

The 15th Rodens et Spatium

International Conference on Rodent Biology

Programme and Abstract Book

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First Edition

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Foreword

Dear participants,

it is my great pleasure to welcome you to the 15th International Conference on Rodent Biology, Rodens et Spatium. It is for the second time when this unique conference found its way to the Czech Republic. It happened in 2000 and the conference venue was České Budějovice, southern Bohemia. Sixteen years have since elapsed, the conference continuing to move over the map of Europe, from the west (Louvain-la-Neuve, Belgium) to the East (Myshkin, Russia) and from the north (Rovaniemi, Finland) to the south (Lisbon, Portugal). Hence, it seems to be appropriate to return to the Czech Republic, the heart of Europe. This meeting takes place in the eastern part of the Czech Republic, called central Moravia. Located on the Morava River, the city of Olomouc is the ecclesiastical metropolis and historical capital of Moravia. Today, it is an administrative centre of a central Moravia region in which landscape was predominantly used for agricultural production, mainly cereals, due to highly productive soil.

Olomouc is an ancient university city and has more than one hundred thousand residents. Olomouc has several large squares. The main one, the Upper Square is adorned with the Holy Trinity Column, designated as a UNESCO World Heritage Site. Olomouc is the natural centre of a historical ethnic region Haná covering the productive lowlands in the Upper Moravian Vale along the river Morava. It is among the warmest areas in the Czech Republic where rodent populations and communities play an important role in ecosystem functioning. In farmland, the common vole is among the most abundant ones followed by *Apodemus* mice. There are still natural populations of the common hamster in Czech lowlands and Eurasian beavers are now quite common in Czech rivers, including the Morava river running through Olomouc.

I am very happy to host this meeting in Olomouc. In R&S 15, roughly 140 participants from 34 countries have registered. With 96 lectures on various rodent topics we offer a broad range of research perspectives covering all fields of current ecology, genetics and conservation biology.

I hope that this meeting will represent a unique opportunity contributing to the exchange of new and exciting scientific points and to developing new networks and collaborations. I believe that you will also find some time to enjoy the city of Olomouc by walking through downtown and beautiful city parks.

Welcome!

Emil Tkadlec

Committees

Local Scientific & Organizing Committee

Emil Tkadlec, *Palacky University Olomouc, Olomouc*

Josef Bryja, *Institute of Vertebrate Biology AS CR, Brno*

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Jan Zima, *Institute of Vertebrate Biology AS CR, Brno*

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Olga Osipova (Russia)

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Takuya Shimada (Japan)

Grant Singleton (Australia)

Mustafa Sözen (Turkey)

Alexey Surov (Russia)

Emil Tkadlec (Czech Republic)

Nigel Yoccoz (Norway)

Jan Zima (Czech Republic)

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Programme



**RODENS
ET
SPATIUM**

**JULY 25 — 29
OLOMOUC 2016**

Sunday, July 24

16:00–19:00 Registration, at the entrance of the Faculty of Science, Floor 1

Monday, July 25

07:30–09:00 Registration, in front of Aula of the Faculty of Science, Floor 2

Aula

Opening ceremony

09:00–09:15 Welcome: Emil Tkadlec, Ivo Frébort, the Dean of the Faculty of Science

Plenary lecture

09:15–10:00 Nancy Solomon: Dispatches from the field: intraspecific variability in prairie vole sociality
Chair: Tkadlec

10:00–10:30 Coffee break

Aula

Symp 1: Monitoring Rodent Populations

Chairs: Torre and Viñuela

10:30–10:45 Koprowski: Montane mammals at risk of loss: squirrels as indicators of global change

10:45–11:00 Jannett, Jr.: Long-term population pattern, habitat, and trappability of the southern bog lemming (*Synaptomys cooperi*) at high population levels in the apparent absence of the northern bog lemming (*S. borealis*)

11:00–11:15 Torre *et al.*: A monitoring protocol for the Spanish small mammal biodiversity (SEMICE) in the light of environmental change

11:15–11:30 Debenedetti *et al.*: Wood mouse populations as biological tags of environmental disturbances – A twenty two-year study in a burned Mediterranean ecosystem

11:30–11:45 Benedek *et al.*: Which factors shape rodent communities' structure and diversity in the typical rural landscape of central Romania?

11:45–12:00 Torre *et al.*: A monitoring program for the edible dormouse (*Glis glis*) in the Iberian Peninsula

12:00–12:15

12:15–12:30

12:30–14:00 Lunch (Student's Cafeteria)

Lecture Hall 2.005

Symp 5–I: Parasites and pathogens

Chairs: Henttonen and Krasnov

Costa *et al.*: Ecology and patterns of pathogenic *Leptospira* shedding of *Rattus norvegicus* from a Brazilian urban slum community

Debenedetti *et al.*: Rodents and parasites: what can they tell us about wildfires?

Fichet-Calvet *et al.*: Lassa virus infection in *Mastomys natalensis* populations: abundance, prevalence and force of infection

Henttonen *et al.*: Ecology of Puumala hantavirus in Finland

Tagliapietra *et al.*: A recent outbreak of Dobrava-Belgrade hantavirus in a population of wild rodents in northern Italy: causes and implications

Imholt *et al.*: Comparative hantavirus dynamics in two rodent reservoir species

Khalil *et al.*: A diverse ecosystem promotes human health: the dilution effect and Hantavirus infection

Ulrich *et al.*: Viral pathogens in exotic and indigenous squirrels, Central Europe

	Symp 2: African rodent ecology and evolution Chairs: Bryja and McDonough	Symp 5–II: Parasites and pathogens Chairs: Henttonen and Krasnov
14:00–14:15	Bryja <i>et al.</i> : African rodents: from biodiversity surveys to general evolutionary models	Kiefer <i>et al.</i> : Plague foci in Mongolia
14:15–14:30	Mikula <i>et al.</i> : Imprints of climate fluctuations in distribution of rodent diversity in the northern part of Zambezi savanna	Goüy de Bellocq <i>et al.</i> : Parasitism in the European house mouse hybrid zone
14:30–14:45	Sousa <i>et al.</i> : Did climatic changes trapped Ctenodactylidae species on Sahara-Sahel mountains and shaped intraspecific genetic variation?	Occhibove <i>et al.</i> : Does biodiversity affect pathogens transmission? Testing dilution effect in Welsh wild rodent communities
14:45–15:00	Aghova <i>et al.</i> : Integrative phylogeography of rodents from Sudanian savanna	Paulauskas <i>et al.</i> : Ticks and mites parasitising small rodents collected from different habitats in Curonian Spit, Lithuania
15:00–15:15	Krásavá <i>et al.</i> : Multilocus phylogeny of grey-bellied pygmy mouse (<i>Mus triton</i>) complex	Rodríguez-Pastor <i>et al.</i> : <i>Francisella tularensis</i> in a wild population of common vole (<i>Microtus arvalis</i>) from agricultural landscapes of SW Europe
15:15–15:30	McDonough <i>et al.</i> : On the use of next-generation sequencing technology and museum specimens to resolve African rodent systematics	Sándor <i>et al.</i> : Rodents, ticks and pathogens: importance of host species and habitat for tick parasitism and pathogens carried by ticks of small mammals in Romania
15:30–15:45		Krasnov and Khokhlova: How do parasites select their host species? Trait-based and phylogenetic associations between fleas and their small mammalian hosts in the Palearctic
15:45–16:15	Coffee break	
16:15–17:15	Poster session	
17:15–19:00	The guided tour through the downtown	
19:30–24:00	Welcome party: Faculty of Science	

Tuesday, July 26

	Aula Plenary lecture Ottar N. Bjørnstad: Causes and consequences of spatial synchrony in population dynamics – data, statistics and theory Chair: Tkadlec	
09:00–10:00		
10:00–10:30	Coffee break	
	Aula Symp 3-I: Rodent population dynamics Chairs: Tkadlec and Jacob	Lecture Hall 2.005 Symp 7-I: Stories from underground Chairs: Šumbera and Burda
10:30–10:45	Fauteux <i>et al.</i> : Lethal and non-lethal effects of predation on arctic lemmings	Hrouzková <i>et al.</i> : Seismic signals in subterranean rodents: how is it in spalacids

10:45–11:00	Bogdziewicz <i>et al.</i> : Negative effects of density on space use of small mammals differ with the phase of the masting-induced population cycle	Malewski <i>et al.</i> : Magnetoreception in rodents – new species, new methods
11:00–11:15	Borowski <i>et al.</i> : Experimental test of a trade-off between breeding dispersal and fitness in males of the root vole (<i>Microtus oeconomus</i>)	Lövy <i>et al.</i> : Soil preference in the speciating blind mole rats <i>Spalax galili</i> : Do they prefer the fertile or the familiar?
11:15–11:30	Ecke and Hörnfeldt: Spatio-temporal patterns in the population dynamics of the field vole (<i>Microtus agrestis</i>) in Sweden	Burda <i>et al.</i> : Mole-rats like it hot
11:30–11:45	Hein and Jacob: Recovery of common vole populations (<i>Microtus arvalis</i>) after population collapse	Šumbera <i>et al.</i> : Light or temperature; that is the question. Circadian rhythms of the silvery mole-rat (<i>Heliophobius argenteocinereus</i>)
11:45–12:00	Petrová <i>et al.</i> : Increased productivity by large-sized individuals leads to high population density in the common hamster	Moshkin: Nasal construction protects rodent brain from inhaled dust and virus
12:00–12:15	Tkadlec and Pavlučák: The effects of vole population variability on annual productivity of barn owls: testing Jensen's inequality using a predator–prey system	Begall <i>et al.</i> : Do breeders and non-breeders in eusocial Ansell's mole-rats (<i>Fukomys anselli</i>) represent different personalities?
12:15–14:00	Lunch (Student's Cafeteria) Symp 3-II: Rodent population dynamics Chairs: Tkadlec and Jacob	Symp 7-II: Stories from underground Chairs: Šumbera and Burda
14:00–14:15	Gasparini <i>et al.</i> : Effects of forest management on density and survival in terrestrial small mammals	Vlasatá <i>et al.</i> : Spatial patterns of activity in the giant root-rat (<i>Tachyoryctes macrocephalus</i>), a fossorial rodent endemic to the Bale Mountains, Ethiopia
14:15–14:30	Imholt <i>et al.</i> : Synchrony of forest rodent abundance and relation to tree damage	Okrouhlik <i>et al.</i> : Huddling and socio-physiological effect in a social African mole-rat, the Mashona mole-rat (<i>Fukomys darlingi</i>)
14:30–14:45	Orozco and Cornejo: Integrated rodent pest management in the campaign against vole in the local board of Plant Health in El Valle Del Fuerte, sin. Mexico	Smorkatcheva and Kuprina: Effect of social environment on female reproduction in the Zaisan mole-vole, <i>Ellobius tancrei</i>
14:45–15:00	Tchabovsky <i>et al.</i> : Species-specific response of desert rodents to human-induced landscape change from desert to steppe	Cerveira <i>et al.</i> : Reproduction, postnatal growth and development of two fossorial pine voles, <i>Microtus duodecimcostatus</i> and <i>M. lusitanicus</i>
15:00–15:15	Damugi <i>et al.</i> : Matrix population modelling of the common hamster life history	Çolak <i>et al.</i> : Notes about reproduction biology of <i>Nannospalax xanthodon</i>
15:15–15:30	Pyzyna <i>et al.</i> : The efficacy of ContraPest®, a contraceptive bait, in the management of wild rats (<i>Rattus norvegicus</i> and <i>Rattus rattus</i>)	Matur: A new hypothesis for the origin of cytotype diversity of blind mole rats in Anatolia
15:30–16:00	Coffee break	
16:00–17:00	Poster session	

Wednesday, July 27

07:30–19:00 Mid-Conference Tour
Museum of Olomouc Cheese, Bouzov Castle, Hydroelectric power station at Dlouhé Stráně

Thursday, July 28

Aula

Plenary lecture

09:00–10:00 Gerald Heckel: Very many and still too few? Charting the limits of vole diversification
Chair: Tkadlec

10:00–10:30 Coffee break

Aula

Symp 6: Rodent behaviour

Chairs: Sedláček and Borowski

10:30–10:45 Frynta *et al.*: Exploratory axes in personality of black rats: repeatability and mutual correspondence in open-field and hole-board tests

10:45–11:00 Borowski *et al.*: The role of kinship in the formation of dormice aggregations in post breeding season

11:00–11:15 Safavian *et al.*: Habitat structure can affect nocturnal activity pattern of jerboas: a comparison of semi-desert and mountainous areas of Iran

11:15–11:30 Schlötelburg and Jacob: Maze runners: common voles (*Microtus arvalis*) in T-maze trials for identifying repelling or attracting substances

11:30–11:45 Sedláček *et al.*: On the determination of personality traits in the common vole

11:45–12:00

12:00–12:15

12:15–14:00 Lunch (Student's Cafeteria)

Symp 8: Physiology and Reproduction of Rodents. Chair: Frynta

14:00–14:15 Gromov and Anisimova: Reproductive success and fitness of male common voles (*Microtus arvalis*)

14:15–14:30 Kuznetsova *et al.*: Seasonality in the physiology and reproduction of the common hamster from urban population

Lecture Hall 2.005

Symp 4-I: Exploring rodent genomes

Chairs: Ruiz-Herrera and Kotlík

Herman *et al.*: Serial colonisation and natural selection in a common rodent, the Eurasian field vole

Chevret *et al.*: Phylogeography, genetic structure and morphological evolution of the house mouse on the Orkney Archipelago

Hánová *et al.*: Genetic-based modelling of population history and spread of the European ground squirrel (*Spermophilus citellus*)

Özkurt and Kandemir: Morphometric, karyologic and mtDNA characterization of *Sciurus vulgaris* and *S. anomalus* in Turkey

Kotlík *et al.*: SNP versus mtDNA: genomic phylogeography of the bank vole in Europe

Strážnická *et al.*: Gene–environment interaction in the bank vole (*Clethrionomys glareolus*)

Ruiz-Herrera *et al.*: Comparative genomics in rodents: genomic signatures of evolutionary reshuffling

Symp 4-II: Exploring rodent genomes

Chairs: Ruiz-Herrera and Kotlík

Maltsev *et al.*: Phylogeography and phylogenetics of the eastern house mice (*Mus musculus*) on polymorphisms of mitochondrial DNA

Mironova and Gromov: Structure of the natural hybrid zone between two chromosomal forms of common vole

14:30–14:45	Guenther and Trillmich: Seasonality and the wild cavy: effects on physiology, reproduction and behaviour of a highly precocial rodent	Poplavskaya <i>et al.</i> : Molecular-genetic analysis of urban populations of common hamster (<i>Cricetus cricetus</i>)
14:45–15:00	Potashnikova and Feoktistova: The hormonal response of chinese hamster males exposed to con- and heterospecific olfactory signals	Russell <i>et al.</i> : Phylogeography of invasive rats in New Zealand
15:00–15:15	Wang: Geographical physiological adaptation in energy and water metabolism in Mongolian gerbils (<i>Meriones unguiculatus</i>)	Shenbrot <i>et al.</i> : Phylogeography and taxonomy of the northern three-toed jerboa (<i>Dipus sagitta</i> Pallas, 1773) species complex
15:15–15:30		D'Elia <i>et al.</i> : A phylogenomic appraisal of the sigmodontine radiation (Cricetidae)
15:30–15:45		Renaud <i>et al.</i> : Bank voles in Southern Eurasia: vicariance and adaptation
15:45–16:00		Dabrowski <i>et al.</i> : How cold-tolerant species coped after the last glaciation: the case study of the <i>Microtus oeconomus</i> subspecies in Europe
16:00–16:30	Coffee break	
16:30–17:30	Poster session	
19:30–24:00	Banquet (Archbishop's Palace, Würmova 9)	

