent genera, with the rapid acquisition of a large first lower molar contemporaneous to their radiation. Our study provides alternative evolutionary hypotheses for mammals with different trajectories of development.

Molecular systematics, life traits and ecological niches of the mongooses (Herpestidae, Carnivora)

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The Herpestidae are small carnivores comprising 34 African and Asian species. It is an ecologically and behaviourally diverse family that occupies a broad range of habitats, and displays a wide range of social behaviour, from solitary to social species. Our work suggests that there are two subfamilies within the Herpestidae: the Mungotinae, small, social mongooses (occurring in Africa) and the Herpestinae, large, non social mongooses (occurring in Asia and Africa, with an Asian monophyletic group). We inferred an Early Miocene African origin for the Herpestidae, and a Middle Miocene origin for the Asian mongooses. Our phylogeny allows us to infer the evolution of some life traits (social organisation, activity, and habitat preferences). The ecological niche preferences of four Asian species provide an explanation for their distributions and the impact of barriers on their population structure.

The factors involving the evolution of locomotor apparatus in moles

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Digging of moles is unique among all the burrowers. In the others the forelimb movement is directed from the front to the back and slightly laterad, whereas in moles the arm goes only sideways. The humerus hyperabduction changes the bone orientation: the distal end is upward and forward, the medial side becomes lateral. The articulation between scapula and clavicle hinders the motion of the limb, therefore in moles the clavicle associates with the humerus. The humerus broadening in moles results in the lengthening of the force's lever of the m. teres major which is especially enlarged. However the m. teres major cannot pronate the humerus since the m. flexor digitorum profundus prevents from it. Thus the m. teres major functions for the strengthening of the hand pressure on the ground. It is necessary to transfer the power from one side to another, so in moles the clavicle become shorter and has a cuboid form. In the specialized moles the forelimb can be moved far ahead without its lengthening, because of the long presternum. Else the force's lever will increase with lessening the hand pressure on the soil. The fixation of the forelimb makes the force's lever shorter. The holding in the elbow joint is performed by the elongation of the olecranon; on the contrary the muscles are weakened.

Evolution of lactation: when, how and why. New perspectives for paleontologists

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Lactation, a complex secretion designed to optimize newborn development and health, is unique to mammals. Its origin is still debated. It is unclear whether it appeared suddenly, in line with the punctuated-equilibrium theory, or gradually, through progressive acquisitions, in accordance with the classical Darwinian model. Biochemical, endocrinological, ultrastructural analogies of the different mammary glands prove that lactation was developed by the Mesozoic common ancestor of all mammals. The lineage that led to mammals first appeared about 305 Ma. Mammalian features appeared during the next 100 Ma among different mammal-like synapsids. The mammary gland can phylogenetically derive either from epidermal apocrine glands associated with a hair follicle, and/or from the innate immune system. The ventral mammo-pilo-sebaceous units of oviparous monotremes, connected with nipple-free areas, are a possible living example of the archaic glandular concentration that evolved to keep moist synapsid ***parchment***-shelled ***eggs*** during incubation, which are at risk of dehydration. The evolutionary success of lactation was also ensured by the inclusion of antimicrobial factors in epydermal secretes, which enhanced offspring survival in an environment infested with parasites. In this reconstruction, proto-mammary glands provided hydration and immunity to developing embryos and neonates prior to nutritional support. The conclusions of genomic analyses and physiological studies suggest that paleontologists should perhaps focus on various skeletal changes (i.e., smaller size, secondary palate, diphyodont dentition, and epipubic bones) that seem to be more or less directly correlated with the acquisition of mammary glands and higher metabolic rates.

Poster Communications

Morphological study of molar teeth in *Neosaimiri* and *Saimiri*

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The lower molar of *Neosaimiri*, which is a fossil species of *Saimiri*, has a postentoconid notch present mesiobuccally to an entoconid. This is believed to be a feature of *Neosaimiri*. In addition, the position of wear facet 8 in extant *Saimiri* is same as that of the notch in *Neosaimiri.* However, *Saimiri* with notch was confirmed. There is a possibility that same dental microwear as the one formed to facet 8 exists there if notch and hypocone during chewing each other. Moreover, there is *Saimiri* with notch by the height of hypocone and the size of upper molar and is the same size as *Neosaimiri* possibility. In the present study, the correlation between notch and hypocone of the two species was examined. The microwear pattern on facet 8 at each developmental stage was observed by SEM and digital microscopy (20–500×). Hypocone height and molar size were measured using callipers. Microwear formed on facet 8 due to a hypocone was similar to the pointed part that existed in the object forming the notch observed. Hypocone height in the *Saimiri* with a notch was greater than that in normal *Saimiri*, that was almost the same as *Neosaimiri* and usual. In addition, the size of upper molar was also larger than that in normal *Saimiri*. Since evolution to the *Saimiri*, height of the hypocone of the upper molar has gradually decreased and the number of individuals with a hypocone height sufficient for chewing a notch has decreased.

Evolution of molar proportions in rodents: Macroevolutionary and developmental hypotheses

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Dental material, usually well preserved and abundant in the fossil record, is frequently used to study mammalian history based on the evolution of morphological characters, conjointly to several recent studies improving the knowledge of tooth development (Jernvall and Thesleff 2000, Peterkova et al. 2006). A development model, based on murines (Kavanagh et al. 2007), has been proposed to explain relative molar proportions according to an inhibitory cascade and has been extended to other rodent groups such as voles (Renvoisé et al. 2009). The aim of our study is to understand the evolution of molar proportions in rodents through time. In fact, rodents present a decrease in the number of teeth, especially with the disappearance of canines and premolars. The diastema is present since at least the Eocene (Keränen et al. 1999, Viriot et al. 2002) and some species lack of premolars although others remain one or two. Some authors suggested that particular dental phenotypes such as molar elongation could be allowed by the absence of premolars. The influence of the presence of the fourth premolar (p4) on the relative sizes of molars is studied using extinct and extant taxa, distributed on a large time scale from Eocene to Recent and among several rodent families. Our results suggest that old extinct families with p4 show pattern with quite equal molar size whereas recent families show more unequal molars. The p4 has an influence on molar size, especially the m1 is bigger when the p4 is absent. However, p4 has no influence on molar relationships as described by developmental model.

The dental morphology of the rhinoceros of the genus *Elasmotherium* Fischer, 1808 from the late Pliocene – middle Pleistocene of eastern Europe

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Elasmotherium is a peculiar rhinoceros characterized by its very large size and huge (“horn basement”) frontal bone. These animals are known from the Late Pliocene to the Middle Neopleistocene of Eurasia. In spite of the fact that *Elasmotherium* has been studied for more than 200 years by many respected experts, our knowledge about this animal remains very poor. In this connection the objective of our project was to make a comparative study of all available *Elasmotherium* teeth. Our research has shown that the morphological structures and dimensions of the upper teeth changed as worn (age variability). The teeth ontogenesis of *E. caucasicum* Borissiak, 1914 (Late Pliocene – Middle Neopleistocene) differs from *E. sibiricum* Fischer, 1809 (Early - Middle Neopleistocene). The upper teeth of *E. caucasicum* have an open pulp cavity in the early stages of ontogenesis and early root forming. The postfossette functions for a long time. On the contrary, the upper teeth of *E. sibiricum* are characterized by the open pulp cavity which closes in the late stages of ontogenesis. The postfossette of *E. sibiricum* is worn very fast. The comparison of wear stages between *E. caucasicum* and *E. sibiricum* has shown that they differ by postfossette condition (lack or presence). Thus, variability of morphological structures and dentition ontogenesis should be taken into account in taxonomic identification.

Session 21 - Mammalian population ecology

Invited & Oral Communication

Grasses bite back! The role of induced silica defences in vole population cycles

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Long-term studies investigating the causes of cyclic population dynamics in microtine rodents have focussed on the role of top-down processes such as predation or parasitism. We propose an alternative, bottom-up mechanism which may be able to drive vole population cycles in some locations, e.g. those with low amplitudes, and suggest that nutritional constraints imposed by plant defences may limit individuals' reproductive potential. Laboratory experiments have shown that grazing by field voles (*Microtus agrestis*) can increase concentrations of silica in grasses, thereby reducing digestibility and limiting animals' ability to absorb nitrogen, which is essential for growth and reproduction. We tested the hypothesis that past grazing pressure de-stabilises vole population dynamics through delayed density-dependence in silica induction. We carried out experiments in the glasshouse and the field and found that vole grazing is sufficient to induce silica uptake in the grass *Deschampsia caespitosa*, but only after a threshold vole density has been reached. We also demonstrated that induction and post-grazing relaxation of silica are time-lagged processes. Both of these factors are a necessary requirement for the initiation of population cycles. We then used a manipulative field experiment to test relationships between food availability and quality on the reproductive success of individual field voles in Kielder Forest in northern England. Finally, we applied a simple mechanistic model to our empirical data from the glasshouse and a long-term data set of vole population dynamics in Kielder to demonstrate that delayed density-dependence in silica uptake can generate multi-year population cycles in voles.

Trophic interactions key to climatic effects on herbivores

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The regularity of population cycles of several species has recently declined in many areas. Climate change is often implicated as a contributor, although little is known of how weather proximately affects cyclic populations. To obtain reliable estimates of weather effects on animal populations, spatially and temporally extensive data are required. We combined data on vole abundances and weather, collected at 32 locations throughout Finland from 1970 to 2010, to investigate the effects of temperature, rainfall and snow depth on vole population growth, allowing for geographical, seasonal and species differences. Overall, during the past 40 years summer growth rates of voles have increased and winter declines become steeper. However, these changes differ between vole genera. *Microtus* population densities have generally increased, whereas *Myodes* densities have declined. Consistent with these trends, *Microtus* populations are more resilient to weather variations, especially during winter. Summer and autumn weather influences vole populations immediately but also with a delay. The direct and delayed effects may synergistically drive vole populations towards seasonal dynamics and alter vole communities by exacerbating the differences in the effects on different species. Conversely, winter weather and snow depth appear of minor importance to vole population growth. Our results challenge the currently predominating view of the importance of winter snow depth on the demography of cyclic populations, and underline the weight of trophic interactions mediating population responses to climate change. The changes in vole densities and seasonal growth rates due to climate change may result in altered vole community composition and population dynamics. Ultimately, these changes are likely to influence trophic interactions and ecosystem dynamics.

The impact of predation on small rodent population dynamics as exemplified by the root vole (*Microtus oeconomus*)

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Population cycles of many herbivorous small mammals are a well known phenomena which have mainly been described at high northern latitudes. The results of numerous studies and experiments conducted in Fennoscandia have accumulated evidence that specialist predators are the key factor in generating small-mammal population cycles. In the presented paper I analyzed long-term root vole population dynamics and tested the role of specialist predators (least weasel, stoat and avian predators) in root vole population dynamics in NE Poland. This root vole population exhibited endogenous five-year cycles. This study is the first empirical analysis of inter-annual cycles for this species. The results show that avian predation only reduced root vole survival in late winter and early spring, whereas from late spring to early winter predation by birds had no impact on vole population dynamics. Small mustelid population density had no impact on root vole population growth rate, whereas vole density did affect weasel population size. There was no time lag in the change in the weasel population in response to root vole population dynamics. Additionally, excluding weasels and stoats did not prevent the root vole population from crashing during the downward phase of the root vole cycle. Moreover, there were no changes due to predator exclusion in the basic root vole population parameters: population density, population growth rate, sex ratio and survival rate. This research indicates that the two groups of predators, small mustelids and avian predators, are not able to generate negative feedback loops in endogenous root vole population cycles.