Friday, July 29

Aula Plenary lecture

09:00–10:00	Stuart J. E. Baird: Introgression across the European house mouse hybrid zone: mouse genes, mitochondria and parasites Chair: Tkadlec
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10:00–10:30	Coffee break
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Aula Symp 9: Ecology and Biology of Rodents Chair: Le Boulengé

10:30–10:45	Rivarola and Simberloff: Categorization and effectiveness of protected areas: comparative study of small mammal communities in Nahuel-Huapi National Park, Argentina
10:45–11:00	Jeon <i>et al.</i> : Changes of rodent community and habitat structure with time elapse after thinning in Japanese larch (<i>Larix kaempferi</i>) plantations

11:00–11:15	Ghazaryan <i>et al.</i> : New data on Armenian birch mouse
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Lecture Hall 2.005 Symp 10: History and morphology of rodents Chair: Horáček

Horáček <i>et al.</i> : Rodents in Central Europe along the Pleistocene/Holocene transition

Naderi <i>et al.</i> : Cranial morphometric analysis of the Transcaucasia mole vole in Iran and Caucasian region
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Romaniuk and Herman: Rodent osteology from a zooarchaeological perspective – rodent skeletal remains from a Neolithic site at Skara Brae, Orkney, United Kingdom
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		Symp 11: Food of rodents Chair: Verde Arregoitia and Heroldová
11:15–11:30	Sözen and Şenol: Population size estimates for <i>Apodemus</i> spp., <i>Myodes glareolus</i> , <i>Glis glis</i> and <i>Muscardinus avellanarius</i> inhabit a deciduous forests in Zonguldak Province	Verde Arregoitia: Rethinking omnivory in rodents
11:30–11:45	Amirmardfar: The amount of organic phosphates (like DPG) existing in blood is determining factor of mammal's bulk	Mühlböck and Sedláček: Food preference of the bank vole (<i>Clethrionomys glareolus</i>) and yellow-necked mouse (<i>Apodemus flavicollis</i>) in a laboratory experiment
11:45–12:00	Kazanis <i>et al.</i> : Where does size matter? Common and different aspects in the life of adult Neural Stem Cells in the mouse and the rat brain	Dell'Agnello <i>et al.</i> : The diet of Savi's pine vole: a new quantitative approach
12:00–12:15		Li <i>et al.</i> : <i>Ochotona curzoniae</i> physiological adaptation to <i>Oxytropis ochrocephala</i> toxin
12:15–12:30	Closing Ceremony	
12:30–14:00	Lunch (Student's Cafeteria)	

Plenary presentations



**RODENS
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Introgression across the European house mouse hybrid zone: mouse genes, mitochondria and parasites

Stuart J. E. Baird

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Environmental change can both divide organism ranges into sub-ranges and subsequently reunite those sub-ranges. One outcome of this secondary contact is formation of a stable transition zone where taxa produce less fit hybrids due to incompatibilities accumulated during isolation. Such tension zones are permeable to geneflow despite maintaining distinct taxa, forming natural laboratories for studying evolutionary process: do some types of gene preferentially introgress across taxon boundaries, do others systematically impede such introgression? Isolation and re-contact does not however only shape process at an organism's nuclear loci. Genomes of fellow-travellers from commensal mitochondria through to selfish parasites will also diverge during their host isolation, with a range of architectures, mutation rates and effective population sizes. What happens to this diverged meta-genome on secondary contact? We use the European House Mouse Hybrid Zone (HMHZ) to address this question empirically. Two synanthropic taxa of mice (*Mus musculus musculus* and *M. m. domesticus*), previously isolated for about 0.5 million years, form a 2500km long ≈ 20 km wide tension zone dividing western and eastern Europe. They differ in pelage, allometry and behaviour. Allozyme analyses suggest many tens of incompatibility loci contribute to their taxon barrier. SNP analyses show this barrier to geneflow operates throughout the nuclear genome, most strongly on chromosome X, with numerous local 'punctures' of higher introgression. The mitochondrion appears relatively free to introgress in either direction along the course of the HMHZ. The Y chromosome tends to introgress east to west, with large variation in penetrance. Several 'specific' parasites show a taxon boundary coinciding with the HMHZ centre, while one generalist (multi-host) shows no such structure. Work is underway to ask whether parasites hybridising at the host contact allow introgression of genes that subvert host defences.

Causes and consequences of spatial synchrony in population dynamics – data, statistics and theory

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Spatial synchrony refers to coincident changes in geographically disjunct populations. This phenomenon has been documented in studies of a variety of taxa across a range ecological systems. Synchronization may arise from a number of mechanisms including (1) dispersal among populations reducing the size of relatively large populations and increasing relatively small ones; (2) congruent dependence of population dynamics on synchronous exogenous random factor such as temperature or rainfall (the “Moran effect”); (3) trophic interactions with populations of other species that are themselves spatially synchronous and mobile; and (4) endogenous cyclicity which promote synchrony through the dynamical process of “spatial phase locking”. In contrast, spatial de-synchronization may be caused by opposing forces such as (i) landscape heterogeneities that makes local populations follow different density-dependent trajectories or (ii) locally unstable fluctuations leading to spatially chaotic decorrelation. I will use data and models to illustrate these effects in a range of systems and discuss statistical methods that may be useful for distinguishing among them.

Very many and still too few? Charting the limits of vole diversification

Gerald Heckel

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Speciation research has gained momentum in the last decades through the explicit consideration of an adaptive contribution to the diversification process. Currently, the scientific literature is taxonomically highly skewed regarding the relevance of adaptive versus neutral processes in the onset of speciation. Rodents are the group of highest taxonomic diversity among mammals and feature extraordinary diversification rates. However, compared to other vertebrate groups both the rate of diversification and the level of diversity achieved in millions of years of evolution appear almost feeble. This contribution reflects on spatial, temporal, and other factors contributing to – and potentially limiting – the diversification of rodents. With a focus on the radiation of the *Microtus* genus, I report on recent investigations of the spatial patterns of divergence and the build-up of (incomplete) evolutionary boundaries in contact zones of multiple species and lineages of voles and their pathogens. Genetic and behavioral data show that the critical stages of divergence before completion of full reproductive isolation among incipient species are often associated with sex-specific processes at pre- and/or post-zygotic levels. The time needed for reaching these critical stages might be shorter than often assumed as suggested by recent genetic analyses. The contribution of sexual selection and adaptive processes appears to be less prevalent relative to other vertebrates, although – surprisingly – important phenotypic and ecological traits and their consequences for the diversification of voles and their pathogens appear understudied. It will require the analysis of more complex phenotypes and processes to better understand the apparent evolutionary stasis of some traits despite very rapid speciation in many taxa.

Dispatches from the field: intraspecific variability in prairie vole sociality

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Understanding the factors that influence the evolution and maintenance of sociality is an important question in animal behavior. In my research group, we have taken an integrated approach to this question by studying some potential intrinsic and extrinsic factors involved in sociality as well as consequences for individuals that live and breed in various types of social units. The prairie vole is an excellent species for testing proximate and ultimate hypotheses about sociality because they live and reproduce as single adults, male-female pairs, or groups containing more than 2 adults with or without philopatric offspring. In addition, male prairie voles appear to display alternative reproductive tactics: some adult males are trapped at the nests of more than one female (wanderer) while others are residents at only one nest (residents). Few manipulative experiments have been conducted in the field and there are also few studies that examine the consequences on the reproductive success of prairie voles. We have studied prairie voles in multiple natural populations as well as in semi-natural enclosed populations at the Miami University Ecology Research Center where we can manipulate demographic or ecological factors. We can also breed animals with particular genotypes or, with the advent of some of the newer molecular methods, manipulate the density of receptors in particular brain areas and examine the voles' behavior and reproduction in our enclosed populations. I will share some results from our studies and discuss what we still need to more fully understand the evolution and maintenance of sociality.

Oral presentations



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Integrative phylogeography of rodents from Sudanian savanna

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Sudanian savanna forms a wide belt of more or less open habitats spreading from Senegal to western Ethiopia. Although several phylogeographic studies of species associated with the Sudanian savanna have been published, there is still no clear agreement on the main evolutionary processes that have influenced the diversification of these species during the Plio-Pleistocene. Here we gathered recently published and new DNA sequence data from eight Sudanian savanna rodent taxa with the aim of analyzing simultaneously their phylogeographic patterns. As a first step, we produced a well resolved and time-calibrated phylogenetic tree of the whole family Muridae based on a supermatrix (10 genes) of 165 taxa using a novel set of calibration points (13 well documented fossil records). As a second step, we relied on one single Bayesian analysis to simultaneously date the divergences between georeferenced phylogeographical lineages within each of the nine model taxa. This approach allowed us to investigate the degree of synchrony between (both inter and intra-specific) lineage divergences. The inferred split events were also analyzed in the framework of known past climatic/environmental past events that occurred in this part of Africa. Altogether, the results obtained following this meta-phylogeographic study provided new insights into the impact of the evolution of the African savanna on mammalian rodent communities as a whole.

The amount of organic phosphates (like DPG) existing in blood is determining factor of mammal's bulk

Ramin Amirmardfar

Independent Scholar

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The diet, its quality and quantity considerably influence population parameters. It is essential that oxygen is transported by the blood to all cells of a mammal at any moment. This ensures survival of all cells in a mammal's body. In case a mammal's bulk is large, the distance between cells in different tissues and the mammal's heart is larger. Therefore, red blood cells in bulky mammal's bodies should be capable of conveying oxygen to farther distances. To make it practical, oxygen should be glued to red blood cells tenaciously. In other words, the cohesion of oxygen to red blood cells should be stronger in bulky than in small mammals. In mammal's bodies, the controlling factor of amount of cohesion of oxygen to red blood cells, are organic phosphates (like DPG). The less DPG in red blood cells of a mammal, the more cohesion of oxygen to red blood cell at the same rate. If oxygen is glued more tenaciously to red blood cells, oxygen could be carried to farther distance allowing mammals to have larger bulk at the same rate. The amount of organic phosphates (eg. DOG) of red blood cells decreased respectively with size from mouse, rat, cat, fox, sheep, horse, to elephant.

The mammal species and the oxygen pressure (in mmHg) in which the red cell's hemoglobin sends most of its oxygen to the tissues.

Mouse	45
Rat	42
Cat	38
Fox	35
Sheep	30
Horse	25
Elephant	22.5

Do breeders and non-breeders in eusocial Ansell's mole-rats (*Fukomys anselli*) represent different personalities?

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Ansell's mole-rats (*Fukomys anselli*) are subterranean rodents living in families composed of about 20 members with a single breeding pair and their non-breeding offspring. Most of them remain with their parents for their lifetime and help to maintain and defend the natal burrow system, forage, and care for younger siblings. Ansell's mole-rats display a bimodal aging pattern with reproductive animals having a significantly longer mean and maximum life-span compared to non-reproductive animals. We hypothesize that this difference in lifetime reproductive success is reflected in different personalities. We tested the risk-taking behaviour in 48 adult (>2 years) animals of seven families using three different tests. We found consistent individual responses over time and contexts indicating different animal personalities. However, neither sex nor reproductive status (or a combination of the two factors) had an influence on the results. There was a significant difference between wild-captured animals (living in the laboratory since four years) and those born in the laboratory (these two groups did not differ in age). Discriminant function analysis revealed that members of different families clustered more closely together than expected by chance. The results of our study imply that reproductive status is not decisive for individual differences, but rather family membership and origin. This is consistent with the idea that personality is determined by genetic factors and moulded by social and environmental experience, that about becoming a breeder (king, queen) in mole-rats decides chance but not personality or physical traits and that there is little competition within the respective mole-rat families.

Which factors shape rodent communities' structure and diversity in the typical rural landscape of central Romania?

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Turning grasslands into arable land and deforestation are among the main causes of habitat loss and biodiversity impoverishment. In central Romania the landscape is still highly heterogeneous. Following the political changes in Eastern Europe, most of the land was restituted to its former owners. The villagers own small plots which they cultivate with different crops, partly still using traditional methods. Semi-natural habitats are also well represented in the study area, as pastures, hayfields and woodlands connected by riparian forests. This study focused on the relationships between rodent community indices and habitat characteristics in the typical forest–agricultural landscape in central Romania. Our aim was to answer the following questions: (1) which environmental variables drive abundance and diversity of rodent assemblages in the studied landscape and (2) how do individual species respond to habitat factors? Rodents were live-trapped using box-traps placed in 104 trap-lines set in all the habitat types in the study area during summer and autumn. The forest–agricultural landscape in the researched region sheltered a very abundant and diverse rodent community. Total captures counted 1345 rodents belonging to 14 species. Similarly to other regions in the temperate climate zone, the assemblage was dominated by two species, *Microtus arvalis* and *Apodemus agrarius*, representing 71.4% of the captured rodents. The Monte Carlo permutation test showed that the CCA was highly significant for both the first and all the canonical axes, explaining 41.3% of the variability within the species data. Tree cover was the most important factor for species composition, followed by herbal cover and distance to forest. Herbal height and shrub cover had the strongest influence on rodent community diversity and abundance. Abundance of the whole community and most species was significantly higher in autumn, while no difference was found between seasons for the diversity.

Negative effects of density on space use of small mammals differ with the phase of the masting-induced population cycle

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The space used by an individual (home range) is an important determinant of its fitness. Population density strongly affects the size of a home range, but separating its influence from other factors (e.g. food availability, kin structure) is a difficult task. We used spatially explicit capture recapture models (SECR) to examine how population density affects home range size in the yellow-necked mouse (*Apodemus flavicollis*). The relationship between population density and home range size was studied at two distinct phases of population fluctuations induced by beech (*Fagus sylvatica*) masting: post-mast peak in abundance (one year after mast, $n = 2$) and subsequent crash (two years after masting, $n = 2$). We live-trapped mice during summers (from June to October) to avoid confounding effects of autumn seedfall (i.e., changes in food abundance) on home range size. In accordance with general predictions, we found that population density was negatively associated with home range size. However, after controlling for the effect of density, home ranges of mice were larger in post-mast years than during the crash phase. This indicates a higher spatial overlap among neighbors in post-mast years. We speculate that the increased clumping is caused by negative density-dependent dispersal that leads to high relatedness of individuals within population in the peak phase of the cycle.

The role of kinship in the formation of dormice aggregations in post breeding season

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In late summer and autumn during the day dormice aggregate in large groups. This is an important period for this species, because animals must intensively forage to accumulate fat reserves before hibernation. If places for diurnal rest are related with food resources we should expect the competition between individuals for food. However, competitive interactions between members of group could be mitigate by their kinship. That is why we analyzed the pattern of dormice diurnal aggregations in nest boxes in their free-living population in Central Poland on four trapping grids (25 ha each) located from 1 to 10 km from each other. In total we analyzed over 300 animals which were caught in autumn 2013. The number of individuals per aggregation varied between analyzed population and was positively dependent on their population density. On the trapping area with the highest dormice population density (123 ind. per 25 ha) the mean number of animal per aggregation amounted to 5. Despite the fact, that analyzed populations were characterized by different population density and different aggregation size, their kinship did not play any role in observed aggregations' structure. Contrary to the evolutionary expectations we did not observe that next boxes were more frequently shared between mother and their offspring or between siblings. How to explain this paradox in kin selection theory? At the moment we have two explanations. The first one is that in our study area the natural holes are very (the pine forest), therefore dormice aggregations are artificially created by nest boxes availability. The second one is that foraging areas of these species are not related with the diurnal resting places.

Experimental test of a trade-off between breeding dispersal and fitness in males of the root vole (*Microtus oeconomus*)

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In presented study we tested a trade-off between breeding dispersal and fitness in males of small rodents on the root vole example. During three years of the study (2013, 2014, 2015) we analysed reproductive success of migrating and resident males as well as selected physiological, behavioural and morphological traits which are known to be related with dispersal and fitness. There were: behavioural profile (personality traits), social status (SS), testosterone level (T), resting metabolic rate (RMR) and body mass (BM). To test above mentioned trade-off we designed a field experiment by building four enclosures (0.5 ha each) which were grouped in two temporarily connected pairs in the natural root vole's habitat (Biebrza National Park, NE Poland). Surprisingly, results of the experiment show that the overwhelming majority of analysed males did not participate in reproduction. The minority of breeding individuals was characterized by higher BM, higher probability of dispersion and lower RMR and was less proactive. Such seemingly obvious small rodents' traits as T level and male's SS did not influence on males participation in reproduction. In the next step we focused on diversity in reproductive success among these males which had an offspring. In this case the following males' traits influenced on diversity in number of offspring: BM, SS, probability of migration, T level and RMR. Almost all mentioned above traits had a positive impact on male's breeding success, with exception of RMR which has been found an inverse relationship. These findings indicate the strong sexual selection pressure for males which operate on the following traits: BM, RMR and probability of migration. Obtained results also show that there may be no relationship between breeding dispersal probability and following physiological and behavioural traits of small rodent males: RMR, SS, personality traits and the level of T, which was previously suggested by studies of other groups of animals.

African rodents: from biodiversity surveys to general evolutionary models

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Africa is a region well known for its high ecosystem diversity (from deserts to tropical rain forests), reflected in high diversity of fauna and flora. In rodents, nearly every ecological, behavioral, and locomotory adaptation are represented on a single continent. Given these factors, African rodents may lend themselves as a model for studies related to ecology and evolution. However, until now the majority of rodent studies only have described basic ecological requirements of individual species and patterns in the distribution of biological diversity. Current boom in the use of genetic approaches not only allows us to reconstruct phylogenies and to resolve taxonomic problems, but also provides the opportunity to use rodents as general evolutionary models. For example, thanks to intensive large-scale collection of fresh tissue samples of small mammals assembled in last decades, it is now possible to use the comparative phylogeographic approach to assess the role of past climate and geomorphology on evolution of African biodiversity in particular ecosystems. Knowledge of detailed phylogenies allows us to study the mechanisms of adaptive radiations. The characterization of contact zones between differentiated populations provides new models for speciation studies. Such contact zones also represent important hot-spots for organisms associated with rodents, (e.g. viruses or host-specific parasites), and understanding their evolution can provide insight into their role in human health. In our contribution we will shortly present several case studies demonstrating huge opportunity of African rodents in evolutionary studies.

Mole-rats like it hot

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The naked mole-rat, a subterranean rodent (Bathyergidae) gained popularity within the last 35 years thanks to its hairlessness, eusociality, heterothermia, longevity, resistance against cancer, and tolerance of pain mediated by skin receptors. While before 1980 almost unknown, today it is kept in many zoos and institutions all over the world and it has become a prospective model animal in biomedical research. Its alleged uniqueness is, however, a complex of traits which frequently characterize also other bathyergids or even other subterranean mammals. Here we studied the reduced perception of pain (nociception) due to skin irritation. Chemoreceptors at free nerve endings which participate in nociception react on protons and in mammals (not in birds and amphibians) on capsaicin. The naked mole-rat does not react on subcutaneously injected capsaicin because neuropeptides SP and CGRP which are needed for nociception are missing in skin and mucosa. The changes in the nociceptive system of the naked mole-rat are considered an adaptation to high concentration of carbon dioxide in burrows which can result in acidosis of tissues and thus in pain. If this is a real ecophysiological adaptation we have to expect convergent adaptations also in other subterranean mammals. We have tested this hypothesis, yet have chosen a non-invasive "voluntary" method – instead of injecting capsaicin under the skin of tested animals we offered them food soaked in solution of capsaicin of different concentrations. We found that all the tested species of subterranean rodents (*Heterocephalus glaber*, *Heliophobius argenteocinereus*, *Fukomys anelli*, *F. darlingi*, *F. kafuensis*, *F. mechowii*, *F. micklemi*, *Spalacopus cyanus*) accept readily capsaicin-treated food (even in very strong concentrations) and do not exhibit any behavioural changes indicating pain or discomfort. The epigeic species (*Microtus arvalis* and *Acomys dimidatus*) under study avoided capsaicin and in the case of contact showed distinct reactions.

Reproduction, postnatal growth and development of two fossorial pine voles, *Microtus duodecimcostatus* and *M. lusitanicus*

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The Lusitanian and the Mediterranean pine voles (*Microtus lusitanicus* and *M. duodecimcostatus*) are fossorial sister species occurring in the Iberian Peninsula and southern France. Reproduction, postnatal growth and development of both species were investigated in the laboratory from birth to day 100. Both species had a mean litter size of 2 pups per litter, ranging between 1 and 4 in *M. lusitanicus* and between 1 and 5 in *M. duodecimcostatus*. The sex ratio was not significantly different from 1:1 ratio. Interval between litters (IBL) and gestation period was also similar in both pine vole species (mean \pm SE; *M. duodecimcostatus* IBL = 47.0 days \pm 4.437, gestation 21 days; *M. lusitanicus* IBL = 37.6 days \pm 2.972, gestation 21 days). The ontogenic sequence of both species followed that described for other *Microtus*; pups are altricial, born naked with folded ear pinnae, closed eyes, fused toes and no teeth, weighing an average of 1.9 ± 0.27 and 2.5 ± 0.34 g respectively. The body weight of both species increased rapidly on the first 30 days, attaining its full weight of about 15.9 ± 1.53 g in *M. lusitanicus* and 28.2 ± 4.07 g in *M. duodecimcostatus* around day 60 and day 80, respectively. *M. lusitanicus* showed a faster mean growth rate in body size (K in the Gompertz sigmoidal curve) compared to *M. duodecimcostatus* (0.064 ± 0.001 and 0.047 ± 0.009 respectively). Although growth rate was not affected by litter size in *M. duodecimcostatus*, *M. lusitanicus* pups born in litters of one or two newborns grew significantly faster than pups born in litters of three or more. Overall results suggest that both species are K -strategists, and although not strictly subterranean, their reproductive strategy and development seem to reflect some degree of adaption to the subterranean ecotope.

Notes about reproduction biology of *Nannospalax xanthodon*

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We recorded the observations of the reproduction behavior of blind mole rats which subjected to our several projects about blind mole rat diversity in Anatolia between the years of 2000 and 2016 in order to better understand the reproduction biology of Anatolian blind mole rats. We detected the reproduction data at 93 individuals out of observed 690 individuals during the studies. According to the data, the vaginal opening and large testicles were seen at females and males, respectively in September when the reproduction period started. The enlargements of testicles at male individuals could be seen till end of March. The males aim to reach nest of their potential female partners by digging reproduction tunnels, of which the length reach tens of meters even sometimes hundreds of meters, in a straight line without changing the direction. The females do not dig reproduction tunnels and the mating probably occurs in the nest of female individuals or in the reproduction tunnels which are constructed by male individuals. The females give birth in the period from the beginning of February to the its end. The pups after birth could vary between 1 and 4. At the first birth of the females gave frequently 2 and sometimes 1 pups. At the cases when the number of pups is 1, we observed that there is another embryo and this is immature. If mother is old, then it may give pups up to 4. We see that the number of pups do not depend on cytotype while it is related with the mother age. On the other hand, the climatic differences at the area do not seem to effect the number of pups. In mid april, the pups learn first underground experiences with their mothers. In the end of november, young blind mole rats have all skills for living by themselves in their isolated nests from the mother nests and other pups.

Ecology and patterns of pathogenic *Leptospira* shedding of *Rattus norvegicus* from a Brazilian urban slum community

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Leptospirosis is a zoonosis that causes large seasonal epidemics in slum settlements worldwide. We conducted prospective investigations of leptospirosis in a slum community in the city of Salvador, Brazil to characterize the dynamics of *Leptospira* in *Rattus norvegicus*. Initial studies have focused on defining if seasonal variation in the rat population and shedding of leptospires by rats are associated to the increased risk of leptospirosis infection in slum residents. During three years (2013–2015), we completed systematic trapping and track plates campaigns in three valleys within the study site during the wet and dry seasons. We also apply spatial genetic analyses to rats collected across Salvador and genotyped at 16 microsatellite loci. We captured more than 1000 rats and found that rat abundance varied between valleys. Although the proportion of adult rats was higher during the wet season (we did not identify seasonal differences in abundance, and other rat demographic parameters. The prevalence of *Leptospira* infection was significantly higher among adults and young rats when compared to juveniles (but was similar between rats trapped during the wet and dry seasons and in different valleys. The overall mean leptospire pathogen load in urine from positive rats was $3.1 \times 10^6/\text{ml}$ and varied between valleys and seasons. The genetic data clearly suggest that valleys can be considered separate units and identified high traffic roads as barriers to rat movement. Our results indicates that rat population structure, abundance, and ultimately the amount of leptospires shedding, varies significantly within the slum microenvironment and may influence the spatial and temporal risk for human infection.

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

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

How cold-tolerant species coped after the last glaciation: the case study of the *Microtus oeconomus* subspecies in Europe

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During the last glacial maximum, the cold-tolerant species *Microtus oeconomus* (Pallas, 1776) occupied continuous area across central Europe, in contrast to most other temperate species that remained isolated in the Mediterranean refugia. During postglacial expansion *M. oeconomus* spread from central Europe northward, leaving behind isolated populations in the middle Europe (Pannonian area) and the Netherlands. Today the subspecies *M. oeconomus mehelyi* (Éhik, 1928) inhabits Hungary, Slovakia and Austria while the subspecies *M. oeconomus arenicola* (Selys-Longchamps, 1841) occurs in the Netherlands. In this study we were looking for signs of possible deterioration of genetic variability in populations of the two subspecies living in isolation since the last glaciation. More precisely, we aimed at assessing genetic variability in the two subspecies of *M.oeconomus* and comparing it with the variability of the population of *M. oeconomus stimmungi* (Nehring, 1899) inhabiting north-eastern Poland thus located in the continuous range of the species. To achieve this we genotyped 14 microsatellite loci of 192 individuals sampled in Austria, Hungary, Slovakia, the Netherlands and Poland. Initially detected putative null alleles in the loci were found to be false positive according to null alleles verification procedure results with use of NullAlleleGenerator. Our analysis did not reveal any decrease in the genetic variability at any study site or within the isolated subspecies. We did not detect any signs of the genetic bottleneck but we found well pronounced genetic structure reflecting the past and present environmental changes, as well as high values of the effective number (N_e) of individuals. Evidently, the originally cold-tolerant species has adapted to the local conditions, very different from the original ones. Our findings are important in the evolutionary and conservation context and require further studies. Acknowledgments: Research supported by LIFE 08 NAT/SK/000239.

Matrix population modelling of the common hamster life history

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Population numbers of the common hamster (*Cricetus cricetus*) have declined dramatically over last decades not only in western but also in eastern European countries. Several hypotheses have been suggested to explain this population decline. Some of them focused on reproductive parameters, namely the number of litters produced over the breeding season, others focused on higher mortality rates due to more numerous predators and farming practices. Matrix population models have increasingly been used to analyse life history strategies in many organisms, including rodents. More importantly, these models can conveniently be used to explore feasibility of the proposed hypotheses. The key step in the analysis of age-structured populations is the construction of a projection matrix. This process entails reviewing empirical data from field populations and literature sources to parameterize survival probabilities and reproductive contributions for all structural elements of the matrix. Here I will describe the methods of deriving matrix models for the common hamster, paying attention either to low reproduction or high mortality hypotheses. The results of modelling will be discussed with respect to the local studied field population in the periphery of Olomouc.

Rodents and parasites: what can they tell us about wildfires?

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Responses of the host/parasite system provide accurate information about the recovery of a disturbed ecosystem. Particularly, the close relationship between rodents and their helminth parasites can offer information not only about the host population ecology, but also about the environmental status. Herein the binomial *Apodemus sylvaticus*/helminth is proposed as a biological tag of post-fire regeneration, determining the epidemiological changes of this system in a burned Mediterranean ecosystem throughout the regeneration process. Data were collected for 21 years (from the 2nd to the 22nd post-fire year) in the Serra Calderona Natural Park (Valencian Community, Spain), a Mediterranean ecosystem which suffered a devastating wildfire in 1992. A total of 1,078 wood mouse individuals was helminthologically analysed: 798 from the burned area and 280 from a non-burned control area. Eighteen helminth species were detected (1 Trematoda, 8 Cestoda, 9 Nematoda), which were morphologically and ecologically analysed. Besides, the influence of intrinsic and extrinsic factors on the prevalence, abundance and biodiversity were considered. After 22 years, the global prevalence and the mean abundance were significantly higher in the burned area, and the biodiversity and the species richness were also greater. Helminths transmitted by a free-environmental stage were dominant. Host age was the most influential intrinsic factor in both areas. Generally, extrinsic factors had a greater influence on the disturbed area, suggesting a greater susceptibility of the ecosystem to external changes. However, along time, this influence decreased, finding an increasing similarity in the dynamics of the system *A. sylvaticus*/helminth community in both areas. These results allow the definition of several biological tags based on the epidemiological changes of the helminth community of the wood mouse that can be extrapolated to other Mediterranean ecosystems.