Small mammal population cycles in the Urals southern taiga and "predator-prey" scenario

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The density of small mammals in the study area (N57°22′402″, E59°46′409″) was characterized by surprisingly regular two-component dynamics (since 1984 up to 2007), consisting of weak seasonal and strong three-year cycles. The number of small mustelids caught preceded the prey crash occurring every three years (but, 2007-08 in sequence) and was associated with a high prey density in the previous autumn and in the current spring. We used GLM and model selection technique to determine the relative importance of different lags in the delayed response of the least weasel to prey density. The strongest support ($w=0.96$) was found for a model with a lag of about 9 months. In the next step we developed a dynamical model – a system of two differential equations with delays. In contrast to our model we added seasonality in the prey carrying capacity and a delay in the prey self-limitation term. At least two features in the dynamics of our model were similar to reality: the high winter prey survival at the transition from "increase" to "peak" and inconstant intra-year trajectories in these phases. When the predator term is excluded from the model ($\eta \equiv 0$), the prey dynamics has a seasonal oscillation only. We noted that the mortality caused by specialist predation remains uncompensated due to discontinuity in prey reproduction under seasonal environments. We argue that a strong predator–prey interaction is the key factor behind small mammal population cycles in the Middle Urals southern taiga.

Dynamic and structure of lemming populations in the western sea coast of Taimyr

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We studied populations of Siberian (*Lemmus sibiricus*) and Collared (*Dicrostonyx torquatus*) lemmings at the Pyasina Bay coast in north-western Taimyr (74°10´ N 86°45´ E). Lemmings were captured by three different methods: by snap-traps on permanent lines and plots in the main types of habitats and by live traps on permanent plots in the dominant type of habitats. The dominant species - Siberian lemming from 1981 to 1995 in the study area had a 3-year cycle and coincided with dynamics of collared lemmings. After 2000 there was a peak abundance of Siberian lemming in 2005 with especially high local densities followed by an extremely deep depression. A similar situation we observed after peaks in the 1990s. We did not identify a peak in 2008 as we expected. However, indirect indices (abundance of avian predators, arctic fox and least weasel) showed that at the end of the snow melting period the number of lemmings was quite high. Based on these, we suggest a tendency of 3-year cyclicity to be present in the fluctuation of lemmings in this region, especially in Siberian lemmings. The proportion of Siberian lemming females was smaller during the peak of 2005 than in 1994. But average litter size was significantly bigger in 2005 than in 1994. Perhaps this is one of the mechanisms which supports high population densities an increase in litter size when the proportion of females is low.

Do population cycles promote different life history tactics? Experiments with the bank vole

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Cyclic fluctuations in population densities are a common phenomenon in free-living animals. These fluctuations can maintain genetic variation or even promote the existence of specialized genotypes, however, evidence for this is still surprisingly scarce. We set out to investigate this in the bank vole (*Myodes glareolus*) by conducting enclosure experiments both during the breeding season and during the winter. In the experiments, we used common garden reared individuals that originated from founders caught during the high or low phase of a vole cycle. Breeding characteristics and survival of individuals were monitored in full factorial experiments where, in addition to the origin of individuals (low or high cycle phase), population density (low or high) was manipulated. In the summer, females had a lower breeding success when the density was high, but it did not interact with the origin of individuals. However, in winter experiments, females from the high phase of the cycle initiated reproduction significantly earlier in the spring than females from the low phase, thereby leading to higher reproductive success. Our results suggest that cyclic fluctuations may promote genetic variation in life history tactics, which then could facilitate the existence of specialized morphs in populations of cyclic rodents.

Spatial genetic structure and dispersal pattern of the mandarin vole (M*icrotus mandarinus*)

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Dispersal behavior is a complex phenomenon affected both by natural environment, as habitat fragmentation, and by species biology, including type of social system and breeding behavior. The mandarin vole is an excellent model for studies of population ecology in connection with dispersal behavior. It is a territorial subterranean rodent with a sophisticated social system, which is unusual for most voles. Nevertheless, its dispersal behavior and spatial genetic structure in natural environments is almost unknown. The vole population from the Transbaikal region of Russia, which is apparently isolated from the rest of the range, was studied on different spatial scales. We investigated three localities, separated by distances from 35 to 100 km. Observed high genetic differentiation (pairwise F_{ST}=0.06, 0.24 and 0.17, P<0.001) indicates considerable gene flow restriction between the fragments. On a moderate spatial scale (several km between patches comprising one locality), genetic differentiation levels vary between sexes, being greater for females (F_{ST}=0.053) than for males (F_{ST}=0.036), thus gene flow is male-biased. The finest scale analysis of one particular patch showed that mandarin vole females do tend to stay philopatric, their dispersion distances being limited to 300 m, compared to 600 m and more for males. Thus, gene flow in the Russian population of the mandarin vole is significantly restricted at various spatial levels, though the dispersal pattern is similar to that in other vole species.

Predation risk and supplemental food: opposite effects on overwintering success and onset of breeding in the boreal rodent

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In the seasonal environment, survival and optimal onset of breeding play major roles in fitness of an individual. It is assumed that many physiological or behavioral factors related to the breeding increase the risk of predation. This means that an individual should make breeding decision based on current risks and benefits. In certain circumstances it may be beneficial to postpone breeding if current predation risk is high. In north food availability is declining during winter and it is lowest just before onset of breeding in spring. Food constraint may also cause physiological incapability to start breeding. We studied effects of food supplementation and predation risk (weasel, *Mustela n. nivalis* odour) as determinants of survival in winter and onset of breeding in bank voles (*Myodes glareolus*) in 2 x 2 factorial experiment. The experiment was conducted in 20 outdoor enclosures (0.25 ha) in central Finland. Survival probabilities in founder populations were highest in food supplementation while they were significantly lower in predator risk treatment. Voles with supplemental food started to breed earlier than the voles in control and in predator treatments. Predation risk affected negatively vole condition and survival also in combination with supplemental food. We conclude that during energy constrained harsh conditions in winter, the high risk of predation has important negative survival and fitness effects for small mammals. Generally, predation risk effects should be taken in to account more carefully in issues related to conservation or population management.

Regime shifts in mammalian population ecology

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Climate change and persecution of large carnivores are processes which can trigger pervasive changes in the structure and function of ecosystems. The impacts may act on the ecology of individual species, but also cascade through the ecosystem and alter the relative importance of top-down and bottom-up control. Fennoscandia comprises a bioclimatic gradient from temperate forests to Arctic tundra. Top predator extirpation characterised the 19th century, whilst the 20th century faced top predator recovery and climate warming. Changes in top predator status caused regime shifts in the mammal community. Historic persecution of wolf (*Canis lupus*) and Eurasian lynx (*Lynx lynx*) caused mesopredator release of red fox (*Vulpes vulpes*) in Sweden. In the 20th century, lynx recolonisation caused cascading shifts between top-down and bottom-up regulation of fox and shared prey, the mountain hare (*Lepus timidus*) in Finland. Importantly though, top-down impacts were mediated by bioclimatic conditions. Predator abundance had to increase with ecosystem productivity to counteract the bottom-up impact of productivity on prey. Consistent with these findings, theory predicts that predator impacts are weaker in unproductive northern ecosystems. Hence, a warmer climate should strengthen predator control, allow establishment of resource-demanding species and cause regime shifts as tundra/boreal ecosystems turn temperate. This is supported by fading population cycles in Norwegian lemmings (*Lemmus lemmus*) and voles (*Microtus/Myodes spp.*), and by red fox range expansion in tundra habitat which causes behaviourally-mediated exclusion of the arctic fox (*Vulpes lagopus*). A future challenge is to investigate the interacting processes underlying these regime shifts.

Diet changes in American mink population in the Snæfellsnes Peninsula, West Iceland

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The alien invasive American mink *Neovison vison* is fully established in the low biodiversity and competitor-free environment of Iceland. The population appears to have peaked in 2002-2003, followed by a continuous decline until 2009. In an effort to reveal the causes of the population decline we analysed the stomach contents of 662 mink obtained from hunters in 2001-2009. Prey remains were classified to order and species level if possible. During the period in question there was an increase in total fish consumption in spring in both sexes while we found no trends in marine fish. Birds in the minks' diet showed general strong negative trends, which were mostly apparent for all mink in spring, when all groups of birds were decreasing in the diet. Invertebrates, however, showed increasing trends which were most apparent in the warm months for males but in the cold months for females. Rising sea temperatures and various marine changes have occurred in Iceland in recent years. The numbers of wintering waders have decreased steadily since 2002 and Iceland has also seen a recent decline in a number of seabird species. The decrease in seabirds has been linked to a recent collapse in the sandeel population around Iceland. Thus we suggest that changes in the marine environment are an indirect cause of the change in mink diet.

Tendencies of hunting mammals population dynamics: analysis of long-term account data, mathematical modeling, priorities and ways for mammal conservation

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A detailed analysis of long-term account data for the main hunting mammal animals is carried out. The population size dynamics of the following hunted animal species is analyzed: herbivores - Ussurian moose, Manchurian deer, Manchurian roe; Ussurian wild boar; predators- Ussurian brown bear, Siberian forest wolf, Ussurian fox, Siberian river otter, Siberian sable, Manchurian weasel; rodents and hares – Sakhalin-Amur squirrel, Amur blue hare and Manchurian hare. The approach based on mathematical modeling is used for the description of tendencies in population size dynamics. A general mathematical model of the population dynamics of the harvest species has been developed. It reflects a periodicity of the reproduction process and focused on the description and research of demography, population dynamics and hunting influence results. Model parameters are estimated on the basis of harvest statistics and account data for the hunted mammal animals. Modeling retrospective forecasts made it possible to show adequacy of the model to the majority of game species. It is shown that maintenance of the population size and age structure for many game species is determined by their migration activity. Reserved territories promote preservation of hunting species and determine even some growth in their population size, but it is obviously insufficient. It is necessary to expand the territories free from harvesting and transfer to the strategy of rigid restrictions of hunting for the populations with a depressive regime of dynamics.

How to mitigate effects of climate change on arctic fox viability – a field experiment

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Populations often go extinct during periods of unsuitable climate. The arctic fox went extinct in central Europe during Late Pleistocene. Today a similar scenario is enacted in Scandinavia where arctic foxes are close to extinction due to climate related changes in the ecosystem. The main threats are the small population size constrained by low food availability due to fading lemming cycles and competition from the larger red fox. In a large scale action programme in Sweden, Norway and Finland (SEFALO+, 2000 – 2010), we experimentally added food (commercial dog pellets) at active arctic fox dens. In the same areas we also reduced red fox numbers by culling. Yearly monitoring of about 1000 known arctic fox dens showed that the population doubled as a response to the actions. Detailed path analyses revealed that 20% of the increase was related to the feeding programme, 20% to red fox culling and 50% to lemming peak years. These results demonstrate a specific consequence of climate change in a sub arctic ecosystem and the importance of lemmings as a key species. It also demonstrates that it is possible to halt population declines by intensive actions programmes and even to turn negative population trends into positive increases.

Contribution to the study of the biology of populations of three endangered species of bovidae: scimitar-horned oryx (*Oryx dammah* (Cretzschmar, 1826)), addax (*Addax nasomaculatus* (De Blainville, 1816)) and mhorr Gazelle (*Nanger dama mhorr* Bennett, 1833) In Bou Hedma National Park (Central Tunisia)

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Scimitar-horned oryx (*Oryx dammah*), addax (*Addax nasomaculatus*) and mhorr gazelle (*Nanger dama mhorr*) are very endangered species in the world. The two first species have been re-introduced in Bou Hedma National Park (Central Tunisia) in 1985 while the introduction of the mhorr gazelle has taken place between 1992 and 1995 in this same protected area. Survey of the three populations has permitted the analysis of the evolution of the numbers and the study of some demographic parameters of these species living in semi-natural conditions. Monthly data spanning 15 years has been used for this study. Thus, although births and deaths of the three species are extended to the whole year, autumn and winter are the seasons of the maximum births of oryx (with 26.86 % of the total annual births in each of the two seasons). Winter is also the season of the maximum births of mhorr with 33.33 % of the total annual births. The births of addax are at the maximum in spring (38.33 %). Births of oryx (21.71 %) and addax (11.6 %) are at the minimum in summer and those of mhorr (16.66 %) in winter. Mortality rates of the three species are at the maximum in winter (31.65 %, 39.70% et 40 % of the total annual deaths respectively of oryx, addax and mhorr) and minimum in summer (14 %, 16.17 % and 19.42 %). The resort to the autocorrelograms allowed to envisage the future tendency of the three species and suggest a certain rhyth in the three populations with successive periods of increase and decrease in numbers.