Wood mouse populations as biological tags of environmental disturbances – A twenty two-year study in a burned Mediterranean ecosystem

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Monitoring rodent populations can be used as an efficient way of studying the environmental changes, including human and natural disturbances. The present study shows the results of a long-term project in a disturbed Mediterranean ecosystem which suffered a devastating wildfire in 1992. The aim was to investigate the population dynamics of the small mammals present in the ecosystem related to the post-fire regeneration process, focusing on the behavior of the wood mouse, *Apodemus sylvaticus*. The study area is located in the Serra Calderona Natural Park (Valencian Community, Spain) where periodical surveys were carried out seasonally from the 2nd post-fire year. Within 22 years, a total of 2800 mice have been captured, 2132 from the burned area and 668 from a control non-burned area. Dynamics of the wood mouse have been studied calculating the number of individuals captured per 100 trap-nights at each site, year and season. The χ^2 test was applied to study the differences along the post-fire regeneration process, and linear regressions were used to estimate the influence of intrinsic and extrinsic factors on the population. From a global point of view, the population was higher in the perturbed ecosystem, with statistically significant differences in 13 years of the 22-year study period. However, both areas presented a similar tendency in the annual dynamics of the wood mouse trapping success, and the differences between them are lower along time, even finding a higher presence of the rodent in the control area in the 21th post-fire year. Thus, the similar evolution of the wood mouse population from both sites in the final years suggests a positive progress in the regeneration process of Serra Calderona Natural Park. The behavior of this rodent can be correlated to vegetal succession after the wildfire, among other factors. The wood mouse must therefore be considered a useful biomarker for the environmental changes in a burned Mediterranean area.

A phylogenomic appraisal of the sigmodontine radiation (Cricetidae)

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Cricetid rodents of the subfamily Sigmodontinae constitute one of the largest radiations of New World mammals; currently more than 400 living species, allocated in ca. 88 genera, are recognized. Historically, sigmodontine genera have been united into groups that have been formalized at the rank of tribe. With few exceptions, recent phylogenetic analyses have stabilized the number and contents of the distinct tribes. However, most relationships among tribes remain unresolved or poorly supported. Here, we present results of an analysis, based on 11070 orthologous genes analysed with distinct methods, aimed to assess sigmodontine intertribal relationships. In addition, we also assessed relationships among the five subfamilies of Cricetidae. Financial support: FONDECYT 1141055 and 3150604.

The diet of Savi's pine vole: a new quantitative approach

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Savi's pine vole (*Microtus savii*) is a fossorial rodent distributed in open areas and croplands of the Italian peninsula. Their diet is strictly herbivorous and in some contexts this species can be considered as a pest of arable crops and orchards. The aim of this study was to analyze the diet of Savi's pine vole throughout the year in a peach orchard of northern Italy. From November 2014 to September 2015 we analyzed stomach contents of 98 voles. Food availability was evaluated by sampling vegetation in 40 (2 × 2 m) plots in order to determine species composition and richness. A total of 36 Taqman assays were designed on plant-specific polymorphisms of the RuBisCO gene. Real-Time PCR products were approximately 100 bp long. Standard curve experiments were then conducted to assess presence and quantity of each species from the content of each stomach. Results showed a high variability in food ingested and high adaptability of the species during each season. The methodology presented here provides new opportunity for the analysis of the diet of small mammals species where food ingested is a mixture of degraded fragments.

Spatio-temporal patterns in the population dynamics of the field vole (*Microtus agrestis*) in Sweden

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In the last decades, long-term declines in the population size of voles have been reported from several European regions. Our knowledge on detailed spatio-temporal patterns of these changes is however limited. Here, we analyzed the population dynamics of the field vole (*Microtus agrestis*) in six different climatic regions in Sweden and covering time series ranging from 15–44 years. The two regions with the longest time series (1971–present and 1973–present, respectively) in the lowland areas of south-central and northern Sweden, respectively, were characterized by similar high-amplitude cycles until the late 1980s. From the early 1990s, *M. agrestis* showed low-amplitude cycles, with indications of recovery to high-amplitude again during the last two cycles. The low-amplitude periods in these two regions were also characterized by more seasonal dynamics, caused by an increased frequency of winter declines. Except for a period with similar seasonal dynamics in the late 1990s, the population dynamics of *M. agrestis* in the mountain areas showed distinct high-amplitude cycles with a lower frequency of “disturbing” winter declines from the early 2000s. We discuss these results in relation to changes in landscape structure and weather conditions.

Lethal and non-lethal effects of predation on arctic lemmings

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Predation has often been identified as the most susceptible factor to cause cyclic fluctuations in small herbivore populations due to its delayed density-dependence character. Recently, studies have shown in cyclic hares that predation can also have non-lethal effects on prey by inducing high stress levels, which can have negative effects on reproduction. The objective of our study was to identify the lethal and non-lethal effects of predation on brown lemmings on Bylot Island, Nunavut, Canada. This population fluctuates regularly according to 3–4 yr cycles. In order to reduce predation experimentally, we built an 8 ha fence (or enclosure) covered by an anti-avian predator net in which lemmings were trapped. A control trapping grid was located nearby. Both trapping grids were active since 2008, which allowed us to compare the demography (survival, reproduction, prop. of juveniles) of lemmings before and after the construction of the enclosure. In 2014–2015, fecal samples were collected in both grids to measure stress levels quantified with the glucocorticoid metabolites. Our results are striking: densities, survival, and proportion of juveniles were higher in the enclosure, whereas stress was lower inside the predator enclosure. However, fecundity was not affected by predation reduction, which suggests that despite elevated stress levels, lemmings succeed in maintaining high reproduction. Thus, direct effects of predation appear to be sufficient to regulate lemmings in the High Arctic.

Lassa virus infection in *Mastomys natalensis* populations: abundance, prevalence and force of infection

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Lassa fever is a viral haemorrhagic fever, affecting 200–300,000 persons with 5,000–10,000 fatalities per year in West Africa. Lassa virus has a rodent reservoir *Mastomys natalensis*, and is transmitted to humans through direct contact, their body fluids or droppings. According to a mathematical model (Davis et al. 2005), the correlation between the reservoir abundance and viral prevalence in the reservoir can show 4 scenarios: (1) positive linear, (2) positive logarithmic with a threshold, (3) negative or (4) null. Consequently, the correlation between reservoir abundance and force of infection to humans can be: (1) positive exponential, (2) positive linear with a threshold, (3) null or (4) positive linear. We therefore intended to investigate these 2 outcome variables: rodent abundance, and Lassa prevalence in the rodent population by conducting an experimental study in a high endemic zone in Upper Guinea. In 2013, 2014 and 2015 the rodent populations were sampled in 4–10 villages, all located in remote dry forest savannah. In 3 villages only, the rodent populations were reduced by performing a rodent control and level of abundance was checked before and after control. During 3 days, 120 traps were set inside the houses along a transect through the village, dispatching 2 traps per room. Necropsies were done each day in situ following the BSL3 procedure. In total, 779 rodents were collected of which 728 were *M. natalensis*. Their abundance, measured by the mean trapping success varied from 1.7% to 16.4%. Lassa prevalence, measured by a double molecular testing (PCR) varied from 0.0% to 33.3%. First analysis showed no relationship between rodent abundance and Lassa prevalence (scenario 4). Nevertheless, the relationship between rodent abundance and force of infection was positively correlated, according to the mathematical model. The Lassa incidence in humans could therefore be amplified when rodent populations remain abundant.

Exploratory axes in personality of black rats: repeatability and mutual correspondence in open-field and hole-board tests

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Personality, or behavioural differences among individuals, which are stable both in time and across contexts, is a highly popular topic. Currently there has been an increase of interest in the relationship between personality and repeatability, which is a methodical approach developed to measure the stability of interindividual differences in time. The aim of this study is to evaluate the personality of wild black rats (*Rattus rattus*) according to behavioural patterns exhibited under widely used testing procedures in new environment (open field test, hole board test) and to compare, how behavioural traits in these tests mutually correlate and change over time. Each test trial was repeated eight times with different intervals (24 hours, 6 days, 4 weeks). The results suggest that most of the recorded behavioural variability can be explained with three principal axes. The first one is associated with loco-exploratory activity of the subject. The elements of behaviour associated with this axis are the most repeatable and best correlated with markers of stress, such as defecation. The second axis is mostly associated with the amount of time the animal spent in the central part of the arena and the third axis represents the interest in the holes in the hole board test. These two axes are less repeatable. A significant effect of the identity of the animal was found in all behavioural traits associated with these axes. This effect was repeatedly found in all behavioural traits, associated with all the axes of variability mentioned above. The behavioural traits correlate across the tests as well, which means they are stable in different contexts. We found no behavioural differences between males and females, which is in contrast with some other studies.

Effects of forest management on density and survival in terrestrial small mammals

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Several studies have shown that small mammal communities are influenced by silvicultural activities possibly because these affect the quality of wildlife habitats. Previous research mainly focused on community parameters and abundance of target species, however the most robust approach to study the impacts of forestry is to follow a demographic-response approach. Investigating multiple demographic measurements is essential to understand how populations respond to forest management, nevertheless studies focusing on multiple demographic parameters are lacking. Our analyses targeted individual survival and population density, aiming to understand the demographic mechanisms by which forest management exerts its effects on small mammals. We focused on the populations of *Apodemus flavicollis*, *A. sylvaticus* and *Myodes glareolus*, constituting the guild of forest- and ground-dwelling rodents in central Italy. Populations were monitored for three years in a continuous forest subject to different management practices. We identified four forest management types (three coppice stands logged in different years and a conifer plantation) where we selected 12 sampling areas. We sampled a total of 31752 trap-nights capturing more than 1350 individuals. We also gathered quantitative data on the amount of trophic and cover resources in each area to interpret the response of populations to silvicultural activities. For all the three species, forest management had strong effects on the population density, which were, in some cases, matched by similar effects on individual survival. We found that different types of forest management, such as the recently coppiced stands, did not create high-density sinks but, rather, enhanced the carrying capacity of the habitats by increasing the availability of cover and food resources. Our analyses encompassing multiple population parameters allowed us to highlight the mechanisms by which forest management affects small mammal populations.

New data on Armenian birch mouse

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The unique population of poorly known Armenian birch mouse (*Sicista armenica*) was studied more than 20 years ago. The listing of this species in the Red Data Book of Armenia provides *S. armenica* with nominal protection as a threatened species. The description of this species was done by Russian scientists. They found three specimens on Pambak Ridge in the vicinity of village of Ankavan, in the upper side of river Marmarik, right tributary Razdan river of Armenia. Armenian birch mouse belongs to a group of morphologically similar species of monochrome Caucasus birch mice, so a number of respects it is indistinguishable from other species of this group of closely related species. Studies on distribution of Armenian birch mouse was started in 2012. Pregnant female were captured by live traps on 2015. Morphological measures were done, the biotope of species were characterized. DNA analyses of Armenian birch mouse were done. Final identification of species were done by DNA analysis. Further researches on population status will be done.

Parasitism in the European house mouse hybrid zone

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Hybrid zone studies of host-parasite systems have largely taken a host-centric viewpoint: does parasitism affect the outcome of host hybridization by differentially impacting the fitness of host taxa vs their hybrid descendants? This viewpoint neglects the possibility that host taxa have distinctive genetic clusters of parasites that may themselves potentially hybridize. Hybridization, bringing together combinations of genes previously untested by natural selection, may affect parasites in similar ways to free-living organisms: revealing a barrier to gene flow, promoting divergence via reinforcement, homogenizing genetic clusters or leading to rapid adaptive diversification via the formation of hybrid parasite species. We use the European house mouse hybrid zone (HMHZ) between *Mus m. musculus* and *M. m. domesticus* and their parasites to explore these issues. First, from a host-centric viewpoint, we tested whether hybrids have greater or lesser helminth load than additive expectations. Sampling 689 mice from 107 localities across the Bavaria–Bohemia region of the HMHZ we found hybrids have significantly reduced worm load, but similar age structure, contradicting the idea that helminths reduce host hybrid fitness through increased load. Second, from a parasite-centric viewpoint, we analyzed the genetic structure of several parasites: the murine cytomegalovirus (MCMV), the fungus *Pneumocystis murina* and 2 nematodes (*Trichuris muris* and *Syphacia obvelata*). We found distinct genetic clusters meeting and forming hybrid parasites at the host HZ centre for 3 out of 4 parasite species. The parasite's host specificity may explain this pattern: while MCMV, *P. murina* and *S. obvelata* are highly specific to their hosts and form host-specific genetic clusters, *T. muris* can be found on sympatric murine species and does not form clusters specific to any of these hosts. In conclusion, this model system offers strong opportunities to dissect the processes of host-parasite adaptation.

Reproductive success and fitness of male common voles (*Microtus arvalis*)

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Pup survival and growth were monitored to determine whether paternal care potentially contributes to reproductive success of male common voles. The subjects were 143 pups from 24 litters obtained from adult voles trapped in the wild. One group of litters (I, $n = 12$, 72 pups) was raised by adult females without sires, and another group of litters (II, $n = 12$, 71 pups) was raised by both parents. Litter size was recorded at parturition and again when young were 12, 21 and 30 days old. Pups in each litter were weighed at parturition and also again when young were 12, 21 and 30 days old. The study has shown that all the pups have been successfully survived in the group I, whereas in two litters of the group II, some pups have been died during the first 10 days of their life. Hence, the presence of the sire may negatively affect pup survival in litters of the common vole. As for the body mass, there was no difference between the groups at parturition and when the pups were 12 days old. Next weighing revealed that body mass of the pups from the group I was significantly higher (in average, 15.3 ± 0.1 g) than that of the pups from the group II (in average, 14.7 ± 0.2 g): one-way ANOVA, $F = 6.80$, $df = 1/132$, $p = 0.010$. The last weighing (when the young voles were 30 days old) revealed a much more prominent difference in their body mass: for group I, it was averaged 19.3 ± 0.3 g; for group II, it was averaged 18.2 ± 0.2 g ($F = 8.18$, $df = 1/132$, $p = 0.005$). Thus, growth rate was found to decrease in the presence of the sires. This finding indicates a decrease of fitness of male common voles living in family groups. The study is supported by the Russian Foundation for Basic Research (grant 15-04-00819).

Seasonality and the wild cavy: effects on physiology, reproduction and behaviour of a highly precocial rodent

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Pronounced seasonal variation in day length, temperature and resource availability influences animals living in temperate regions. To survive and reproduce successfully, animals usually adjust their timing of breeding to the most adequate season. The wild cavy (*Cavia aperea*) is a South American rodent that occurs in temperate regions but reproduces year-round. We have investigated reproduction, physiology, life history characteristics and behaviour across seasons in outdoor enclosures and in the laboratory. We find unusual adjustments to seasonal variation. Cavies adjust the litter size, pup birth weight and growth rate as well as maternal investment during lactation to season. Litters born in summer are nearly three times larger than litters born in winter, but winter born pups are much heavier. Furthermore, the offspring differs in timing of maturation, innate immune function and resting metabolic rates, indicating differences in life history. Several behavioural traits such as boldness towards unknown objects, open field behaviour and exploration develop differently depending on the season in which pups are born. These findings suggest that in cavies strong maternal effects operate. In addition, lifelong plasticity in physiology and behaviour allows individuals a highly differentiated adjustment to seasonal variation.

Genetic-based modelling of population history and spread of the European ground squirrel (*Spermophilus citellus*)

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Glacial cycles during the Pleistocene have been one of the major drivers of contemporary patterns in natural diversity and species ranges in Europe. Individual species repeatedly expanded and shrank their distribution ranges according to their preferred habitats. The European ground squirrel (*Spermophilus citellus*), as a typical inhabitant of steppe habitat with the core distribution in the southeastern Europe, represent a suitable model to study the evolutionary changes of species requiring continental climate. Here we review the current knowledge of evolutionary history of *S. citellus* and model its past population changes, especially spreading in Central Europe after the Last Glacial Maximum (LGM). The current *S. citellus* populations in the Czech Republic form a genetically distinct homogeneous cluster whose history during the Holocene remains unclear: either they survived LGM and humid periods at the beginning of Holocene in a refugium in Central Europe or immigrated later from the long-term refugium in Pannonia following the Neolithic human-mediated deforestation. To clarify this we use the Approximate Bayesian Computation approach (ABC) which allows estimation of the most likely evolutionary scenarios based on comparison of the real dataset with many simulated ones. The modelling based on nuclear microsatellite data from populations throughout the whole current range supports relatively recent recolonization of the Czech Republic from the southeast rather than surviving the early Holocene in potential central European microrefugia. The research was funded by GA AV ČR (KJB601410816).

Recovery of common vole populations (*Microtus arvalis*) after population collapse

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In European countries, the common vole (*Microtus arvalis*) is an important pest species in the agricultural landscape and can cause tremendous crop loss during outbreak years. Although there has been intensive research on the species, little is known about its recovery behavior after population collapse due to rodenticide application. Such information is relevant for spatial and temporal aspects of management and may be useful for optimizing management. We investigated whether population recovery works via immigration, survival of residential individuals and in situ reproduction or a combination thereof; additionally, we determined population recovery time and recovery rate. To obtain data under realistic management conditions, we conducted a replicated and controlled live trapping study from June 2014 to October 2015 in alfalfa in Central Germany. We applied zinc phosphide in July 2014 and March 2015 on parts of the alfalfa field according to the product label. In July, there was no effect of the treatment on population density. This may have been due to massive reproduction of surviving voles and voles outside the treated area easily offsetting mortality caused by the rodenticide treatment. After rodenticide application in March, before the start of the reproductive period, the population was reduced by 90%. However, population densities in treated alfalfa reached the density of populations in untreated control sites after 3 months. The response of common voles suggests that during outbreaks a single application of rodenticides is insufficient to limit population growth sustainably.

Ecology of Puumala hantavirus in Finland

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The infection risk of humans by Puumala hantavirus (PUUV) is highest in northern Europe, where populations of the rodent host (bank vole, *Myodes glareolus*) undergo cyclic fluctuations. During 1995–2015 about 35000 human cases of NE (nephropathia epidemica) have been diagnosed in Finland. We conducted a 7-year longitudinal capture-mark-recapture study, mostly at monthly intervals, to monitor seasonal and multiannual patterns of the PUUV infection rate in bank vole populations exhibiting a 3-year cycle in the highly endemic area in boreal taiga in Central Finland. Infected bank voles were most abundant in mid-winter months during years of increasing or peak host density. Seroprevalence of PUUV infection in bank voles exhibited a regular, seasonal pattern reflecting the annual population turnover and accumulation of infections within each cohort. In autumn, the PUUV transmission rate tracked increasing host abundance, suggesting a density-dependent transmission. However, prevalence of PUUV infection was similar during cyclic increase and peak years despite a twofold difference in maximum host density. This may result from the high proportion of young individuals carrying maternal antibodies in summer of the peak year delaying transmission during the cycle peak years. This increase/peak dilemma is reflected in the human NE incidence in the region: even though the bank vole density is clearly higher in the peak year, the number of NE cases can often be similar or even higher in the vole increase year. As a comparison we analysed the annual NE incidence in various parts of Finland, from coastal areas to inland and from south to north, reflecting declining proportion of agricultural land and forest fragmentation. There was a trend for one year NE peaks in coastal and southern regions while two year peaks occurred inland, possibly indicating more restricted dispersal of host and virus in the increase phase in former ones.

Serial colonisation and natural selection in a common rodent, the Eurasian field vole

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Serial waves of colonisation, involving the partial or complete replacement of lineages, may be one of the means by which current phylogeographic patterns have arisen. The process has previously been implicated in the colonisation of the British Isles by small mammals, including several species of rodent. The distribution of genetic variation in Eurasian field voles (*Microtus agrestis*) from the British Isles is examined here, using existing mitochondrial sequence data together with new data from the Y-chromosome and a panel of microsatellite loci to represent the autosomal nuclear genome. Both the mitochondrial and Y-chromosome sequence data show extremely skewed patterns of variation, which may be attributed to lineage replacement or selective sweeps on standing variation. The field vole therefore provides a useful model to examine the process of serial colonisation and the effect of natural selection on phylogeographic patterns.

Rodents in Central Europe along the Pleistocene/Holocene transition

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Dramatic environmental rearrangements during the last glacial and the post-glacial period present a key factor patterning rodent communities of Central Europe and distributional history of individual species. The extensive fossil record of the Vistulian/Holocene faunal history provided by ca 200 continuous sedimentary sequences from Czech Republic and Slovakia reveals a replacement of (i) the glacial elements with (ii) the interglacial elements, more or less gradual in most sites, with considerable interregional differences in timing of particular faunogenetic events and a peak of diversity in the Boreal stage. Yet, the high resolution record provided by a recently excavated 10-m thick sedimentary sequence in Býčí skála cave (Moravian karst), which covers the earliest stage of the Pleistocene/Holocene transition (12 to 8.5 ky) with 21 horizons and 4525 MNI of 52 mammalian spp., bring a new light on the topic. It convincingly demonstrate an abrupt expansion of all interglacial elements including the (iii) Holocene apochoric elements, not recorded in Central Europe during previous cycles, which were expected to invade Central Europe only due to the anthropogenic environmental changes associated with the post-Neolithic period. The core stage of faunal transition started with abrupt changes in community structure by the end of the Young Dryas (11.2 ky) and terminated by the 9.3–9.5 ky event associated with a drop of alpha diversity but significant increase of the beta-diversity. The respective period was associated with dramatic fluctuations in role of particular species and pronounced phenotype rearrangements including patterns of phenotype variation documented in details in the most common community elements (*C. gla.*, *A. flav.*, *M. arv.*, *M. agr.*, *M. oec.*, *M. greg.*, *A. ter.*). The trends characterizing the Holocene phenotype dynamics (such as enlarging complexity of M3 posteroconid complex in *C. glareolus*) were obviously established just during that stage.

Seismic signals in subterranean rodents: how is it in spalacids

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Seismic communication in blind mole rat (*Spalax ehrenbergi*) has been known for several decades, they use seismic signals as territorial signals. Blind mole-rats use headthumping for production of seismic waves. The same way of production is used also by Demon mole rat (*Tachyoryctes daemon*). Demon mole rat has even two types of seismic signals – fast and slow used as territorial respective courtship signals. We were interested in two more spalacid species Giant root-rat (*Tachyoryctes macrocephalus*) and Gansu zokor (*Eospalax cansu*). Giant root-rat belongs among fossorial rodents with largest body size and high aboveground activity, whereas Gansu zokor has middle body size and low aboveground activity. Despite these difference both species produce seismic signals and they use same behaviour – headthumping. The seismic waves in underground environment are transmitted better than sound waves and can be used also for communication between unconnected burrow systems, which makes them perfect territorial signals. All so far studied spalacid species use them in this way.

Synchrony of forest rodent abundance and relation to tree damage

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Several rodent species can cause significant damage to forest trees especially in stands of young broadleaf tree species such as oak (*Quercus*) and beech (*Fagus*). Field voles (*Microtus agrestis*) and bank voles (*Myodes glareolus*) inhabit afforestation stands and can damage trees. For assessing inter-specific synchrony and environmental drivers of rodent damage we analysed time-series of rodent abundance (standard snap-trapping in northern and eastern Germany) and time-series of rodent damage to trees (visual estimates in eastern Germany) covering up to 60 years in northern and 12 years in eastern Germany. Data were collected by State Forest Authorities for adjusting rodent management activities to damage risk. There was considerable large scale synchrony of population abundance of field voles and bank voles. Growth rates of both species were positively related to beech mast intensity. Beech mast in the previous year particularly affected bank vole dynamics and to a lower degree field vole dynamics. Rodent damage in forestry was associated with autumn abundances of rodents (adj. $R^2 = 0.53$) while beech mast as such and snow cover did not further contribute to variation in damage. Beech mast is a good indicator of long-term rodent abundance in German afforestation areas. However, rodent damage to forestry in Central Germany was not dependent on environmental parameters beyond rodent abundance at the large scale. Rodent abundance in autumn did explain about half of the variation in damage. Systems for forecasting rodent damage in forestry can be developed based on autumn abundance but further experimental work is required to identify additional drivers beyond beech mast and snow cover to improve quality of predictions.

Comparative hantavirus dynamics in two rodent reservoir species

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Hantaviruses circulating in rodent populations are a major issue in public health because human infections can be numerous and severe. It is therefore imperative to understand the effects of host density and population specific demographic factors to estimate the relative contribution of different functional groups to virus transmission within the host population. This might however vary between different host/hantavirus systems. Here we present results to highlight seasonal changes in density dependence and demographic drivers (age, sex, reproductive activity) of hantavirus transmission in the two most common rodent host/hantavirus systems (bank vole (*Myodes glareolus*)/Puumala virus; common vole (*Microtus arvalis*)/Tula virus) in Germany. Trapping was conducted between 2010 and 2013 in four federal states with 3 woodland (bank vole) and 3 grassland (common vole) replicates per state resulting in 3,246 individuals tested for hantavirus-specific antibodies. There was strong seasonality in the density dependence and the probability of carrying hantavirus-reactive antibodies for different functional groups of both species. For bank voles, demographics played a significant role during summer and autumn, while for common voles effects were restricted to autumn when populations on grassland reach their peak densities. A clear impact of hantavirus-specific maternal antibodies was found during peak reproduction in summer for bank vole populations. No such impact at any level could be demonstrated for the common vole system. In both systems older individuals and males were associated with higher seroprevalence. These results highlight underlying similarities and dissimilarities of hantavirus transmission in two different host/hantavirus systems, and the need to consider functional groups in future efforts to understand hantavirus transmission and predict human health threats

Long-term population pattern, habitat, and trappability of the southern bog lemming (*Synaptomys cooperi*) at high population levels in the apparent absence of the northern bog lemming (*S. borealis*)

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Inventory of rare species, the northern bog lemming (*Synaptomys borealis*) and heather vole (*Phenacomys ungava*), at the margins of their respective ranges in northern Minnesota, USA, yielded no *S. borealis* but many southern bog lemmings (*S. cooperi*). Three types of traps (pit, baited and unbaited Museum Special) yielded different patterns of capture. Although more *S. cooperi* were secured on bogs and at more bog sites (23 of 25), many were captured at 21 of 25 upland dry sites dominated by heather [*Vaccinium* sp(p).]. Long-term research at other sites (e.g., 18 to 21 annually over 1984–2015) indicated that the 2001 inventories were undertaken coincidentally in a year of relatively high population numbers of *S. cooperi*. The results are discussed in the contexts of inventory strategies and the significance of cycles of arvicoline rodents.

Changes of rodent community and habitat structure with time elapse after thinning in Japanese larch (*Larix kaempferi*) plantations

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This study was conducted to investigate the change of rodent community and habitat structure after thinning, with retrospective approach. Among the Japanese larch (*Larix kaempferi*) plantations, unthinned control and three treatment stands were selected (1S: 1 year after thinning stand, 3S: 3 years after thinning stand, 7S: 7 years after thinning stand). Forest structure was different between each stands. Coverage of tree and shrub layer, tree crown ratio, number of shrub stems, and number of CWD (coarse woody debris) were significantly different among stands. We trapped four species and 468 individuals of small rodents: *Apodemus agrarius* (Aa), *Apodemus peninsulae* (Ap), *Myodes regulus* (Mr), and *Tamias sibiricus* (Ts). Total number of individuals were significantly higher in thinned stands than unthinned. Also, there was significant difference in rodent community between each stands. Canonical correlation analysis (CCA) revealed the relationship between habitat variables and rodent species. Aa showed the lowest relationship with most of variables, slightly associated with rock coverage and herbaceous plants, Ap and Mr showed positive relationships with volume of CWD and tree canopy coverage. Ts was highly related to number of shrub stems, and increased coverage of shrub layer and leaf litter depth. The vegetative change after thinning may affect rodent community, by altering habitat structure. Based on these results, thinning can act as a positive habitat management to the small terrestrial rodent species at Japanese larch plantations in Korea.

Where does size matter? Common and different aspects in the life of adult neural stem cells in the mouse and the rat brain

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Cytogenesis from postnatal brain Neural Stem Cells (pbNSCs) persists in mammals. However, as the brain became larger and more complicated during evolution the number and activity of pbNSCs became more limited. Here, we will present data from the comparative investigation of the biology of pbNSCs and of their niche in mice and rats. In the 5-times larger rat brain we found that the volume of the stem cell rich area of the Subependymal Zone (SEZ) of the lateral walls of the lateral ventricles was also 5-times bigger. Surprisingly, the number of pbNSCs was only 3-times higher, being directly correlated with the similar 3-fold expansion of the surface of the ventricular wall and of the number of ependymal cells that line it. Notably, the localization of pbNSCs was similar in the two species, next to the ependyma, whilst their daughter cells were more widely distributed within the larger rat niche. Rat pbNSCs were also found to be more oligodendrogenic than the mice ones and the morphology of ependymal cells showed adaptations to the larger SEZ volume in rats. These data, along with other observations regarding the differential ability of mice and rat pbNSCs to synthesize extracellular matrix components and to respond to growth factors, as well as with the description of the features of the primate SEZ lead to new hypotheses in the evolutionary adaptations of pbNSCs and of their niches in mammals.

A diverse ecosystem promotes human health: the dilution effect and Hantavirus infection

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The “dilution effect” implies that where species vary in susceptibility to infection by a pathogen, higher diversity often leads to lower infection prevalence in disease hosts. For directly transmitted pathogens, non-host species may “dilute” infection directly (1) and indirectly (2). Competitors and predators may (1) alter host behavior to reduce pathogen transmission or (2) reduce the density of hosts. We tested the dilution of the zoonotic *Puumala* hantavirus (PUUV) infection in bank voles (*Myodes glareolus*) by two competitors and a predator through species-specific hypotheses. Our study was based on long-term PUUV infection data (2003–2013) in northern Sweden. The field vole (*Microtus agrestis*) and the common shrew (*Sorex araneus*) are bank vole competitors and Tengmalm’s owl (*Aegolius funereus*) is a main predator of bank voles. Infection probability in bank voles decreased when common shrew densities increased, suggesting that common shrews reduced PUUV transmission. Field voles suppressed bank vole density in meadows and clear-cuts and indirectly diluted PUUV infection. Further, Tengmalm’s owl decline in 1980–2013 may have contributed to higher PUUV infection rates in bank voles in 2003–2013 compared to 1979–1985. Our study provides further evidence for dilution effect and suggests that owls may have an important role in reducing disease risk.