Cryptic structure, and unusually high proportion of breeders in grey wolf (*Canis lupus*) population under hunting pressure

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In general, assessments of population viability typically rely on limited data, often involving only estimates of population census and harvest rate, while largely ignoring the impacts of hunting on population structure, breeding behaviour and social structure. To investigate the population structure and genetic diversity of a grey wolf (*Canis lupus*) population under strong hunting pressure, we genotyped 16 microsatellite loci of 166 wolves sampled in northern Europe, namely in Estonia and Latvia. Instead of a panmictic population in the relatively small area occupied fairly evenly, wolves in Estonia and Latvia were structured into four contrasting genetic groups. The sub-structuring was further supported by a spatial analysis that indicated that the three of the groups are clearly disjointed. The presence of such sub-structuring was unexpected regarding the limited extent of the study area, high mobility of the wolf and the absence of obvious movement barriers. Moreover, analyses revealed unusually high effective population size (*Ne*), *i.e.* the proportion of breeders, compared to other wolf populations that are protected or under mild hunting pressure. Thus, the high *Ne* and population sub-structuring are most likely the consequence of intensive hunting, which has disrupted the natural social structure of wolves. As being highly social animal, disrupting the natural social structure reduces fitness and survival and has also evolutionary consequences. From the general population conservation and management point of view this study provides a cautionary example of consequences of strong hunting pressure.

Climate destabilisation and agricultural intensification linked to changes in hare population dynamics and long-term decline

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Hare populations are renowned for their complex dynamics, and more recently, their widespread decline. Regular cycles in abundance are best known from arctic species, most notably snowshoe and mountain hares, whilst population crashes have characterised recent temporal trends in southerly species, most notably the European hare. The 'tri-trophic' or 'predator-prey-winter food' hypothesis is frequently invoked to explain regular cycles in the abundance of high latitude species, contingent on snow conditions affecting food availability and predation whilst agricultural intensification has been attributed as the main cause of declines among farmland species throughout Europe. We demonstrate that the dynamics of a hare population, located at intermediate latitudes and free from severe winters and significant predation pressure, was also driven by climatic oscillations during a stable regime in the past (1852-1908). Specifically, the hare population throughout Ireland and the autumn Northern Atlantic Oscillation Index ($aNAO_t$) exhibited a coherent 8 year cycle in which the $aNAO_t$ was the leading wave. Moreover, hare population growth was positively correlated with the $aNAO_{t-1}$ which we speculate may have modulated dynamics by influencing grass growth and the maturation of late born leverets. However, climate destabilisation during the early 20th century was coincident with the collapse of regular cyclicity whilst the initiation of agricultural intensification a few years later was correlated with a dramatic 86% decline in numbers (1909-1968) similar to the magnitude of hare declines throughout Europe. This is the first study to demonstrate the joint effect of early climate change and agricultural intensification in disrupting mammal population dynamics driving long-term declines.

Poster Communications

Pulsed resources and habitat selection by rodents: a case study in managed beech stands of western Poland

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We evaluated the effects of habitat structure (shaped by different types of forest management) and masting on rodent populations in beech stands of western Poland. Animals were live-trapped during summers of 2009 and 2010 (11 710 trapnights in total) on four grids located in undisturbed forest, two in partially logged (shelterwood) stands and two grids in scarified shelterwood stands. The yellow-necked mouse *Apodemus flavicollis* and the red-backed vole *Myodes glareolus* represented the majority of individuals captured (69% and 23%, respectively). In 2009, the overall rodent abundance was very low and almost all (26 out of 28) rodents were found at only two grids (one undisturbed and one partially logged). In 2010, rodent abundance was high due to large crop of beech seeds. In June, average abundances of *A. flavicollis* differed significantly among management types, with 9.5 individuals captured per grid in scarified shelterwood, 18.5 in undisturbed stands, and 53.5 individuals in shelterwood stands. Later in the season, the abundances of mice evened out. Abundance of *M. glareolus* differ among management types during whole season in the same pattern as *A. flavicollis* in June. In 2010 the patterns of habitat selection could have been suppressed by high densities associated with masting. This phenomenon was stronger for granivorous *A. flavicollis* then for herbivorous *M. glareolus*. When population dynamics is controlled by rare food pulses such as masting, it might take data from multiple years to evaluate responses to habitat alterations. Therefore, the study is ongoing and more data will be collected.

The breeding behavior of a mediterranean mammal subspecies introduced on an atlantic island: the wild rabbit (*Oryctolagus cuniculus algirus*) in Azores (Portugal)

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The wild rabbit (*Oryctolagus cuniculus*) is endemic from the Iberian Peninsula, where two subspecies (*cuniculus* and *algirus*) are distributed along segregated (NE and SW, respectively) but partially overlapped ranges. Domestication and most colonization events outside Iberia were performed using the *cuniculus* subspecies, being the Azores one of the few known cases where *algirus* subspecies was introduced. Due to its importance as a game species, rabbit sustainable hunting requires knowledge of local breeding cycles. However, little is known about *algirus* breeding behavior outside Iberia. Since climate in Azores is Atlantic we hypothesized that rabbit breeding cycles would be different in relation to Mediterranean populations from SW Iberia. To test this hypothesis we adjusted a predictive model, previously validated for this species, to environmental data from Azores. Additionally, a total of 563 adult rabbits were collected monthly from November 2006 to October 2008, on Flores Island (largest of western group) to record the following parameters: testis (position) and epididymis weights; ovaries and uterus weights, number of embryos, and mammary glands development. Despite the climatic differences between the Atlantic and Mediterranean regions, both model predictions and observational data on reproduction suggest similar breeding cycles in Azores and SW Iberia, with annual peaks in March-April, a reproductive pause during summer (July-October), and mean litter sizes of 3.65±0.21. The main limiting environmental factor seems to be high temperatures, since green pastures are available throughout the year. This study is ongoing as part of a project aimed at improving game species management in Azores.

Does ecological isolation and population size influence genetic diversity in the European ground squirrel, *Spermophilus citellus?*

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Genetic diversity is considered of paramount importance to maintain evolutionary potential in populations or individual fitness. Particularly for conservation issues it is crucial to know how genetically diverse an endangered species is, and what factors may explain genetic variation among populations. In this study we investigated whether genetic diversity of local populations (four in Hungary and five in Austria) of the declining European ground squirrel was influenced by census population size and ecological isolation of the populations. We genotyped 144 individuals at eleven polymorphic microsatellite loci to assess population-specific allelic richness by a rarefaction approach to account for different sample sizes. We based estimates of population size on standardized counts of numbers of entrances of burrows, and we used the isolation index of Rodríguez and Delibes to obtain population-specific values of ecological isolation; they were calculated using grid-based presence/ absence data of ground squirrels around each local population. Using a generalized least squares fit by maximum likekihood approach and following AICc-based best fit model selection and model averaging, we found higher allelic richness in the Austrian populations than in the Hungarian populations (relative variable importance: 0.98), but no significant influence of either ecological isolation (rel. variable improtance: 0.40) or census population size (rel. variable importance: 0.03). Increased levels of ecological isolation seem to reduce allelic richness of populations as well, but more populations are needed to acertain that. The unexpected region effect might partly result from generally higher population densities in Hungary, which might reduce effective population sizes because of relative high proportions of non-reproducing yearling males (corresponding to the ”scramble-competition polygyny hypothesis”).

Monitoring a wild boar population from hunting data a protected area in Western Spain

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Hunting in protected natural areas may be important to maintain population density within the carrying capacity of the ecosystem, thus preventing negative impacts on vegetation or other animal populations. In this study we analyzed data from hunted wild boars (*Sus scrofa*) from a population in the natural park Tajo Internacional (Central-West Spain). Information on hunting bags was obtained for hunting seasons 2008-2009 and 2009-2010 from 86 estates that conform the area of the park (25,088 hectares). Also, individuals wild boars from hunts were examined to determine their age, development and reproductive status. Mean number of wild boars hunted was 1.18 individuals per 100 hectares. This figure was low compared to other areas in Spain and it was not uniformly distributed throughout the area, ranging from 0 to up to 5 individuals per 100 hectares in some estates. Mean age of hunted wild boars was 2.8 years, similar to that found in previous studies in Spain. Litter size averaged 4 piglets per litter. Males older than 4 years were less than 10% of hunted animals. These results highlight the importance of the wild boar in the area and the need of hunting management to control its density. Also, our study shows how data from hunting activity can be a good source of information both for research and for population management.

Multiannual population cycle of common vole (*Microtus arvalis*) in South-Hungary based on barn owl pellet analysis

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Although the examination of periodic fluctuations is primarily based on trapping surveys the pellet analysis of the cosmopolitan barn owl can be used not only for its feeding analyses but also for examining the small mammal fauna of the given area. It is explicitly applicable by defining population dynamics, since the changes of the density of prey animals in prey-predator relationships are traceable in the nourishment of the owls. The conservation management and parallel pellet analyses of barn own began in 1985 in Baranya, the southernmost county of Hungary. We processed data from the 1995-2009 period, while we examined 38828 pellets and determined 110570 small mammal individuals. We examined the temporal changes in the abundance of the indirectly detected common vole for two landscape scales (county and meso-region) based on quarterly time scale. We analyzed the periodic fluctuation of the relative abundance of common vole with autocorrelation, examining the regular cycles of demography of this species. Our results have shown that the population dynamics of common vole follows a three-year-long cycle with regular oscillation. We examined the effects of meteorological factors in the function of temperature and drought index in the change of the quantity of common vole, although the negative correlation by the latter parameter was not significant. Our result in the examination of the demographic fluctuation of the common vole suggested that long-term pellet analyses for examining the population dynamics of this agricultural pest rodent can be used by considering the III. type functional response of the barn owl.

Ecogeographical analysis of the red fox (*Vulpes vulpes* l., 1758) range in the holarctic

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Distributional range is one of the most important characteristics that shows the ecological connections of a species over time. The recent (2010) and historical (1600-1800) distribution of the red fox was defined both in the Palearctic and Nearctic. The verification of independent data on red fox population density in European Russia and in North America (harvest statistics, winter tracks count and offspring count on dens) has allowed cartographical interpretation of range structure of this species. The methods of historical biogeography can be used to reconstruct the history of range formation. The distribution of the red fox in the Palearctic is different from that in the Nearctic. Thus, in the Palearctic the species has polyzonal distribution with highest densities (annual average density 20-30 foxes per 100 km^2) in temperate semiarid and arid regions, where the genus *Vulpes* has its world centre of diversity. Throughout history, considerable changes have occurred in the structure of the range. However the border of the range has remained relatively constant. In the Nearctic, the original range of the red fox was predominantly in the northern (boreal) part of the continent. The mordern fox's range doubled in size with the highest densities (>35/100 km^2) in the mixed and broad-leaved forests of the Eastern USA. In natural semiarid and arid landscapes, the red fox occurs at relatively low density (<5/100 km^2).Ecogeographical analysis reveals that disproportion in the red fox distribution in the Palearctic and Nearctic is caused by the different ways of the range formation.