Plague foci in Mongolia

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In human history, no other disease claimed more victims than plague. The causative agent of plague, *Yersinia pestis*, caused approximately 200 million of deaths during the three major pandemics in the 6th, 14th, and 19th century. According to the WHO, 1000 to 5000 human cases and 100 to 200 resulting fatalities were detected annually in the last two decades. The estimated number of unreported cases is considered much higher. Being a multi-host multi-vector zoonosis involving more than 233 mammal species and 263 flea species as well as other haemaphageous arthropods like ticks and lice, the plague transmission cycles show a high complexity. Phylogenetic analysis suggests Central Asia, and ecological studies indicate more specifically Transbaikalian and Mongolian steppes as the place of origin for *Y. pestis*. Mongolia offers a broad spectrum of ecotopes resulting in diverse composed plague foci with different hosts, vectors and *Y. pestis* biovars. Current studies show a change of hosts and vektors in the known plague foci due to anthropogenous factors like hunting and climate change. Thus monitoring of these changes is crucial in order to be able to evaluate the risk potential of the corresponding vectors as well as the plague foci in general.

Montane mammals at risk of loss: squirrels as indicators of global change

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Models of global climate change predict temperature profiles that will increase 2–5 °C by the end of the 21st century. Such changes will undoubtedly result in considerable modification to ecosystems and result in challenges for conservation and management of biodiversity. I assessed patterns of elevational distribution of mammals within the Madrean Archipelago of the SW USA. I estimated that 15 to 20% of mammal diversity is at risk of loss by 2100 based solely on predicted patterns of upslope migration of biotic communities driven primarily by climate change. Squirrels demonstrate great promise as harbingers of change and provide excellent model systems for mechanistic and landscape level studies of global climate change. North American red squirrels store cones within larderhoards known as middens. Middens are believed to keep cones cool and moist thus deterring cone opening and promoting retention of protected seeds. In addition, middens may serve as hotspots of diversity and abundance in forests for mammals and birds. Changes in forest structure and microclimate induced by natural or anthropogenic agents may have profound impacts on midden occupancy and red squirrel populations. Habitat structure was assessed at occupied and unoccupied middens as well as at random sites, while also monitoring microclimate. Cone opening is indeed influenced by temperature and humidity and these factors vary between middens and random sites. Furthermore, this research relates midden microclimates to forest structure suggesting that changes in forest structure due to natural and anthropogenic disturbance can impact the suitability of sites for cone storage. Finally, I discuss the potential impacts of climate change on squirrel cache sites and promote the use of seed storage sites as important global models for climate change.

SNP versus mtDNA: genomic phylogeography of the bank vole in Europe

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The golden age of mitochondrial DNA (mtDNA) in phylogeography has clearly passed, but data derived from this marker have made an enormous contribution to our understanding of the process of post-glacial colonization and other aspects of population history in many species. However, it often remains unclear how well mtDNA findings represent genome-wide patterns. Despite the recent advent of population genomics, it's still uncommon to have high coverage genomic studies relating to phylogeography of non-model organisms. We have been able to apply the genotyping-by-sequencing (GBS) approach to discover and genotype 10,000+ SNP loci for 150+ bank voles (*Clethrionomys glareolus*) from all over Europe with the aim to determine how well the genome-wide population structure matches with mtDNA phylogeography. The knowledge of the detailed genomic phylogeography is essential to the study of adaptive differences between bank vole populations and their role in post-glacial colonization.

How do parasites select their host species? Trait-based and phylogenetic associations between fleas and their small mammalian hosts in the Palearctic

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To understand the assembly rules of (a) species composition of parasite assemblages exploiting a given host species and (b) species composition of a host spectrum of a given parasite species, we investigated the associations between ecological (density, shelter structure), morphological (body mass, hair morphology) and physiological traits (basal metabolic rate) of small mammals and ecological (seasonality of reproduction, microhabitat preferences, abundance, host specificity) and morphological (presence and number of combs) traits of their flea parasites that shape host selection processes by fleas. We adapted the extended version of the three-table ordination and linked species composition of flea assemblages of host species with traits and phylogenies of both hosts and fleas. Fleas with similar trait values, independent of phylogenetic affinities, were clustered on the same host species. Fleas possessing certain traits selected hosts possessing certain traits. Fleas belonging to the same phylogenetic lineage were found on the same host more often than expected by chance. Certain phylogenetic lineages of hosts harbored certain phylogenetic lineages of fleas. The process of host selection by fleas appeared to be determined by reciprocal relationships between host and flea traits, as well as between host and flea phylogenies. We conclude that the connection between host and flea phylogenies, coupled with the connection between host and flea traits, suggests that the species compositions of the host spectra of fleas were driven by the interaction between historical processes and traits.

Multilocus phylogeny of grey-bellied pygmy mouse (*Mus triton*) complex

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The grey-bellied pygmy mouse (*Mus triton*) of the African endemic subgenus *Nanomys* is widespread rodent species inhabiting mountain areas of eastern and central Africa. Although *Mus triton* has been long considered as a single species, validity of the single species status was questioned. In order to evaluate current taxonomy of this species, we analysed sequences of one mitochondrial and six nuclear genes from the mayor part of its known distribution range. Three well-supported phylogroups at species level, differentiated during the Plio-Pleistocene, were evidenced. The basal lineage (*Mus triton*), is distributed in the Kenyan highlands and northern part of Albertine rift. The second distinct genetic lineage within the triton group (*Mus* sp. “Kikwit”) was detected in two localities in south-western Democratic Republic of Congo. The last lineage (*Mus* cf. *callewaerti*) occurs over a huge range from northern Tanzania to southern Malawi with presence also in Angola. According to our results we propose scenario where Plio-Pleistocene climatic oscillations together with highly diverse topography of eastern Africa shaped the diversification of *Mus triton* species complex.

Seasonality in the physiology and reproduction of the common hamster from urban population

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During the recent 45 years the numbers of the common hamster (*Cricetus cricetus*) have dramatically decreased in the wild. Along with that, the common hamster has been actively populating urban areas. The cause of this phenomenon is unclear but it could result in the physiological and behavioral changes revealed in present study. The animals were captured ($n = 16$) and brought to the lab from the city of Simferopol and maintained under a natural photoperiod and temperature regime. The body mass, biochemical parameters, leucogram, body temperature, hormone levels were monitored monthly during the year. Concurrently, some of these parameters were measured in the wild. The dynamics of sex hormones indicates that the breeding season in the city starts in February. In fact, the level of sex hormones increased in February to decline to Sep–Oct. The body mass did not change significantly in adult animals during the year. The period of hypothermia (if ever occurred) did not exceed 2.5 months and the bout was never longer than 5 days either in lab or in the wild. The white blood cell counts declined during the autumn–winter season, but it rose in January to remain stable during in the rest of the year, which distinguishes the urban hamster from truly hibernating species. The seasonal dynamics of some investigated indices differs from that of the true hibernators. The glucose level in the blood was the lowest during autumn–winter. The seasonal changes in total protein and albumin levels were similar: the concentrations of these substances remained constant during the autumn and winter to subsequently rise in spring. These features could be associated with the low depth and duration of torpor bouts of the animals concerned. The results suggest that the urban population of the Common hamster differs greatly from the non-urban in terms of hypothermia, reproduction, the seasonal changes in the blood biochemical indices and leucogram. Supported by a RFFI grant № 16-34-01071 mol_a.

Ochotona curzoniae physiological adaptation to *Oxytropis ochrocephala* toxin

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Ochotona curzoniae is a unique small mammalian herbivore inhabiting the alpine meadow ecosystem in the Qinghai–Tibet plateau. Genus *Oxytropis* is plant species on the Qinghai–Tibet alpine meadow ecosystem with long growth season from early spring to late autumn. The species has 10%–20% protein content, and is one of major summer food sources and main haypile items for *O. curzoniae*. However, oxytropis contain the indolizidine alkaloid swainsonine (SW) that is toxic and even lethal to most livestock as an inhibitor of lysosomal α -mannosidase and Golgi mannosidase. *O. curzoniae* growing under extreme climatic conditions with hypothermia and hypoxemia, not only cope with the severe environment to maintain nutrient intake required to keeping their growth and reproduction, but also overcome against plant chemical defense. Therefore, in the long process of natural selection, *O. curzoniae* has developed a wide range of behavioral and physiological mechanisms to mitigate the negative effects of PSMs, and formed herbivore-plant co-evolution. This study from the view of physiology, nutrition, and foraging ecology, by feeding *O. ochrocephala* and SW crude extract, aim to explore *O. curzoniae* digestive strategies on *O. ochrocephala*, and analyze *O. curzoniae* physiological response on hepatic cytochrome P450 exposed to SW toxic. According to *O. curzoniae* foraging oxytropis in the wild, we propose and test the following two hypotheses: (1) based on optimal foraging theory, then maximizing nutrient and energy absorbed with compensation for the energy loss from detoxification, *O. curzoniae* may increase the intake and improve digestibility; and (2) when exposing *O. curzoniae* in *O. ochrocephala* with the range of ecological concentration, *O. curzoniae* has a certain degree of tolerance to oxytropis SW, and its liver cytochrome P450 content may have compensatory adjustments responsible for with the increase of diet SW does and exposed time. (1) The result of which the effect of *O. ochrocephala* on *O. curzoniae* digestibility showed plateau pikas improved food intake, absorption and digestibility of neutral detergent fiber when exposed *O. ochrocephala*. This result supports our hypothesis about the oxytropis promoting plateau pikas digestibility. (2) Swainsonine ingestion by *O. curzoniae* resulted in the liver CYP450 level to decrease initially, but the inhibitory effect of the toxin on CYP450 level was overcome over time and the CYP450 level even increased. These results may suggest that *O. curzoniae* is capable of adjusting its production of CYP450 enzymes when the enzymes are needed for SW detoxification.

Soil preference in the speciating blind mole rats *Spalax galili*: do they prefer the fertile or the familiar?

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Sympatric speciation is a highly controversial topic in the current evolutionary biology. Subterranean blind mole rats (Spalacidae) are suitable model organisms to study speciation in action. In Israel, the superspecies *Spalax ehrenbergi* is an actively speciating taxon with four chromosomal species. So far, speciation in this complex has been assumed to be allopatric/peripatric. Surprisingly, at a microsite sharply subdivided ecologically, ongoing sympatric speciation in one of the four species, *S. galili*, has recently been proposed on the basis of the whole-genome population divergence. There, mole rats inhabit abutting rendzina and basaltic soils that differ dramatically in chemical, physical and vegetational characteristics. Our aim was to test digging preferences of mole rats from both soils in a T-maze. We tested (1) whether mole rats from each soil would show digging preferences for the soil of their origin (the soil which they had been captured from), or the other soil and (2) whether digging preference would be the same in wet and dry soil. In wet soil, mole rats from both soils spent more time excavating in the arm filled with the soil of their origin. In contrast, irrespective of their origin, they preferred to dig in rendzina when soils were dry. We suggest that mole rats distinguished between the two soils by olfaction and oriented their digging on the basis of the presence of soil-specific odorous cues detected in each of the soil. This ability was probably ineffective in dry soils with odorous cues being absorbed onto soil particles and mole rat dug in a better workable soil. In the context of sympatric speciation in blind mole rats, distinguishing between different soils by olfaction can be an important factor in the evolution of natal habitat preference (philopatry), which applies during dispersal at the end of the rainy season when soil is wet. This study was supported by the Czech Science Foundation (GACR, 14-31670P).

Magnetoreception in rodents – new species, new methods

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Unlike classic sensory modalities, i.e. vision, audition, smell and touch, the magnetic sense is poorly understood. Since the beginning of research on magnetoreception (the ability to perceive magnetic fields) 50 years ago, the magnetic sense has been demonstrated in many vertebrate taxa, including several mammalian species. Rodents are highly appropriate for magnetoreception studies, because they show a relatively stable magnetic orientation behaviour, which can be tested using diverse assays. Among rodents, the Ansell's mole-rat (*Fukomys anselli*) became the model species of choice. But also more common species, like mice, voles and hamsters, possess a magnetic sense. Here, we focus on the identification of further magnetosensitive species, as this would be beneficial to study proximate factors, i.e. magnetoreceptors and transduction mechanism. First, we demonstrate magnetosensitivity in other (subterranean) rodent species. Additionally, data of a previous study with negative results in the coruro (*Spalacopus cyanus*) have been reanalyzed, with a positive result. Second, we evaluate different experimental setups used in studies of magnetoreception in rodents, like the established nest-building assay, a digging assay and a magnetic object assay. We review the benefits and caveats of diverse assays and their suitability for biomagnetism research in rodents.

Phylogeography and phylogenetics of the eastern house mice (*Mus musculus*) based on polymorphisms of mitochondrial DNA

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M. musculus, known as the eastern European house mouse, is a widespread polytypic commensal species whose range encompasses Eastern Europe and a considerable part of northern Asia. Modern authors identify three to seven subspecies. The following morphological and/or cytogenetically diagnosed subspecies were used in this work: *M. m. musculus*, *M. m. wagneri* and *M. m. gansuensis*. We examined the phylogeography and genetic diversity of these subspecies in Russia and adjacent territories. 150 samples from 25 localities of house mice are included in the present study. Analysis of the control region of mtDNA and cytochrome b gene has been used to reconstruct the phylogenetic relationships and phylogeographic patterns of intraspecific forms. The genealogy of matrilineages was constructed using Bayesian tree. Additionally, the *SplitsTree4* software package was employed to build a split network. The phylogenetic analysis has identified four distinct clusters of control region and three for cytochrome b gene. Basal monophyletic clade as well as control region and cytochrome b gene was lineage of Transcaucasian hybrid zone. Samples of *M. m. wagneri* divided into two clades, the first from the European part of Russia, the second of middle Asia from Kazakhstan. In *M. m. musculus* we identified distinct clade “Siberia”. All identified specimens in this lineage were collected from west Siberia to Far East. House mice could disperse with human by railway. In conclusion, our results confirm previous suggestion, that in middle of Asia and Transcaucasia could exist the centre of expansion of house mice *Mus musculus*. Supported by grant the Russian president № MK-3909.2015.4.

A new hypothesis for the origin of cytotype diversity of blind mole rats in Anatolia

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Turkey is located within a structurally complex geological part of the recently folded mountain belt of Eurasia. A wide variety of tectonic processes shaped the Anatolian complex landscapes over millions of years and continue still as evidenced by frequent earthquakes. The fault lines formed by the earthquakes are known to release radon gas, which is radioactive and highly mutagenic. A number of studies claim that ionizing radiation can induce a variety of chromosomal aberrations. Because mole rats spend all of their lives in the underground tunnels, and have limited movement/dispersal ability compared to other species, they could be particularly exposed to the radon gas. This, in turn, might trigger chromosomal aberrations in the mole rats more often than in other rodents. If the aberrations fix in the germ line, the new chromosome sets can disperse in the population through sexual reproduction. In this study I briefly review the previous studies that provide a clue for my new hypothesis: the radiation emerged from fault lines affect the distributions of cytotypes in the mole rats.