SNOW DEPTH INCONSEQUENTIAL TO VOLE POPULATION GROWTH

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The regularity of population cycles has declined in many areas. Climate change is often implicated as a contributor, although little is known of how weather affects cyclic populations. To obtain reliable estimates of weather effects on animal populations, spatially and temporally extensive data are required. We investigated the effects of weather on vole population growth, allowing for geographical, seasonal and species differences. We combined data on vole abundances and weather, collected at 32 locations throughout Finland from 1970 to 2010. The effects of temperature, rainfall and snow depth on winter and summer population growth were modelled separately. Candidate models were compared with AICc. Weather effects on winter population growth were uniform throughout Finland. Effects on summer growth varied regionally. Rain, especially in summer and autumn, emerged as a key weather factor, while snow depth had no effect on population growth. Mid-winter weather appeared inconsequential to population growth. Summer growth rates have increased and winter declines become steeper since the 1970's. *Microtus* population densities have generally increased, whereas *Myodes* densities have declined. The altered vole densities and seasonal growth rates may result in transformed vole community composition, population dynamics and ultimately change trophic interactions and ecosystem dynamics.

Population dynamics of European mink M*ustela lutreola* in Spain: population trends, prospective analysis and management targets

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Demographic analyses are essential for the conservation of small and endangered populations. Management targets can be determined by testing which factors, such as survival and fertility, have the greatest influence on a population's rate of growth (λ). In this study, population trends (deterministic and stochastic growth rate) and prospective analysis (elasticity, sensitivity and quasi extinction probability) were determined for the critically endangered European mink (*Mustela lutreola*) in Spain. As expected, population tends to decline ($\lambda < 1$ and $\lambda_s < 1$) with a quasi-extinction probability >0.5 in less than 50 years. Elasticity (proportional changes) pointed out adult survival (P_a) as the vital rate with largest effect on proportional changes on the population growth rate λ; while sensitivity (absolute changes) of λ was highest for adult survival (P_a) and fecundity (F). Hence, both vital rates should be considered main management targets. We call for analyses and review of factors affecting adult survival (i.e. road casualties) and fecundity; and consequently further evaluation of management actions for the Spanish population of European mink.

Impact of the management of the habitat on the community of small mammals of the Doñana national park (SW Spain)

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One of the main management practices carried out in the Doñana National Park, as part of the *Lynx pardinus* and *Aquila adalberti* recovering plans, is the clearing of mediterranean scrubland to create open areas for rabbit feeding. This practice positively affects rabbits but also provokes significant changes in the scrubland structure. No studies have been performed to evaluate the effect of this habitat change on other species inhabiting scrubland. In this study we evaluate the effect of the scrubland clearing, through prescribed burning, over small mammal community. We compare the composition, specific richness, age structure and abundante of species and the temporal evolution of these parameters between six different plots burned in different years and other three no treated (control plots). Data were obtained through capture-mark-recapture methods in eight seasonal trapping campaing, from summer 2005 to spring 2007. The results show that the specific richness was very low, with only four captured species (*Mus spretus*, *Apodemus sylvaticus*, *Crocidura russula* and *Eliomys quercinus*). The abundante values were different depending on the species, season and plot type. Abundante was higher in autumn and winter, and was very low during summer. The most abundante species was *Mus spretus*. The prescribed burn of ageing Mediterranean scrubland in Doñana favour presence and abundante of the small mammals, mainly in the surrounding scrubland of the burned plots. The colonization process of burned plots seems to finish three-four years after treatment and it is conditioned by other factors, like annual precipitation.

On set of spring and reproductive strategies in bank voles (*Myodes glareolus*)

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My aim is to test how the quality of nutrition and fluctuations of temperature affects to the onset of breeding in bank voles after winter. The idea of this experiment is to mimic the possible effects on environmental conditions caused by the climate change. The experiment is carried out in four temperature adjustable clima chambers. There will be four different treatments, one in every clima chamber, manipulating temperature and food quality. In the chamber with high quality food and constant temperature the voles are fed with pellets with high protein content(30%), and the temperature is stable. In the high quality food and variable temperature treatment the food is same as above but the temperature fluctuates between low night temperature and higher day temperature. In the low quality food treatments the pellets have lower protein content(8%) and the temperatures are same as above. All the test laboratories have the same light period rhythm. The voles living in stable temperature with high quality food are supposed to start breeding first, for despite the constant cool temperature the conditions are predictable. The voles in the treatment of low quality food and fluctuating temperature are supposed to start breeding last if all. The groups in the middle are actually the main interest for it shows the significance of the factors affecting on the onset of breeding.

Phase-dependence in antipredatory behaviour of cyclic bank voles

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Predation risk is not uniform across space and time. Furthermore, some individuals become more experienced in avoiding predators while others remain more naïve. Under high predation risk and high predation related mortality, selection pressures are very different than under low risk and low predation mortality. In the latter situation other behavioral characteristics evolve at the cost of antipredatory behaviours. Under long-lasting high predation risk, individuals should evolve better antipredatory behaviours than individuals living under low predation risk due to experience and/or selection. In cyclic vole populations, where predator numbers follow vole numbers with a time delay, it is assumed that voles living in decline phase of the cycle should exhibit more efficient antipredatory behavior compared to voles from the increase phase. We tested this hypothesis by capturing voles from different areas that were in different phases of the population cycles and by testing their antipredatory behaviour in the laboratory. Our results demonstrate differences between populations in different phases of the cycle. However, these differences were not always in a line with our predictions. We also observed seasonal and sex-related variation in antipredatory behaviour. We cannot exclude the effect of different geographical origin of test voles as source of variation, and therefore a long-term study of the local populations is needed to fully understand behavioural changes associated with population cycles.

A comparison of marsh vegetation types using occupancy studies of small mammal populations in Louisiana

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There is considerable variation between sites in freshwater marshes in Louisiana in terms of vegetation structure, and presumably, faunal occupation. Current wildlife management uses salinity zones as habitat descriptors, regardless of how different habitats may be in terms of the plant communities within a zone. Small mammals are key consumers in the marsh food-web and could serve as a good indication of the potential for a marsh to support higher level predators. We conducted a study to determine whether small mammal occupancy varies among the plant communities in freshwater marshes, and if vegetation stand structure affects small mammal occupancy. The study was conducted in the marshes of Southeastern Louisiana during May and early June 2010. We sampled small mammal presence at 36 sites, using livetrapping, on four different occasions. We collected vegetation from five plots at each site at the end of the study. Mammalian diversity was low; only one species, the marsh rice rat (*Oryzomys palustris*) was captured at any of the sites. The only significant difference in stand composition between sites occupied or unoccupied sites by *O. palustris* was the presence of bull tongue (*Sagittaria lancifolia*). Upon modeling occupancy, with and without *S. lancifolia*, we determined that *S. lancifolia* presence predicts occupancy of a patch by *O. palustris* even at low levels of plant biomass. It is unclear whether *S. lancifolia*'s influence on the presence of marsh rice rats was due to the plant's influence on cover or food, or if *S. lancifolia*'s abundance was correlated with an unmeasured factor that also influenced small mammal use.

Session 22 - General session

Invited & Oral Communication

Does food limitation in winter explain Dehnel's phenomenon in soricine shrews?

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It is widely assumed that winter is a critical time for homeotherms because of decreased ambient temperatures coupled with reduced food supply. Shrews are excellent models for investigating overwintering strategies, not only because of their particularly small size, high energy requirements and short fasting endurance, but also the dramatic reduction in body size (Dehnel's phenomenon) exhibited by soricine shrews in northern temperate winters. The cause of Dehnel's phenomenon is poorly understood but food supply is implicated. To test the hypothesis that winter at higher latitudes is a period of reduced food availability for small homeotherms, we compared feeding habits and food supply of the common shrew, *Sorex araneus*, in winters and summers in NE Poland using scat analysis combined with pitfall and ground core sampling for invertebrates. Ground-surface activity and numbers of invertebrates in pitfall traps were greatly reduced in winter but, contrary to prediction, no significant differences between winter and summer were found in total numbers and biomass of prey invertebrates in ground core samples. However, certain prey types changed seasonally with respect to numbers, biomass and distribution in the soil profile, which was reflected in shrews' food composition and foraging behaviour. Dehnel's phenomenon appears not to be caused by food limitation and reduction in total prey numbers. Smaller body mass coupled with lowering of absolute food requirements may have important survival value in winter with fewer preferred prey available, reduced prey accessibility and high energetic costs of foraging.

Sexual conflict over testosterone – antagonistic selection pressures between sexes in the bank vole

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Sexual signaling and reproductive success in male mammals is generally understood to be largely determined by the circulating level of the hormone testosterone (T) through its various physiological and behavioral effects. If so, the T-level should be subjected to positive directional selection that reduces genetic variation in this trait. However, due to its costly immunosuppressive effects, the T-level (and associated level of sexual signalling) could also work as a honest signal of male genetic quality. Current 'good genes' theories of sexual selection hypothesize that females receive indirect genetic benefits via offspring fitness by choosing males with the most elaborate sexual signals. This traditional view is currently being challenged by new concept of sexually antagonistic selection, which illustrates a difference in the fitness of a certain trait value between the sexes. Using the bank vole *Myodes glareolus* as a study species, we present a series of experiments where the T-level of males was manipulated and subsequent fitness effects were studied both in the laboratory and in the field. Our results illustrate a close interplay between T and immunocompetence where these two traits are both phenotypically and genetically negatively correlated. With the help of selection lines divergent for male T, we also reveal a sexual conflict through a significant negative intersexual correlation for reproductive success. To conclude, 'good genes' in this system may be highly gender specific, such that whilst a female mating with the highest T male may produce fit sons, daughters may only show average fitness.

Competitive release of the mediterranean water shrew (*Neomys anomalus*) living in Portugal

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Shrews usually occur in communities of multiple species, coexisting in the same habitat. In these communities, due to their high food requirements, interspecific competition can play an important role in separation and shrinking of their ecological niches. Changes in the composition of shrew communities, as absence of main competitors, can lead to an opposite situation: niche extension due to competitive release. For instance, in coexisting populations, niches of Eurasian (*Neomys fodiens*) and Mediterranean (*Neomys anomalus*) water shrews clearly segregate: *N. fodiens* inhabits microhabitats closer to deep water and eats much more aquatic prey than *N. anomalus*. In the present study we investigated the potential ecological release in an allopatric population of *N. anomalus* living in Serra da Estrela, Central Portugal, i.e. occurring free of the competition with *Neomys fodiens*. Small mammals were live-trapped in four seasons over two years on a fix grid covering different habitats with increasing wetness (from pine forest to river bank). Besides *N. anomalus*, two other shrew species were captured (*Crocidura russula* and *Sorex granarius). C. russula* was the most abundant shrew species in all seasons followed by *N. anomalus* and, captured only sporadically, *S. granarius*. *N. anomalus* were always captured within 1-meter-distance from river, i.e. in places much closer to water than usually found in populations syntopic with *N. fodiens*. Our results suggest that the absence of *N. fodiens* allowed Portuguese *N. anomalus* to extend its ecological niche to more aquatic microhabitats and food resources.

Wintering adaptations of the pygmy shrew *Sorex minutus* and the Eurasian water shrew *Neomys fodiens*

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Although it is assumed that severe winter is a critical period for all soricine shrews (tiny, non-hibernating mammals with an extremely high metabolic rate), the considerable differences in their body size, metabolic rate, life-style and diet can result in differentiation of their wintering adaptations. Therefore, we compared seasonal changes in body size, ecology and behaviour of terrestrial pygmy shrews *Sorex minutus* (3 g) and semi-aquatic Eurasian water shrews *Neomys fodiens* (15 g). CMR-trapping and invertebrate prey sampling were performed during January-February and June-July of 2007-2011 in a lowland river valley in eastern Poland. Foraging behaviour was investigated in laboratory tests performed at 6-7°C (winter) or 19-22°C (summer), using video-recording. Intensity of Dehnel's effect (winter decrease in body size and mass) was assessed by morphometric analyses. Population numbers changed between seasons in both shrew species, however *N. fodiens* was more abundant in summer than in winter, while *S. minutus* displayed a reverse pattern. *S. minutus* shifted its activity peak from night-time in summer to daylight in winter, whereas *N. fodiens* was most active at night-time in both seasons. Neither species displayed significant seasonal changes in food hoarding behaviour, however *N. fodiens* hoarded proportionally fewer food items and lower food mass than *S. minutus*. The species differed considerably in Dehnel's effect: pygmy shrews reduced their body mass and skull height by 14% in winter; in contrast, the skull height of water shrews decreased only by 2,5% and body mass increased by 5%. These findings can be explained by interspecific differences in metabolic rate, energy reserves in body and availability of prey.

Exploratory behaviour relates to life history strategy in shrews

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Exploration of the environment is a key behaviour in many animals. The exploratory behaviour of species or populations depends on different aspects of their ecology, like diet or habitat characteristics. New data suggest that differences in exploratory behaviour might also be related to life history strategies, with fast-paced, short-lived animals being the faster explorers than slow-paced, long-lived ones. We tested this hypothesis in shrews. Shrews divide into two large phylogenetic groups, which differ tremendously in life history. We compared the exploratory behaviour of three species, covering both phylogenetic groups, in a simple exploration experiment using video motion tracking analysis. Our results corroborate the hypothesis that exploratory behaviour relates to life history strategy: Shrews of the fast-paced subfamily Soricinae were quicker to start exploration and to locate the first patch with food. They also performed more, but shorter exploration bouts, and moved faster than the slow-paced subfamily Crocidurinae. While the two subfamilies in general differ in the climatic zones they inhabit, our study species all occur sympatrically in wide parts of Europe and face similar ecological conditions. Thus, the differences in their exploratory behaviour can likely be explained by their highly diverse life histories and not by their actual habitats. The different life histories are presumably a result of the different evolutionary histories of the two phylogenetic groups.

Habitat preferences of wild goats (*Capra aegagrus*) in Agh-Dagh protected area, Iran

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We studied habitat selection by wild goats in North West of Iran. This species is known to choose highly sloped, rocky and steep areas as habitat. I studied wild goats habitat preferences in Agh-Dagh protected area during two years. The species habitat selection was best explained by incorporating various physical and biological variables using logistic regression. Topographic features alone, however, ranked better than components of vegetation in explaining habitat selection and were often excellent predictors of habitat use.

Habitat associations of iranian jerboa (*Allactaga firouzi* Womochel 1978)

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We studied habitat preferences of the only known population of Iranian jerboa in Iran. Binary logistic regression was used to identify habitat variables that might be important to Iranian jerboa. The number of candidate variables was reduced using logistic regression retaining variables that differed between occupied (presence) and non-used (absence) plots. Logistic regression model could successfully distinguish between used and non-used areas. Habitat use of Iranian Jerboa is mainly affected by vegetation type and percent cover of bare soil.

Seasonal changes in space use, activity and foraging behaviour as elements of wintering strategy of the common shrew

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It has not been known if and how soricine shrews (tiny, non-hibernating mammals with an extremely high metabolic rate) modify their "summer" behaviour to survive through severe winters. Therefore, we investigated seasonal changes in population density, space use, circadian and locomotor activity, and food hoarding behaviour of common shrews *Sorex araneus*. CMR-trapping of shrews and invertebrate prey sampling were performed during the coldest (January-February) and warmest months (June-July) in lowland river valley at Białowieża (eastern Poland). Locomotor activity and foraging behaviour were investigated in laboratory "cafeteria tests", performed at 6-7°C (winter) or 19-22°C (summer) and using video-recording. Population density was 4-5 times lower in winter than in summer but winter populations comprised a higher proportion of residents. Winter home ranges were 2-3 times smaller and overlapped less than summer home ranges. In summer, shrews were more active during night than day hours, whereas in winter they were active night and day. Also in laboratory tests, the total activity was longer in winter then in summer, though shrews moved more in summer. Shrews entered the shelter more frequently in winter than in summer, which is related with the fact that they hoarded significantly more food in winter. This tendency can result from depletion of its main prey (earthworms) which descent deeper into the soil in winter. The results suggest that the wintering strategy of common shrews includes: 1- being more territorial, 2- travelling shorter distances, 3- allocating more energy for foraging then exploration, and 4- making larder food stores.

Patterns of variation and development in the mammalian axial skeleton

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Patterns of vertebral variation across mammals have seldom been quantified, making it difficult to test hypotheses of covariation within the axial skeleton and mechanisms behind the high level of vertebral conservatism among mammals. Here, we discuss variation in vertebral counts across monotremes, marsupials and major clades of placental mammals. These data show that xenarthrans and afrotherians have, on average, a high proportion of individuals with meristic deviations from species' median series counts. Monotremes, xenarthrans, afrotherians and primates show relatively high variation in thoracolumbar vertebral count. Among the clades sampled in our dataset, rodents are the least variable, with several species not showing any deviations from median vertebral counts, or vertebral anomalies such as asymmetric ribs or transitional vertebrae. Most mammals show significant correlations between sacral position and length of the rib cage; only a few show a correlation between sacral position and number of sternebrae. The former result is consistent with the hypothesis that adult axial skeletal structures patterned by distinct mesodermal tissues are modular and covary; the latter is not. Variable levels of correlation among these structures may indicate that the boundaries of prim/abaxial mesodermal precursors of the axial skeleton are not uniform across species. We do not find evidence for a higher frequency of vertebral anomalies in our sample of embryos or neonates than in post-natal individuals of any species, contrary to the hypothesis that stabilizing selection plays a major role in vertebral patterning.

Interesting features of the specialized urogenital tract in Xenarthra Cope, 1889.

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In spite of presenting a highly specialized morphology, the magnaorder Xenarthra retains anatomical and physiological characters thought to be primitive for placental mammals It's comprised by two orders: Cingulata (armadillos) and Pilosa (sloths and ant-eaters). Previous works showed peculiar features about the male urogenital tract, however they were scarcely placed in an evolutionary context. Macroscopic identification and morphometric measurements were carried out on adult male urogenital tracts of: the ant-eaters *Tamandua tetradactyla* (4)*,* and *Myrmecophaga tridactyla* (2); and the armadillos: *Dasypus hybridus* (3), *Chaetophractus villosus* (25), *Chaetophractus vellerosus* (5), *Zaedyus pichiy* (3), *Chlamyphorus truncatus* 1- and *Tolypeutes matacus* (4). Testes were located ventrally in the pelvic cavity in all species. Armadillos presented separated testes while ant-eaters presented joined testes. Kidneys were located in the abdominal cavity in armadillos while in ant-eaters kidneys descend and locate inside the pelvic cavity. Testes length in proportion to body length was greater in *C. villosus* (13.92%) than in *D. hybridus* (8.59%) and the ant-eaters (8.02%). Penis length in proportion to body length was 15.98% in *D. hybridus,* 28.94% in *C. villosus,* and 8.79% in ant-eaters. Testes in xenarthrans represent the beginning of testicular descend in eutherians denoting an intermediate state between the testicondid afrotherians and the scrotal mammals. Penis length in proportion to body length of *D. hybridus* resembles what happens in most mammals (medium length penis), while derived lengths like large penis, appears in the rest of armadillos and short penis in ant-eaters as it also happens in sloths.

Paleopathology of *Ursus spelaeus* from Bear's Cave, Poland

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There are very few descriptions of pathologies visible in fossil animal material. One of them is be a monograph concerning Bear's Cave in Kletno presenting, among others, examples of post-traumatic lesions visible on selected bones. The bones of the cave bear (*Ursus spelaeus*) constitute 90% of bone material (40 000 bones and their fragments) and they present in silt in all the known parts of the cave. Considering the importance of the site, it was agreed that it was worth describing the bone tissue structure changes in the bear coming from the Quaternary deposits of cave in Kletno and determining their possible reasons and results using classical and non-standard radiological techniques as well as selected methods. After the initial analysis, 1516 bones were selected for further examination. Several mutually supplementary examination methods were applied which allowed complex analysis of the bone tissue structure of the osseous remains. The applied methods of: morphological, radiological and histological analysis served, apart from macroscopic and microscopic description, for the determination of pathological lesions as well as individual age. The examination performed allowed determining the irregularities in bone tissue structure, and constitute the first study of pathology of Pleistocene animals from Poland. The studies allowed determining the possible limitations on normal animal functions as well as a possible cause of death of the individual. The analysis results of the occurrence frequency of diseases in the investigated population allow concluding that these diseases were not the reason for the species extinction during Pleistocene in this region of Poland.

Rival presence leads to reversible changes in male mate choice in a desert dwelling ungulate

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Most studies on sexual selection have investigated female mate choice, but increasing evidence demonstrates that also males exhibit mating preferences. Mate choice can be sensitive to social cues from neighbouring individuals, especially in group-living animals, which often choose their mating partners within social aggregations. By-standing individuals may extract and subsequently use information from observed (sexual) interactions to refine their own mating decisions ('social eavesdropping'). In internally fertilizing species males face increased sperm competition risk (SCR) when other males copy their mate choice decisions. Strategic male behaviours in response to increased SCR (audience effects) have thus far been examined primarily in live-bearing fishes (familiy Poecilidae), while experimental studies on mammals were as yet lacking. Here we demonstrate that male mating preferences of a desert dwelling ungulate, the sand gazelle (*Gazella marica*, kept at the King Khalid Wildlife Research Centre in Saudi Arabia), are affected by the presence of a rival male. We gave males an opportunity to choose between two females (1st test part, 24 hours) and repeated trials while an audience male was present that could observe the focal male's mating behaviour (2nd part, another 24 hours). When considering focal males' preferences over the entire observation period, high consistency in male mate choice was uncovered. However, during the 1st hour upon presentation of the audience, a marked change in focal males' preferences could be seen, and males spent more time interacting with the previously non-preferred female. It seems, therefore, that audience induced changes in male mate choice behaviour are short-term responses to the presence of rivals.

Blind as a bat? Comparative genomics iluminates the evolution of colour vision in bats

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Within mammals, bats exhibit the greatest level of sensory specialization. The complex and highly evolved process of laryngeal echolocation allied with the capability of flight have given bats the ability to exploit most ecological niches throughout the globe. The Megabats have large eyes specialized for nocturnal vision, whereas the Microbats rely more on laryngeal echolocation and have questionable visual capabilities. It has been argued that bats developed their echolocation at the expense of other senses such as vision, however this hypothesis has never been fully explored. Molecular data suggest that the ancestor of modern bats was most likely capable of echolocation and that the Megabats may have lost this sense by "trading" hearing for vision and olfaction. To date the molecular analysis of color vision in bats and other mammals has linked changes in vision genes to differences in ecology as well as other sensory capabilities. With the aim of establishing the evolutionary patterns and functionality of visual photoreceptors, the Short-wavelength opsin gene (SWS1; UV/blue) and the Medium-to-long wavelength opsin gene (MWS/LWS; yellow/green) were sequenced in all bat families. This molecular dataset covers species that exist in very divergent ecological niches and that possess divergent sensory capabilities. Our data shows that the MWS/LWS is functional and conserved, while the SWS1 opsin has undergone gene defects, leading to leading to a loss-of-function and consequently to monochromacy in several yinpterochiropteran and yangochiropteran lineages. We will evaluate evolutionary patterns and the genetic consequences of nocturnality, laryngeal echolocation and ecological niche specialization on vision in bats.

Cellular architecture of laboratory mice selected for high and low basal metabolic rate

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There is a general agreement that the basal metabolic rate (BMR) scales allometrically with body mass. However, despite decades of research, understanding of determinants of scaling of metabolic rates still remains unsatisfactory. A recently proposed Cell Metabolism Hypothesis postulates that variation in metabolic scaling could be largely attributed to differences in cell size, where larger cells are metabolically more frugal due to relatively smaller surface to volume ratio. Thus, independently of body size, organisms built of smaller cells should have higher MR than those built of larger ones. To test this hypothesis, we measured cell sizes and metabolic rates in laboratory mice subject to artificial, divergent selection on basal metabolic rate (BMR).We found a negative correlation between BMR and erythrocyte and skin cell size, and a positive correlation between BMR and hepatocyte, duodenum epithelium as well as kidney cells. Our results therefore provide partial empirical support for cell size being an important determinant of metabolic rate variation and consequently, its allometric scaling. The results call attention to the significance of long-neglected integration of cellular and organismal perspectives in studies of body size- metabolic rate relationships.