On the use of next-generation sequencing technology and museum specimens to resolve African rodent systematics

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The recently published compendia *Mammals of Africa* and *Rodents of Sub-Saharan Africa* highlight the incredible diversity and endemism exhibited in African rodents. This diversity of taxa (~400 species represented in 15 families and 98 genera) has been described in the taxonomic literature spanning the course of two centuries. Peaks in taxonomic descriptions for African rodents occurred in early and mid 1900s due to the efforts of Oldfield Thomas and Austin Roberts. However, the number of currently recognized valid taxonomic names differs substantially from historically recognized species. Currently we are in a period of taxonomic flux with a new peak in taxonomic discoveries, owing in part to recent advancements in sequencing technologies. Historical museum specimens represent a wealth of natural history information across space and time that can be used to resolve long standing taxonomic issues. Here I describe several techniques for acquiring mitochondrial and nuclear sequence data from historical museum specimens (including holotypes) for resolving taxonomic issues in gerbils.

Imprints of climate fluctuations in distribution of rodent diversity in the northern part of Zambezian savanna

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Zambezian savanna represents a distinct biogeographic region in many vertebrate groups including rodents. In its northern part (Tanzania, Malawi, Zambia and Mozambique north of the Zambezi River) it is divided by Rift Valley lakes (e.g. Lake Malawi) and chains of forested mountains (e.g. Eastern Arc Mountains) both likely acting as dispersion barriers for savanna-dwelling taxa. Indeed, rodent communities are quite distinct on the opposite sides of these barriers and we investigated historical background of this pattern. In present there are several migration corridors connecting different subregions but strength of the barriers may vary in time mainly due to expansion and retreat of forests. Using time-calibrated phylogenies we show that pairs of subregion-specific taxa are of highly unequal age. It suggests that in the past the barriers repeatedly got sufficiently penetrable to allow enrichment of local communities by newcomers from neighboring areas. On the other hand they were still powerful enough to enforce differentiation of newly spread species. By means of species distribution modelling, we also predict distribution of the communities during the last glacial cycle and we discuss a possibility that adaptation to local climate makes the communities as coherent as observed.

Structure of the natural hybrid zone between two chromosomal forms of common vole

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Natural hybridization is an indicator of incomplete reproductive isolation between related, usually young species. Common vole includes two different chromosomal forms: *Microtus arvalis* and *M. obscurus*, which have a controversial taxonomic status. The common voles *M. arvalis* and *M. obscurus* are distributed in the European part of Russia and characterized by parapatric ranges. The boundary between these two forms is extending in the meridional direction through several natural zones and provides a unique opportunity for studying the processes of hybridization, introgression and gene flow intensity in several hybrid zones. The southern part of the hybrid zone located in the forest-steppe zone was probably formed soon after the retreat of the glaciers, while the northern part, located in the forest zone, was presumably emerged after anthropogenic transformation of the area and the formation of large territories of open habitats. We have accumulated a considerable data which revealed significant difference in the structure of hybrid populations in northern and southern parts of the zone. F₁ hybrids are extremely rare in all known hybrid populations, that indicates the presence of selection against hybrids. The northern part of the hybrid zone is dominated by backcrosses with a rare occurrence of both parental forms. The southern part is dominated by pure *M. obscurus* and rarely observed *M. arvalis* and hybrids. Overall hybrid zone is characterized by asymmetric introgression of cytogenetic and molecular genetic markers. Analysis of the cytogenetic markers showed that the width of a hybrid zone is less than 2 km in the southern part, but is more than 10 km in the northern part. According to molecular genetic analysis, the hybrid zone is considerably wider. At the same time, there is some discrepancy in distribution of mitochondrial and nuclear markers, because the mitochondrial DNA is much more easily dispersed through a species boundary without any recombination.

Can ecological niche models predict the effect of climate change on endemic rodents?

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The current climate change affects the distribution and abundance of organisms and recently have developed different methodologies to predict how will the changes. An important tool for learning about the past, present and future potential distribution of species have been ecological niche models. However, uncertainty of future conditions, and the effect of methodologies can be causing bias in the interpretation of results. The aim of this study is to identify whether ecological niche modeling reflects the changing climatic conditions. To answer the question 19 species of Mexican endemic rodents were selected. Each record of presence by species was classified into three periods according to the date of collection (1910–1949, 1950–1979 and 1980–2009) and period model with 19 bioclimatic variables, using three algorithms only presence: Maxent, GARP and BIOCLIM. To identify whether there was a difference with the use of different data sets on the same period, we modeled a period with corresponding data and independently with the other two data sets. For each period we calculate the similarity of the models (value greater than 70% similarity of pixels), with the model with the data for the period and other periods. With the 13 species showed no differences in the use of different data sets for the same period, transfers from one time to the other periods, was valid in the period to which it was transferred performed. With models of the different sets of data per period, a significant difference was observed BIOCLIM and Maxent. However, when the Maxent transfers overestimated the area of the known distribution of endemic rodents were held today. Using past data and validation with the information present, it allows an approach to make inferences to unfamiliar conditions, reducing the bias methodology.

Nasal construction protects rodent brain from inhaled dust and virus

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Inhalation of air-dispersed submicron and nano-sized inorganic and biogenic (virus) particles presents a risk factor for animal health. Here we show that nasal aerodynamics plays a pivotal role in the protection of subterranean mole vole *Ellobius talpinus* from an increased exposure to nanoaerosols. Quantitative simulation of particles flow has shown that their deposition on the total surface of nasal cavity is higher in the mole vole than in terrestrial rodent *Mus musculus* (mouse), but lower on the olfactory epithelium. Using MRI detection, we found a reduced accumulation of magnetic contrast nanomaterials in olfactory bulbs of mole voles in comparison with mice after the inhalation of nano-sized Mn aerosols. Aerodynamic model also predicts higher impact of nanoparticles on the dorsal area of olfactory epithelium than ventral, which also showed different ability to nanoparticle uptake by olfactory nervous. Together, we conclude that nasal geometry and functional heterogeneity of the olfactory epithelium contributes significantly to the protection of brain from accumulation of air-dispersed particles and virus especially in chisel tooth diggers, such as mole vole.

Food preference of the bank vole (*Clethrionomys glareolus*) and yellow-necked mouse (*Apodemus flavicollis*) in a laboratory experiment

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Twenty four individuals of the bank vole and yellow-necked mouse each were given a mixture of seven tree seeds species on first and the second day. Twenty days later the same procedure was repeated. The seeds not eaten were weighed every day with an exactness of 0.1 g and moreover analyzed for nitrogen (protein), starch, glucose, cellulose and lipids. These compounds were evaluated and correlated to each seed species by CANOCO 5. The IVLEV-index of electivity showed the range of rejection and acceptance of the seed species to both animal species in a different stadium of the experiments. Data between day 1/2 and 21/22 were assessed by Wilcoxon–test, normal distribution was tested by a one-way ANOVA. There weren't big differences between both animal species regarding the preference of the tested seed species. Most seeds of *Fagus sylvatica*, *Picea abies*, *Pinus sylvestris* and *Tilia cordata* were consumed, those of *Carpinus betulus* and *Prunus avium* were rejected often. Acorns (*Quercus* sp.) were preferred more from the yellow-necked mouse than from the bank vole. Concerning the consumption between days 1/2 and days 21/22, data of the yellow-necked mouse had smaller differences than those of the bank vole. Latter seemed to cope worse with tree seeds as a food source. Chemical analysis and CANOCO-test points for acorns a lot of starch and glucose, whereas seeds of *Fagus* had much lipids and proteins. Small seeds contained much cellulose (*Carpinus*), lipids and proteins (*Picea*, *Pinus*) respectively lipids and moderate contents of glucose, starch and proteins (*Tilia*). Seeds of *Prunus* had much of lipids and glucose.

Cranial morphometric analysis of the Transcaucasia mole vole in Iran and Caucasian region

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Dramatic environmental rearrangements during the last glacial and the Transcaucasia mole vole is an ideal model species for studying processes driving geographical differentiation because of its large distributional range. We studied geographic variation in the cranial shape of *Ellobius lutescence* along its distribution range in the Caucasian region using geometric morphometric techniques. Our result proved that geographically isolated populations show significantly different skull and mandible morph since positive correlation was found between geographic and morphological distances and among populations studied. The discriminant function analysis performed over the partial warps and uniform components scores matrix showed significant differences among the studied populations. Our results indicated that geometric morphometric approach could successfully distinguished similar pattern of population structure.

Does biodiversity affect pathogens transmission? Testing dilution effect in Welsh wild rodent communities

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Researching rodent disease ecology helps direct wildlife management and conservation, limiting disease spillovers and outbreaks. Here, disease transmission among small rodents in Welsh woodlands was modelled to investigate the effects of host-species and community composition. The dilution effect was tested by assembling a progressively complex community according to ecological criteria whilst modelling eco-epidemiological relationships. Parameters assumed to affect the epidemic were species evenness, reservoir competence, host interspecific contact rates, and competition. To add confidence to the model, field data were collected to evaluate parameters where relevant. Higher species evenness and interspecific contact rates are hypothesised to dilute disease transmission by decreasing encounter rates between the most competent hosts. Small changes in competence between species can also dilute transmission rates, whilst the presence of competitors or predators and the subsequent regulation of host populations are hypothesised to reduce infectious and R_0 . Increasing overall host-species density raised total infections but decreased prevalence; however, reducing host diversity, only retaining the most competent, increased infectious and prevalence compared to a multi-host scenario. Variations in competence and contact rates supported the hypotheses. Most competent species are usually more resilient, so in higher evenness community is more likely the occurrence of less competent species that decrease transmission. Only high presences of competitors and specialist predators reduced total infections and epidemic peak, whereas generalist predators had a limited impact. This suggests that the dilution effect is possible, thus habitat complexity should be preserved to allow a variety of different rodent species and specialist predators to persist. Future work includes model fitting to field data and vector-borne disease modelling.

Huddling and socio-physiological effect in a social African mole-rat, the Mashona mole-rat (*Fukomys darlingi*)

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Lifetime in belowground burrows is among greatest challenges for mammals. Although underground environment is safe from predators and offers relatively stable microclimatic conditions, it is also scarce in food resources and living there requires burrow excavation, which is energetically very demanding. In this respect, energetic savings are extremely important for their survival in subterranean ecotope. We studied the effect of group size on energetic savings by huddling in a social bathyergid, the Mashona mole-rat (*Fukomys darlingi*) at 20 °C. We measured resting metabolic rate (RMR) in isolated individuals and compared it to RMR of pairs and groups from three to eight individuals. This mole-rat species saved 21% of its energetic expenses when housed in pairs. With increasing group size, their energetic savings increased up to 32% in four animals, but diminished in larger groups. In addition, we tested the effect of so called socio-physiological effect, which should be the most conspicuous when metabolic rates of huddling individuals are measured within species' thermoneutral zone (TNZ). Although the mole-rats saved about 5% of their energy expenditure in pairs at 30 °C, the difference was not statistically significant. Even in larger groups no energetic savings were observed at this temperature. Our results about absence of energetic savings in groups within TNZ are in contrast to hitherto published results on other African mole-rat species.

Integrated rodent pest management in the campaign against vole in the Local Board of Plant Health in El Valle del Fuerte, Sin. Mexico

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The Valle del Fuerte, Sinaloa has 150 thousand arable hectares where 3 million tons of foods are produced, with a value of 600 million US dollars. The valley it is characterized by the use of high agricultural technology and the availability of water for irrigation. The main crops are: corn, beans, sorghum, vegetables and chickpea among others. One of the factors limiting agricultural production are vertebrate pests that often cause significant damage if not handled properly. There are 11 species of rodents associated to crops in the valley but only 3 act as plague: *Sigmodon arizonae*, *Peromyscus sinaloensis* and *Oryzomys couvesi*. In Mexico the campaign against vole was ordered of public utility in 1960 since then the Local Board of Plant Health empowered by the Ministry of Agriculture carried out the campaign. In 2009 the local Sugar Company Mill bankrupt and abandonment more than 20 thousand hectares of sugarcane fields causing a major outbreak of rodents that affected other crops. Therefore as a solution an Integrated Rodent Management program was implemented, mainly using chemical and mechanical controls, as well as a permanent monitoring system allowing manage control actions efficiently and consequently act with utmost care to the environment and protecting implemented to non-target wildlife.

Morphometric, karyologic and mtDNA characterization of *Sciurus vulgaris* and *S. anomalus* in Turkey

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A total of 16 *Sciurus anomalus* and 10 *S. vulgaris* samples were collected from distributional areas in Turkey. *S. anomalus* distributed throughout Anatolia while *S. vulgaris* has a natural distribution in North and northeast of Thrace (European part of Turkey) and in Anatolian peninsula its distribution extends from Trabzon to the forested areas of the Kars and Erzurum plateaus. Standard and geometric morphometric approaches were used to assess morphologic characteristics of *S. anomalus* and *S. vulgaris*. Karyology was also studied for both species. Two mtDNA genes Cytb (959bp) and dLoop (482) were sequenced from both species to find the extend of genetic variation and the phylogenetic relationships. Standard morphological measurements were statistically tested for 26 cranial measurements and showed significant differences between two species ($P < 0.05$). A total of 13 landmarks from mandibles and 15 landmarks from ventral side of skull utilized to analyze the shape variation. Although based on the mandibles, two species showed significant differences ($P = 0.013$), but ventral side of the skull did not show any significant differences (0.069). Karyological analyses resulted in the same chromosome number $2n = 40$ but there were differences in the NF (*S. vulgaris* 76 and *S. anomalus* 80) and NFa (*S. vulgaris* 72 and *S. anomalus* 76) values. Both mtDNA gene regions separated two species into two different groups. Cytb sequences combined with the sequences obtained from Genbank and the sequences from both species were clustered with appropriate Genbank *anomalus* and *vulgaris* sequences. Two *S. vulgaris* population in Turkey partially separated from each other. All Northeast samples and the Thracian samples were separated while the Edirne samples (from Thrace) clustered with the Northeast squirrel population. The genetic distance between two species based on dLoop sequences were found to be $d = 0.182 \pm 0.020$.

Ticks and mites parasitising small rodents collected from different habitats in Curonian Spit, Lithuania

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For human health perspective, the rodent-tick associations have a huge importance in most ecosystems. Besides their role as tick hosts, rodents serve as reservoirs of tick-borne pathogens, hence increasing their importance in the eco-epidemiology of diseases like tick-borne encephalitis, Lyme borreliosis, human babesiosis, human granulocytic anaplasmosis or tularaemia. Climatic changes have caused the increasing of distribution in new regions and abundance of ectoparasites, and also have indirect effects on host ecology and abundance, causing emergence of tick-borne diseases. The aim of this study was to investigate ectoparasites (ticks and mites) parasitizing small rodents and estimate ectoparasite infestation patterns in different rodent species in particular habitats in Lithuania. Small mammals were captured with live-traps and snap traps in different locations in the Curonian Spit during 2013–2014. A total of 247 small rodents representing 8 species were trapped. Captured rodents were identified as *Apodemus flavicollis*, *A. agrarius*, *Myodes glareolus*, *Micromys minutus*, *Microtus oeconomus*, *M. arvalis*, *M. agrestis*, and *Rattus rattus*. Collected rodents harbored *Ixodes ricinus* ticks and parasitic mites from suborder Mesostigmata (Gamasida), families Laelapidae, (genus *Laelaps*, *Eulaelaps*, *Haemogamassus*, *Myonyssus*) and Macrochelidae (genus *Macrocheles*). Mites from Laelapidae family dominated between other mesostigmatid members found on rodents. A total 1116 *I. ricinus* ticks and mites were removed from 218 live-trapped small rodents, and 31 *I. ricinus* ticks from 29 rodents trapped with snap traps. Although two stages of *I. ricinus* were found on trapped rodents: larvae and nymphs, considerably higher larval infestation were recorded. Generally, rodents were more infested with Laelapidae mites than with *I. ricinus* ticks. The values of abundance and mean intensity of infestation with *I. ricinus* and mites varied between species of hosts.