Mammals of Argentina: patterns of discovery

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Mammal collectors have visited Argentina for centuries and museum specimens are distributed worldwide. This makes specimen examination difficult. Specialists have not verified the identity of many species and most have not had their taxonomic status upgraded, thus there are many errors in identifications in collections. Using unverified data may lead to a confusing mix of misidentified species. We have studied Argentine mammals for 40 years and examined most of the world's collections. Early collections were often based on personalities, personal situations, or happenstance. About 50,000 mammals from Argentina are in museums, with the majority in Argentina. Most type specimens are in the Natural History Museum in London or in other large museums outside Argentina. In recent years there has been a change in the pattern of mammal collecting, with most being done by Argentine scientists. Only a few naturalists collected most specimens. Too few mammals have been collected to provide a solid database on mammals. Current collecting efforts are inadequate to resolve this problem. A national survey of mammals is required. Given the rate of habitat destruction within Argentina, the need to clarify the distribution and identity of the mammals of Argentina is urgent. Without such foundational data, research in ecology, conservation, behavior, physiology, and other disciplines will be compromised.

Effect of vegetation structure on small mammal communities in different type of forests

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The target of our research was to determine the correlation between of some parameters of small mammal populations and the vegetation-structure. The investigation areas were in semi-natural forests and in forests under forest management. The small mammals were investigated by the CMR method. Diversity, density, habitat and microhabitat preference, home range, condition, rates of sexes and survival were recorded. These data were compared with the following vegetation structure parameters: closure of the foliage, number of the shrubs and wrapping of the sward. For a better examination of the shrub-level, different shrub-classes were categorized. 3 small mammal species were trapped: *Apodemus flavicollis*, *Apodemus sylvaticus* and *Myodes glareolus*. All of them were found in the shrubbiest, and in the moderately bushy area. In the 3rd-area, which has almost no shrub there were only the *Apodemus flavicollis*. The strongest differences of the population parameters were detetected between the first and the second areas, which differ from each other mainly by the number of shrubs. *Myodes glareolus* was trapped enough number only in the 2nd area to calculate population parameters. The reason can be that a moderately bushy area provides variegated microhabitats, and more species can find their living-condition in it. Analyzing the coherence between the amount of animals and the vegetation structure we could determine that the population size correlate mostly with the number of shrubs. The trees and the sward are less important, they have indirect impacts.

Biogeography and hotspots of mammalian species of Iran: implications to reserve selection and conservation

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Studies on species' biogeography, biodiversity are of remarkable significance in biogeographic regionalization and systematic conservation. In this study, distributional information of 172 mammalian species was accumulated to build a database in Iran. The geographical distribution and species richness maps of mammalian species of Iran were analysed by Geographical Information System (GIS). The hotspots were defined as the richness cells in number of species in a global equal-area grid cell map comparable to 1° latitude 1° longitude. Latitudinal distributional pattern and IUCN categories of species in Iran were also evaluated. Our results indicated that the hotspots of mammalian species of Iran with 53 species are located in the north to northwestern Iran where two mountain ranges, Alborz and Zagros, meet each other. Other hotspots were mainly placed in most areas of Zanjan, east of Ghazvin, in south of East-Azerbaijan, east of Kurdistan and east of West-Azarbaijan provinces. Of 172 species of mammals where breeding in Iran about 6.6% and 4.8% of species are vulnerable threat and Endangered species respectively. Our result highly in congruent with the hotspot richness pattern of songbirds in Iran. Complementarity rarity-based analysis could be represented on 200 optimal grid cells in which the entire mammalian species in Iran are included based on IUCN rarity values categories. This study as the first attempt to combine quantitative analysis for mammalian species distribution in Iran could be a bases for further complementary studies.

Effects of global warming on hares in the alps: two sides of a coin

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Global warming is assumed to be a threat to mountain hares (*Lepus timidus*), especially in the Alps where the mountain hare is a glacial relict. Global warming resulted in increase of ambient temperatures within the last decades. With increasing ambient temperature this cold-adapted mammal has to shift it's range to higher altitudes. In line with this, European hares (*L. europaeus*) in the Alps might benefit from global warming as they will find more suitable habitat in high valleys and above timber line. In the contact zone hybridization between the two sympatric species is likely to occur and introgression has been described recently. Both hare species are important game in Grisons with about 2500 hares being shot each year in the last decades. From 1991 until 2008 we asked hunters to fill out protocols with detailed information about the exact place of successful hare hunting events. With this we were able to monitor the altitude of hunting for 17376 mountain hares and 24905 European hares during the 18-year study. In general, mountain hares were shot on average 564 meters higher than European hares. The mean altitude of hunting increased in both species during the study period and this increase correlated positively with an increase in ambient temperature. Moreover, the increase in mean altitude of hunting was more pronounced in European hares than in mountain hares. Our study revealed that global warming is a threat to mountain hares and beneficial for European hares.

Dna barcoding for herbivorous diet analysis

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The study of diet analysis is an indispensable step in determining the biology of a species and its interaction with the ecosystem. Such knowledge is crucial in the case of endangered species, as diet must be taken into account when drawing up conservation strategies. However it can be a real challenge in many herbivores with a secretive life style or when food cannot be identifiable by morphological criteria. The development of DNA barcoding, and the availability of recent DNA sequencing techniques offer new possibilities in diet analysis. DNA fragments shorter than 100–150 bp remain in a much higher proportion in degraded DNA samples and can be recovered from faeces. As a consequence, by using universal primers that amplify a very short but informative DNA fragment, it is possible to reliably identify the plant taxon that has been eaten. We developed such an approach by using the chloroplast *trn*L(UAA) intron P6 loop as a target for plant barcoding. We demonstrated that this new method is efficient for the study of diet of different mammal species. We compared this approach with traditional microhistological method demonstrating that, although the identified plant taxa in the diets matched relatively well between the two methods, DNA barcoding approach gave by far taxonomically more detailed results. This new technique appears to be very robust and can be applied at large scales. It opens new perspectives for determining the diet of wild animals under field conditions.

Carnivores diet analyses using DNA barcoding

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Information about the diet is amongst the basic questions in ecology. This information is even more useful when the predators are endangered and elusive in nature. Various approaches from classical methods to molecular techniques have been used to study the diet. All these methods have their limitations at certain level. Carnivores diet with the universal primers, which can amplify predator and prey DNA simultaneously predominates predator DNA in most of the cases and show biased amplification. We analysed carnivore diet using blocking primer specific to predator sequence in combination with universal primers for vertebrates. These PCR products were sequenced using Illumina Solexa technology. We applied this approach to highly endangered carnivore species of South-Asia, leopard cat (*Prionailurus bengalensis*), common leopard (*Panthera pardus*) and snow leopard (*Uncia uncia*). This system provides complete diet information about the carnivores and no *a priori* knowledge is necessary. This approach is simple to implement to other carnivores diet with a prerequisite of a blocking primer homologous to predator DNA. Moreover, this method is even ideal to study diet of endangered or elusive species where faeces are the only source of information.

Diet variation during food restriction in wild mountain herbivores

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Since last 30 years, populations of large herbivores have dramatically increased in number and geographical range. This raises competition risk, especially in mountain context where overlaps between wild and domestic species become more important. Mountain habitats have also large climate range who conducts to period with resources restriction (like winter). Diet choice should differ between species according to body size, morpho-physiological variation in the digestive functioning and ability to store body fat. Hence, the resources that can be limiting for herbivores species depend to history traits. In case of diet overlap, competition will occur. The Massif of Bauges in France gives us the opportunity to study coexistence with wild and domestic ungulate. We decided to focuses our study on the 4 larges wild herbivores (chamois *Rupicapra Rupicapra*, mouflon *Ovis gmelini*, red deer *Cervus elaphus*, roe deer *Capreolus capreolus*) to show the patterns of diet variation during food restriction. Diet composition is determined using the DNA barcoding which allows identifying plants species eaten from small DNA fragment present in faeces. The diets of the four herbivore species were described. Our results confirm the selectivity gradient between the species, from the most selective, the roe deer, to the most generalist, the mouflon. We found an increase of diet overlap with the restriction of food resources. This kind of study open new perspectives for understands resources portioning among mammal communities.

Estimating of the number of amur tiger population by noninvasive molecular-genetic methods.

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The procedure of noninvasive individual identification of tigers by molecular-genetic methods was developed within the framework of the Program of the Amur Tiger Research in the Russian Far East. The developed method makes it possible to perform noninvasive individual identification of Amur tigers on the basis of feces. As a result of genotyping of 35 samples of feces of the Amur tiger, collected on the territory of the Ussuri Nature Reserve during field research, we determined the number and sex of the animals that use this territory all year round. These were an adult female tiger, which was caught and tagged with a GPS Argos transmitter collar, and its three offspring. In addition, we managed to genotype a male tiger, possibly the father of these three cubs. We also identified one (possibly two) tiger(s) that was not in kinship relationships with the above mentioned animals. In total, we have identified six or seven animals on the territory of the reserve. The results of this study demonstrate the principal possibility of using molecular-genetic analysis methods for noninvasive individual identification of the Amur tiger by feces. This technique is used to clarify the number of animals obtained by traditional methods of accounting for the footprint on the test areas. The obtained data will be entered into the general genetic database for the Amur tigers from Primorye and Khabarovsk Krai based on noninvasive methods. This project was financed by “Konstantinovskiy” International philanthropic found, petrol transportation corporate enterprise “Transneft”, “Tekhsnabexport” and Russian Geographic Society.

Poster Communications

Taxonomy and distribution of the palearctic badgers (*Meles*, Mustelidae)

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The Eurasian genus *Meles* consists of three species –
European badger *Meles meles* (Linnaeus, 1758) with five subspecies: - *M. m. meles* (Linnaeus, 1758) – Sweden, eastern Norway and southern Finland; - *M. m. milleri* Baryshnikov, Puzachenko, Abramov, 2003 – SW Norway (west of Telemark и Siljan); - *M. m. taxus* (Boddaert, 1785) (syn. *britannicus*, *caucasicus*, *danicus*, *europeus*, *heptneri*, *marianensis*, *mediterraneus*, *tauricus*) – continental Europe to the west of River Volga and in the British Islands; - *M. m. canescens* Blanford, 1875 (syn. *minor*, *ponticus*, *severtzovi*) – the Caucasus, Iranian Plateau, Pamir-Alai Mts, South and West Tien Shan Mts; southward to Israel and Iraq; - *M. m. arcalus* Miller, 1907 (syn. *rhodius*) – Rhodes and Crete islands, probably conspecific with *M. m. canescens*. Asian badger *Meles leucurus* (Hodgson, 1847) with two subspecies: - *M. l. leucurus* (Hodgson, 1847) (syn. *altaicus*, *arenarius*, *raddei*, *tianschanensis*, *talassicus*, *blanfordi*, *chinensis*, *leptorhynchus*, *hanensis*, *siningensis*, *tsingtauensis*, *sibiricus*, *aberrans*) – eastward of Volga River throughout Siberia (except Far East), Kazakhstan, Middle Asia to Mongolia and China; - *M. l. amurensis* Schrenck, 1859 (syn. *schrenkii*, *melanogenys*) – Russian Far East, Korean Peninsula. Japanese badger *Meles anakuma* Temminck, 1844 (no subspecies designated) – inhabits at least the larger Japanese Islands of Honshu, Kyushu, and Shikoku, but is absent from Hokkaido. Sympatric zones between *M. meles* and *M. leucurus* found in European Russia (Kirov and Samara provinces) and in West Tien Shan Mts.

Feeding and interactive patterns among przewalski's horse males living in semi-natural conditions during early and fully reproductive period.

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In social equids, males try to control/herd female groups year round, which is at the expense of males’ feeding time. We investigated the temporal evolution of feeding and interactive patterns during four periods from early to full reproductive period (February 10th to April 28th) for 12 Przewalski’s male horses, a non-territorial species, living in a socially natural and enclosed herd. We analyse the structure of feeding bouts of both stallions and bachelors according to their reproductive and social status. A multivariate analysis allows distinguishing three profiles. Short feeding bout and high frequencies of behaviour transition (mainly vigilance and social contact) corresponded to harem stallions in fully reproductive period, the most proactive profile during the four periods. The less proactive profile characterized some harem stallions at the onset of the reproductive period as well as ousted and unstable-status males. However subordinates (bachelors and ousted adult males) might shift from low proactive to high proactive profile as the reproductive period progresses. Some implications of the diversity/alternative reproductive tactics in males on herd stability are discussed.

A novel functional polymorphism in the fatty acis desaturase 2 gene (fads2): possible role in basal metabolic rate

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As membrane components, polyunsaturated fatty acids (PUFAs) play an important role in cellular processes and have been shown to be associated with basal metabolic rate (BMR). While the link between BMR and membrane lipid composition is clear on an interspecific level, the underlying mechanism linking them on an intraspecific level is not well understood. Here we describe a new polymorphism in the fatty acid desaturase (*Fads2*) gene for Δ-6 desaturase (D6D), a key enzyme for PUFA synthesis, in 78 mice from two outbred lines selected for low (L-BMR) and high (H-BMR) BMR as well as for 34 mice from unselected lines. The aim of this study was to verify a possible association between *Fads2* genotypes and BMR. We found a significant correlation between *Fads2* variants and BMR within unselected lines of mice. We also used a F_{ST} outlier test to asses the effect of selection on the variation between L-BMR and H-BMR lines of mice at the *Fads2* gene, using the *Fads2* gene, together with data from the 11 microsatellite loci. Taken together, these results suggest that *Fads2* is expected to become a major focus of membrane, metabolic rate and human metabolic syndrome research.

Population and density estimate of black rat (*Rattus rattus)* in mangrove forest

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Population and density estimate of Black Rat in Mangrove forests was conducted by two independent procedure including Seber-Jolly and Catch-Effort Methods. A selected trapping area with 15 hectare area was studied. We used Color earrings and numerical rings for marking the captured individuals. Seber-Jolly method was performed in 7 steps which population for steps 2 to 6 were estimated 68.5, 96.9, 105.8, 61.7 and 73.6 respectively with density of 4.1 to 7 Rat/ha. Catch-Effort method performed in 6 steps and population estimate was 89.3 with density of 5.9 Rat/ha. For comparing the population estimates with the total population captured in the trapping area, the total number of rats were 96 with density of 6.4 Rat/ha. Considering the results, around 4-7 Black Rats survive in every single Hectare of Mangrove forests of study site, which states low differences between the results of Seber-Jolly, Catch-Effort and total count methods. All of these methods appear to be suitable for population-estimate for this species in this habitat, but because of lower Standard Error(SE) of Catch-Effort method, it is the most recommended to study Black Rats in Mangrove forests. Black Rat is an exotic and pest species in this habitat and removal them for scientific reasons would not damage their population or the ecosystem. The other advantages of the Catch-Effort method is its low cost and efficiency which could lead us to a total population estimate of the area.

Development of the skeleton in Xenarthran evolution

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Previous analyses of how mammals vary in their ossification sequences have focused on monotremes, marsupials, and boreoeutherian placentals. Here, we focus on the sequence of cranial and postcranial ossification events during growth in the xenarthran skull and skeleton, including armadillos, anteaters, and sloths. We use two different methods to quantify sequence heterochrony: sequence-ANOVA and event-paring/Parsimov. Our results indicate that Parsimov is too conservative and does not detect clear heterochronic shifts between xenarthran and boreoeutherian placentals. In contrast, sequence-ANOVA shows that xenarthrans significantly differ from other placentals by a late ossification of the dentary, sternum and clavicle, and an early ossification of the lacrimal, nasal, pedal and manual phalanges, and pubis. We interpret these differences as showing that heterochrony plays a role in the early skeletal development of xenarthrans, a change from previous studies that have emphasized the developmental homogeneity of the skeleton within groups of placental mammals.

Dental eruption sequence and eruption time in patas monkey (*Erythrocebus patas*)

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Erythrocebus patas is unique among the cercopithecines in terms of its life history traits. Inter-birth interval of this monkey is short; the juveniles rapidly develop independence from their mother; females are youngest at first birth; and mortality rate of adult females is high. According to Schultz's rule, molars of fast-growing and shorter-lived primate species erupt early relative to the replacement teeth. Based on the life history of *E. patas*, we hypothesised that the molars erupt before the replacement teeth. The purpose of the present study was to determine the dental eruption sequences and times for *E. patas* and to test our hypothesis. Eruption sequences of permanent teeth are $\frac{\mathrm{M1\ I1\ I2\ M2\ P3\ P4\ [C\ M3]}}{\mathrm{M1\ I1\ I2\ M2\ P4\ [P3\ C]\ M3}}$ in males and $\frac{\mathrm{M1\ I1\ I2\ [M2\ P4\ P3\ C]M3}}{\mathrm{M1\ I1\ I2\ [M2\ P4\ P3\ C]\ M3}}$ in females. Because these sequences constitute the general pattern seen in cercopithecines, Shultz's rule could not be applied to *E. patas*. However, in terms of eruption time, M2 and M3 of *E. patas* appear early within the cercopithecines. Indeed Schult's rule cannot be strictly applied to *E. patas*, but this monkey satisfies the requirements for the rule in terms of the early appearance of M2 and M3. The interval of the eruption time between dp4 and M1 is the shortest among the cercopithecines. In the *E. patas*, the early appearance of M2 and M3 is caused by the short interval of emergence times between dp4 and M1.

Habitat use of bush hyrax in the miombo woodland, Ugalla, Tanzania

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Bush hyraxes (*Heterohyrax brucei*) are diurnal mammals that have adapted to various environments in Africa. However, most researches have been conducted in the *Acacia* savanna where kopjes (rocky isolated hills) exist. In savanna, they form stable polygynous family group. With poor body-temperature regulation and poor defenses against predators, they depend on rocky shelters. Foraging by adults generally take place no more than 50 m away from kopjes. This study aims to give preliminary information of habitat use of them in a different environment, Miombo woodland (Ugalla). Here, they live on the rock outcrops consisting of several blocks. The median size of rock blocks in Ugalla is 269 m^2 (n = 98, range = 25 – 1,105 m^2) much smaller than that of kopjes in savanna. A group and solitary males were directly observed during day time. The group consisted of at least 16 individuals (including 5 adult males and 2 adult females). Although bush hyraxes in savanna are reported to feed mainly in the morning and evening, feeding and foraging was not observed during this study. From the fecal census, we found 151 fecal clumps in 7 days in the study area. There was a large variation in daily number of fecal clumps found in different rock blocks. These preliminary observations suggest that, bush hyrax in woodland live in similar social structure as in savanna. However, they may differ in some behavioral characteristics such that they roam some rock blocks and frequently forage more than 50 m away from rocky shelters.

Sex-specific diet segregation in the iberian red deer during rutting

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A large body of studies have linked sexual segregation in dimorphic ungulates with differential resource selection due to dissimilar nutritional requirements of the sexes. Seasonal fluctuations in resource availability could, therefore, affect patterns of sexual segregation in the different latitudes. We have compared diet and nutritional selection by three sex-age classes in the Iberian red deer (Cervus elaphus hispanicus) according to seasonal availability of feeding resources in a Mediterranean area. Foraging segregation between the sexes was found during the rut (late summer), in opposition to assumptions of general segregation hypotheses. During late summer females and juveniles exhibited a differential selection of dietary and nutritional traits compared to that of males. Female and juvenile selection of shrubs was higher whereas males selected greater grass and forb content. The foraging selection observed relates to a stronger selection of nitrogen, tannins and lignin by females and juveniles, and hemicellulose and cellulose by males. Our findings are associated to the Mediterranean climate, where rut and lactation concur with a shortage period, the extremely dry Mediterranean summer. Foraging segregation between sexes in summer seemed to be shaped by a conjunction of various factors such as low nutritional quality of resources, body dimorphism and differential strategies addressed to fitness enhancement. Male and female foraging patterns overlapped in the post-rutting period, probably due the substantial regrowth and increased quality of herbs and shrubs during autumn. We emphasize the importance of incorporating regional environmental conditions when assessing general hypotheses on ecological segregation.

Ecological Characteristics of Iranian Jerboa *Allactaga firouzi* (Mammalia: Dipodidae)

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Iranian jerboa was discovered in south of Shah-Reza as an endemic species. Its population is limited to semi-arid desert of Isfahan Province in Iran. Since, the ecology of *Allactaga firouzi* in Iran is poorly known; our aim of in this study was to examine some characteristics of ecology of this species in its locality. Because no additional studies on the ecology and behavior of this species have been performed during past 30 years, new data on state of the only population of Iranian jerboa are required. In the study area three major plant types, *Anabasis aphylla*, *Artemisia aucheri* and *Peganum harmalla* constitute the main vegetation cover. The habitat includes perennial grasses as *Scariolla orientalis* and forbs as *Astragalus lateritus* and *Acanthophyllum squarrosum*. There were no trees existing in its habitat The area has a semi-arid climate. Behavior observations were based on the works carried out in captivity and in the field. *A. firouzi* was determined to be an active animal and eager to explore surrounding habitat in the field and movement of it is more rapid. We determined that *A. firouzi* eats plant material such as *A. aphylla* and *A. aucheri*. Active period of this species includes the March to first half November. Pregnant female were found only in June to July. Results showed that *A. firouzi* is not agricultural pest. Iranian jerboa is one of most important species of this study area. Presence of this species that is data deficient and its distribution that limited to single locality in the world causes more important of its habitat. Public awareness campaigns aimed at local communities, nongovernmental organizations and politicians will increase knowledge of the species and provide a baseline for protecting it.

The starvation-predation risk trade-off: response of wood-mice (*Apodemus sylvaticus*) to a scenario of predatory risk

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In small mammals, fat reserves are an insurance against periods of starvation. According with the mass dependent theory these reserves reflect a trade-off between the risk of being predated and the risk of starvation. Carrying fat reserves increases the survival chance in periods of low food resources, but also reduces the ability to be a fast runner, and to hide in small refugees when running away from a predator. Thus, animals use direct cues (*e.g.* odor and sound) and indirect cues (*e.g.* moonlight) to evaluate the risk of being predated in a certain moment, and is expected a change on their physiological and behavioural parameters in response to these cues. In this study, we designed an experiment to analyze energy balance in 18 wild wood mice (*Apodemus sylvaticus*) under a scenario of high predation risk simulated by playback calls of Barn Owl (Tyto alba) and Eurasian Eagle-owl (Bubo bubo). Mice were exposed to playback calls broadcasted for 2 minutes, every 2 hours, during night time (11 pm to 7 am) for 5 consecutive days. During this period, food intake and body mass were monitored daily; resting metabolic rate was measure at the end of the exposure period. We aimed to observe a reduction in body mass, food intake and resting metabolic rate when compared to a group not submitted to the treatment. Perceived risk of predation was estimated through faecal corticosterone levels measured in pellets collected in the last day. The adaptive and ecological significance of the results are discussed.

Fat dormouse survey in a periurban area through combination of three methods

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Fat dormouse (*Glis glis*) is a nocturnal arboreal rodent particularly sensitive to habitat fragmentation and diffused in mature forests, with large trunks and cavitated trees, that provide shelter for daylight hours: this species usually avoids isolated environments and areas in which touristic pressure requires dead trunks’ felling. "Parco della Burcina" is an historical garden, immediately adjacent to the town of Biella (Piedmont, Northern Italy), just behind the foothills of the Alps, characterized by a considerable environmental heterogeneity and instituted for the conservation of peculiar varieties of rhododendron and other exotic plant species,. This reserve is visited by many tourists and local citizens even because it’s the main green area connected to the town of Biella. The presence of fat dormice in this area has been investigated by combining three survey techniques: audible calls counting, evenly distributed inside the study area, hairtubes, placed on different plant species and, nest-boxes, mostly concentrated in the highest part of the park, where it continues uninterrupted with subalpine forests. Methods produced consistent results: despite the constant human presence, fat dormouse seems to be spread throughout the whole reserve, although more concentrated in the northern less managed part, in beech or birch woods and on the edges of the forests.

Large mammal community in the sikhote-alin mountain range

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The Sikhote-Alin is the main mountain range in the southern part of the Russian Far East and has unique natural ecosystems with rich variety of fauna and flora. The purpose of this presentation was to analyze existing information about large mammal fauna of the Sikhote-Alin and to detect differences between southern and central parts of this mountain range. There are two special protected areas (nature reserves) with total area of 5,300 km^2 those were established in 1935. List of carnivores and ungulates of all Sikhote-Alin is represented by 24 species. The central part of the Sikhote-Alin is characterized by the most biological diversity because of flora and fauna combined by both southern and northern elements. Total coefficient of faunistic similarity for mammals between the southern and central parts of the Sikhote-Alin is 88 %. Among key species in large mammal community were eight species: Amur tiger, lynx, brown bear, Asiatic black bear, sika deer, red deer, roe deer, and wild boar. In the Lazovsky Reserve there is one of the most tiger densities for this subspecies – 0,9 animals/100 km^2 because here is highest sika deer density – 8 animals/km^2. The contribution of studies on predator-prey relations is very important for conservation purposes and management plans on rare species. Protection of ecosystems of the Sikhote-Alin Mountains and studying of biodiversity is necessary for ecologically correct sustainable use of natural resources.

Wolf (*Canis lupus*) impact on ungulates community in a new recolonized area of Italian western alps

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Our aim is to investigate wolf-ungulates interactions in a recolonized area of Italian Western Alps (Aosta Valley Region). In this region wolf has been absent since 19th century. Ungulates community comprises chamois (*Rupicapra rupicapra*), alpine ibex (*Capra ibex*), roe deer (*Capreolus capreolus*), red deer (*Cervus elaphus*) and wild boar (*Sus scrofa*). First wolf reproduction occurred in 2007. During our study (May 2007-April 2009) average pack size was five individuals. We used scat-analyses combined with statistical re-sampling techniques to investigate wolf diet. We calculated biomass consumed by wolves basing on volumes of undigested remains in scats through Weaver's biomass model. We estimated wolf impact on ungulate community by biomass values and mean-weight of prey-species. Wolf selection on food-items was evaluated by Manly's index. Chamois was the main prey, it constituted 55.22 – 60.23% of biomass consumed respectively during 2007-2008 and 2008-2009. Roe deer was extremely exploited (21.95 – 28.07%); other prey-categories, including livestock, were relatively unimportant. Assuming that all individuals consumed were killed by wolf, yearly impact was 33.6 chamois and 17.9 roe deer per 100km². These correspond to 3.9% of chamois population censed in summer 2007 and 2.5% of those censed in 2008; roe deer shows percentage equal to 14.7% for 2007 and 18% for 2008. Roe deer resulted to be positively selected by wolf in both years. On the contrary, previous studies in the Apennines indicate wild boar as preferred prey-species. The high susceptibility of roe deer to wolf predation could be due to habitat overlap and to vulnerability of this species in mountainous snowy areas.

First results on the presence of european wild rabbits (*Oryctolagus cuniculus*) on the island of Pantelleria (Sicily- Italy)

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In Italy, one of the greatest populations of European wild rabbits lives in Sicily, where it is hunted for its delicious meat but it is also preyed by wild cat (*Felix silvestris*), the only natural predator in this ambient. On the Pantelleria Island, the over-abundance of wild rabbits causes a lot of damages to the vineyards, famous for "Passito wine" production. The aim of this study was to collect preliminary data on wild rabbits numerousness. We produced a detailed land use map (Arc View 3.2) and, on the basis of direct surveys in March-April 2010, 26 circular plots (1.0 m^2), in three zones representative of this environment, were randomly placed. We estimated rabbit distribution based on the presence/absence of faecal pellets. Using the formula of Eberhardt and Van Etten (1956), assuming a daily average production of 350 pellets, rabbit numbers/ha was calculated. Pellets were present in 20 plots and absent in 6 plots characterised by a higher herbaceous cover. An average of 8, 22 and 80 rabbits/ha for each of the three zones was calculated. Wild rabbit density is higher in comparison with others authors who, in Sicily, found 9.2 rabbits/ha (Caruso and Siracusa, 2001), 10 rabbits/ha in protected areas and 6 rabbits/ha in hunting areas (Lo Valvo et al., 2008). These results suggest that it is necessary to implement effective management strategies, maybe further increasing the number of animal killed from each hunter.

Preliminary results of fatty acid composition of meat from red deer hunted in Tuscany (Italy)

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In the last years, in the north of Tuscany along the Apennine ridge, mainly in Pistoia, Prato and Florence districts, it is recording an increase of red deer number and, therefore, an increasing quantity of derived meat. It is well known that, generally, venison contains less fat than traditional red meats, satisfying consumer demand for lean meat, but less are the knowledge about meat fatty acid profile. Therefore, from the carcasses of ten stags, shot during the last 2009-2010 hunting season at an age of 18-20 months, ten samples of *longissimus lumborum* were excised at the level of 7th-8th ribs to determine pH$_u$ values (pHmeter Hanna pH211) and fatty acid profile (by gas-chromatography after Folch extraction). pH$_u$ values are normal (5.7-5.8) indicating a good acidification of meat and no effect of stress due to hunting method. Meat fatty acid composition shows values similar to other authors on red deer: total saturated content (lauric, myristic, palmitic, margaric and stearic acids) is equal to 42.08%; total monounsaturated (myristoleic, palmitoleic, cis-heptadecanoic, oleic and cis-eicosenoic acids) is equal to 26.04%, while polyunsaturated ones (linoleic, □-linoleic, CLA, arachidonic, EPA, DPA, DHA) are equal to 31.88%. Polyunsaturated/saturated ratio is 0.76 and is similar to the findings of other authors for red deer meat. In conclusion, red deer meat quality competes with domesticates meat and is a good alternative to traditional red meat, even if further research is needed to better know the difference due to sex, age and hunting season.

Capture-mark-recapture study on coexisting dormouse species in the grand duchy of Luxembourg

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The present study is the first research project in Luxembourg dealing exclusively with dormice. It is part of a PhD project, which started in spring 2009. The study site is situated at the river Moselle and characterized by a highly diverse small scale habitat mosaic. It includes inactive and active vineyards with dry-stone-walls, thermophilic forests, limestone escarpments, old mines, a canyon and humid scree forests. One hundred live traps were placed in these different habitat types in a 15m-grid, covering approx. 1 ha. They were activated for three nights twice a month. Nest boxes were also placed at the study site. The habitat around the trapping grid was scanned by foto traps for dormouse presence. During 2009 and 2010, 147 Garden dormice and 63 Edible dormice could be marked with PIT tags. Furthermore, tissue and faecal samples were taken for genetic analysis and information on their feeding ecology. Most Garden dormice were found in the vineyard with dry-stone-walls, a site which was almost completely avoided by Edible dormice. Additionally, the Hazel dormouse could be found at the study site from 2010. Data on habitat use and population structure with regard to the different species, sex and age classes are presented.

Anatomical observation of reproductive organ in Korean water deer (*Hydropotes inermis*)

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The water deer is known to be an endemic species in Korea and some limited areas in East China. There have been no studies of their basic reproduction. To understand the reproductive strategy of this species, their male and female reproductive organs were anatomically observed. The ampulla of deferent duct, vesicular gland, prostate gland (body and disseminate part) and bulbourethral gland were identified. Their shape, location and structure were basically similar to that of goat and sheep. The existence of the spermatozoon was histologically confirmed in the lumen of the convoluted seminiferous tubule of individuals obtained on November and December. Spermatogenesis might take place in specific periods. The uterus was categorized as a bicornuate uterus. The placentomes existed in the whole uterine horns and numbered 6. The volume of each cotyledon was 16-17cm$^{3.}$ The shape of the placentome was convex. The placenta can be classified as an oligocotyledonary placenta. The number of fetus is 3-4 and is exceptionally larger than in other ruminant species. Although the number of placentomes is similar to other cervidae species, there might be some special mechanism or structure in the attachment site of the fetus to accommodate an extraordinary number of fetuses in the water deer. These results may contribute to the management and conservation of this species.

Study of the intestinal microbiota of the faecal samples from the Iberian lynx *(Lynx pardinus)* present of different geographical zones of Spain

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According to the World Conservation Union, the Iberian lynx – *Lynx pardinus* (Temminck, 1827) is the most endangered felid species in the world (IUCN, 2010). The current population is estimated at no more than 280 individuals, distributed in two isolated metapopulations, both in Andalusia, southern Spain: Doñana area (DA), with only about 77 lynxes, and Sierra Morena (SM) with about 190 lynxes. Intestinal microbiota play a very important role as a defensive barrier against pathogens, and it can regulate the expression of an elevated number of genes in the digestive tract but also can contain pathogen bacterial that may threaten its survival. We have analysed faecal samples from 24 different individuals (17 males and 7 females). The samples were obtained along 2010 from animals with different ages (2000 to 2010) in the two areas where the Iberian lynx survives: Sierra Morena and Doñana (Andalusia, southern Spain). We have analysed this faecal samples by molecular methods based on Denaturing Gradient Gel Electrophoresis (DGGE). We have found differences between the microbiota of faecal samples of the studied animals being more similar between the lynxes live in DA that live in SM. These differences may be caused by different diet or environmental conditions.

Eastern boundary of a modern area Mound-Building Mouse

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The area mound-building mouse is not very big: Romania, Hungary, Yugoslavia, Bulgaria, and Austria, the great part of forest-steppe and steppe of Ukraine. In Ukraine the area of mound-building mouse was noted in the territories of Donetsk (Valh, 1927) and Kharkov regions (Zagorodnjuk, etc., 1995), as well as in Dnepropetrovsk (Antonets, 2001) and Kryvyj rig (Evtushenko, 1990) regions, etc. In Crimea mound-building mouse is usual, in Kerch peninsula it is even numerous (Dulitsky, 2001). This species also lives in Podillya (Zagorodnjuk, Berezovsky, 1994). Last results of researches show that the modern area of *Mus spicilegus* is much wider than it was supposed. The species is found out in Lugansk (Zagorodnjuk, etc., 1995; Kondratenko, 1998), in the Rostov (Lipkovich, 2005) regions, it occupies almost all the territory of Kharkov region of Ukraine and also meets in the Belgorod region (present message). During the study of a current state of fauna of rodents in Kharkov area, we had searched for habitats of *Mus spicilegus* in the region from 2002 to 2010. Morphological (exteriors and skull signs), karyological and genetic distinctions between the brownie (*Mus musculus musculus*) and mound-building mice (*Mus musculus hortulanus*) (Mezhzherin, Zagorodnjuk, 1989) were studied. As far as lifetime exterior signs don't allow to diagnose field material precisely, the fact of presence of the species was established on presence of fodder stocks — mounds - which are accurately defined on not opened fields in autumn-winter period. It was also considered that mound-building mouse builds mounds only if an abundance of food takes place and the more accessible it is, the larger mound is. The eastern boundary of a modern area of *Mus spicilegus* passes in limits of Rostov region, grasps a southern part of Belgorod region of Russia. Almost all the territory of Lugansk and Kharkov areas of Ukraine is populated with this species. At a forage abundance mounds are located very densely – near 30 mounds per 1 ha. Often large and doubled mounds with bases either joint or merged completely, forming two-topmost domes with height 40-50 cm can be seen. In the surveyed habitats number of the species in a cold season is from 6 to 189 individuals per 1 ha.

General Index

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