Increased productivity by large-sized individuals leads to high population density in the common hamster

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Body size is known to decrease with increasing population density in many taxa of large herbivores. Conversely, there is the opposite evidence for cyclic small rodents, such as voles, in which body size increases during the phase of high population density. Despite not being a cyclic species, the common hamster (*Cricetus cricetus*) exhibits large variation in population numbers and has a high reproductive potential. However, density-dependent processes in natural hamster populations are still poorly understood. In this study we focused on the variation in body growth rates and body size with population density, using data collected over 9 years in the suburbs of Olomouc, Czech Republic. The productivity index, calculated as a ratio of subadult numbers to adult numbers, increased with population density and length of the breeding season. We found that in years of high population density, adults grew faster, were longer but not heavier and bred longer. These results suggest that variation in asymptotic body size, productivity and population density in the common hamster are driven by interannual variability in adult body growth rates and longevity.

Molecular-genetic analysis of urban populations of common hamster (*Cricetus cricetus*)

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Urbanization is a particularly potent driver of environmental change around the world. Urbanization affects all aspects of animal biology, including on their genetic structure. The high level of isolation habitat in urban landscapes and difficulties for the migration of species lead to a reduction in the genetic diversity of the population of urban animals and increase the degree of relationship within the local groups. This phenomenon known for semi-synanthropic rodents *Calomys musculus* (Chiappero et al., 2011) and *Peromyscus leucopus* (Harris et al., 2016). The population of brown rats (*Rattus norvegicus*), rodents attributed to true synanthropes, in Salvador (Kajdacs et al., 2013) demonstrates rather different genetic structure. We investigated genetic structure of urban populations of common hamster by analyzing nucleotide sequences of the cyt. b gene and mtDNA control region and allelic composition of 10 microsatellite loci. In Simpheropol (Crimea), city with largest of urban population of common hamster, results of our study showed that although some hamster can move on relatively long distances in the city, their population represented by separate small groups of interbreeding animals (demes) confined to different areas of city. These demes have a high degree of genetic isolation and reduced genetic diversity compared with same parameter for summary sample from Simpheropol. Hamsters from Northern Caucasus are represented by rather distanced group of haplotypes from crimean ones, but genetic analysis revealed similar structure of urban population in Nalchik. In both cities were revealed specific mtDNK lineages, which are didn't found in surroundings. So, the analysis of both nuclear and mtDNA markers revealed a relatively high genetic diversity of urban populations of the common hamster and it can be one of the important conditions of successful existence of these species in the urban landscapes. The study is supported by grant of RFBR 16-34-50141 mol_nr.

The hormonal response of chinese hamster males exposed to con- and heterospecific olfactory signals

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The olfactory conspecific signals are known to cause a chain of hormonal reactions to, stimulate and synchronize the sexual behavior of the partners. As a rule, it does not occur when the animals are exposed heterospecific signals. The taxonomic status of a hamster of 4 karyoforms *Cricetulus barabensis* sensu lato is discussed. *C. griseus* males were exposed to the odour of urine of estrous females of the own karyoform and *C. barabensis* and *C. pseudogriseus*. It has been demonstrated, that when exposed to the urine of estrous females in all the experiments the level of testosterone in the male blood increases ($P < 0.05$). However, exposure to heterospecific signals, in contrast to conspecific increased the cortisol level ($P < 0.05$). Moreover, in all the seasons, except autumn the level of testosterone *C. griseus* also increased when exposed to the odour of diestrous *C. griseus* females, but rather not or *C. pseudogriseus*. Thus, the physiological responses in *C. griseus* of to con- and heterospecific signals diestrous females were formed but a positive response the odour of the estrous heterospecific females which were closely related indicates an absent of the mechanisms of the reproductive isolation for odour signals. It is supported by fertile crosses at least in the laboratory. The research is supported by a RFFI grant mol_a 16-34-00820.

The efficacy of ContraPest[®], a contraceptive bait, in the management of wild rats (*Rattus norvegicus* and *Rattus rattus*)

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Commensal rodents are reservoirs for disease and cause extensive damage to infrastructure and crops. Traditional management techniques, such as rodenticides, do not control rodent populations long-term due to population rebounds and increasing resistance to anticoagulant compounds. Sustainable rodent population management requires a new approach targeting the biological source of overabundance: reproduction. In response, we at SenesTech, Inc. (Flagstaff, AZ USA) have developed ContraPest[®](CP): a liquid bait that blocks the reproductive capacity of wild rats (*Rattus norvegicus* and *Rattus rattus*). The two active ingredients in CP, 4-vinylcyclohexene diepoxide and triptolide, deplete primordial and growing follicles and disrupt spermatogenesis. CP formulation is palatable and effective. Fifty percent of free-ranging wild rats in New York City subway trash rooms consumed CP when presented in the near preferred food sources. Research rats produced no pups after consuming CP for 15 days. Wild-caught Norway rats, housed and provided CP for 50 days, produced only 12 pups after 3 breeding rounds, compared to 255 pups born to the control group. A follow-up study conducted with wild-caught Norway rats in an open arena resulted in 255 pups born to the control group compared to 13 pups born to the group provided CP for 56 days. CP was also tested on wild populations of Norway rats at protein production farms, where populations decreased by 30% after 100 days of taking the bait. Studies are currently being conducted on wild caught black rats (*Rattus rattus*) in cage-based experiments and on wild Norway rats in urban settings. Our humane technology can be used alone or in conjunction with integrated pest management methods for the effective, long-term control of rodents in urban, rural or agricultural environments.

Bank voles in southern Eurasia: vicariance and adaptation

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Phylogeographic lineages are interpreted as the product of repeated isolation in glacial refuges, leading to vicariant differentiation. Being restricted to given geographic areas could also promote adaptive divergence in response to local conditions. The role of phylogeny and climate in the evolution of the bank vole (*Myodes glareolus*) was investigated, focusing on molar tooth shape, a morphological feature related to the exploitation of food resource. A balanced role of phylogeny and climate was evidenced. Response to environmental factors led to morphological convergence of bank voles from different lineages leaving in similar environments, and to within-lineage divergence in extreme environments. An important interaction of climate and phylogeny was evidenced, suggesting that each lineage is leaving in a peculiar environment. This lineage-specific adaptation to a range of environmental conditions may have condition the potential of post-glacial recolonization of each lineage. Morphological covariation with environmental conditions further highlights the potential of adaptation of this species.

Categorization and effectiveness of protected areas: comparative study of small mammal communities in Nahuel-Huapi National Park, Argentina

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The increment of Protected Areas (PA) at global scale during the second half of the 20th century reflects the growing concern of preserving lands, facing the biodiversity and habitat loss. However, in most cases, there is no clear evidence of the PA effectiveness. Nahuel Huapi National Park is the first and biggest Argentinean PA (750,000 ha); it hosts few big and medium size mammals' species, however, the number and diversity of small mammals equals those found in temperate forest elsewhere. Our goal was to evaluate the conservation status of the small mammals communities in the Nahuel Huapi protection system, accounting for direct and indirect human intervention. In order to achieve this goal, five plots of 60 × 60 m were established in each level of protection (Strict Natural Reserve, National Park, National Reserve, outside PA), setting 50 traps per plot, over four consecutive nights monthly. Capture effort was 20,600 traps/day. Each individual was identified, marked and released, resulting in 727 individuals (*Abrothrix hirta*, *A. olivacea*, *Oligoryzomys longicaudatus*, *Geoxus valdivianus*, *Chelemys macronix*, *Irenomys tarsalis*, *Loxodontomys micropus* and *Dromiciops gliroides*). Species richness, Shannon–Wiener diversity-index, and abundance were compared by ANOVA, finding only statistical difference for *Loxodontomys micropus* abundance. However, three species were scarcely found; furthermore the unequal distribution of records requires a deeper track in order to elucidate the role that the presence or absence of the PA would be fulfilling in the conservation of these communities.

Francisella tularensis in a wild population of common vole (*Microtus arvalis*) from agricultural landscapes of SW Europe

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In many European regions, most microtine rodents exhibit multi-annual fluctuations in abundance and can cause significant crop damage and economical losses when they are overabundant during population outbreaks. In addition, they can be reservoirs of multiple pathogens responsible of serious zoonotic diseases to humans and livestock. Therefore, understanding the relationships between rodents and their pathogens under a dynamic perspective (density-dependent patterns of prevalence) may be particularly relevant in terms of effective public health management. In NW Spain, the outbreaking common vole (*Microtus arvalis*) recently colonized intensive agricultural landscapes where it has been pointed as a main amplification and spill-over host of *Francisella tularensis* (the etiological agent of tularemia). However, the epidemiological role of these fluctuating vole populations with regard to zoonotic diseases remains largely unknown. Here we describe for the first time the patterns of prevalence of *F. tularensis* along a complete fluctuation in abundance in a wild common vole population. Voles were captured seasonally (March, July and November) during a population outbreak between 2013 and 2015 and were screened for the occurrence of the pathogen. From a total of 243 captured voles, 46 individuals were infected, but prevalence greatly varied in time (range from 0 to 30%). We found a strong effect of vole abundance on tularemia prevalence, in a direct positive density-dependent way. We discuss the implications of the findings for our understanding of vole population regulation and public health. The increasing frequency of zoonotic disease events in rodents encourage us to go on studying the co-infection in common vole populations with other relevant pathogens.

Rodent osteology from a zooarchaeological perspective – rodent skeletal remains from a Neolithic site at Skara Brae, Orkney, United Kingdom

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Despite the presence of rodent skeletal remains in many geological and archaeological contexts, both the scope of the questions addressed and the methods applied to them are limited. In the case of palaeoecology and zooarchaeology, the primary concern has been the identification of the species present and the source of deposition. Apart from the use of cranial and dental morphology as proxies for long term changes, such studies tend to lack the sophistication of those involving larger, especially domesticated, species. A large quantity of rodent skeletal material, retrieved from this Neolithic habitation and the surrounding area, was analysed using classic osteological techniques. The data were used to examine the relationship between the Neolithic people of Skara Brae and the rodents, primarily Orkney voles (*Microtus arvalis*). Accumulations of rodent remains within the settlement were the result of deliberate human activity. While this may reflect an early example of pest control, the accumulations are probably the result of their use as a source of food, supporting the hypothesis that they were deliberately introduced by Neolithic settlers. This is the earliest evidence for the consumption of rodents by people in Europe. It clearly demonstrates the value of detailed osteological analyses to the field of rodent palaeoecology.

Comparative genomics in rodents: genomic signatures of evolutionary reshuffling

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Understanding how mammalian genomes have been reshuffled through structural changes is fundamental to the dynamics of mammalian genome composition, evolutionary relationships between species and, in the long run, speciation. In this work, we defined the evolutionary genomic landscape in Rodentia, the most diverse and specious mammalian order, by whole-genome comparisons of the mouse and those of eleven representative mammalian species. The reconstruction of the evolutionary breakpoint regions across the Rodentia phylogeny show an increase rate of genome reshuffling that is approximately two orders of magnitude greater than other mammalian species. We identified novel lineage and clade-specific breakpoint regions within Rodentia and analyzed their gene content and chromatin modifications. We detected an accumulation of protein-coding genes in evolutionary breakpoint regions, especially genes implicated in reproduction and pheromone detection and mating. Moreover, we found an association of the evolutionary breakpoint regions with 'open' chromatin state landscapes, most probably related to gene enrichment. Our results have important implications for understanding the mechanisms that govern and constrain mammalian genome evolution.

Phylogeography of invasive rats in New Zealand

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Invasive Norway (*Rattus norvegicus*) and ship (*R. rattus*) rats arrived in New Zealand with Europeans in the late 1700s and 1860s respectively. They rapidly spread across the entirety of New Zealand and colonised offshore islands. Today both species are widespread although the distribution of the sub-dominant Norway rat is patchy. Modern and museum tissue samples were obtained from over 350 ship rats and 70 Norway rats from across the two main North and South islands of New Zealand and neighbouring islands. We sequenced a standard 545 base pair section of the mitochondrial D-loop in order to construct a modern phylogeography of the two species and to make inference on historical invasion pathways and spread across the country. We found limited diversity in Norway rat haplotypes, with one widespread haplotype across New Zealand and its offshore islands except for Stewart Island where a separate haplotype most likely corresponded to an independent invasion. In contrast we found widespread diversity in ship rat haplotypes across New Zealand and its offshore islands, most likely corresponding to at least three independent invasions to the main North and South Islands, Great Barrier Island archipelago, and Stewart Island archipelago. The most common haplogroup was found throughout New Zealand and many of its offshore islands, as well as neighbouring islands in the Tasman Sea, and has been documented globally. We also found both geographic partitioning and secondary invasions of haplotypes within the main North and South Island. In addition to distinct haplogroups differing by over three base pairs, which exhibit geographical partitioning suggestive of independent invasion events, for both species we also found instances of single base-pair differences within localities, elevating haplotype diversity. The geographical distribution of pelage colour morphs also correlates with haplotype distribution, lending further support to the hypothesis and role of independent invasion events.

Habitat structure can affect nocturnal activity pattern of Jerboas: a comparison of semi-desert and mountainous areas of Iran

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Investigation about the activity pattern of the Jerboas in different habitat types including semi-desert steppe habitats with low and sparse vegetation in the central parts and mountainous dense steppes in the north-western parts of Iran confirmed that habitat structure can strongly affect nocturnal activity behavior of such small mammals with unique bipedal movement. In both habitat types we recorded more encounter rate with the individuals in the first and last weeks of the lunar nights (low moon period) but the pattern of habitat selection showed significant differences. Statistical analysis for investigating about the mean difference of used plots vegetation percent cover and habitat types in both low and high moon periods showed that habitat structural feature can significantly affect the species habitat usage pattern. Bipedal locomotion pattern of the species require specific anti-predator habitat selection mechanism that is different from other small mammals.

Rodents, ticks and pathogens: importance of host species and habitat for tick parasitism and pathogens carried by ticks of small mammals in Romania

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In Europe, ticks are medically the most important group of arthropods, associated with high health-care costs for most established tick-borne disease and the newly emerging diseases transmitted all over the continent. While their medical importance is acknowledged and most diseases have a long epidemiological history, the majority of tick-borne diseases show an emerging pattern. The vector capacity and transmitted pathogens are known and established for tick species commonly occurring or those which can be collected using dragging. However, our knowledge on the importance of tick species or developmental stages found only or mostly on small mammals is limited. While small mammals are very common in a wide range of habitats and are known reservoirs of a number of zoonotic diseases, their ticks (and their vectorial importance) are unknown in Romania. Here we present data on the zoonotic potential of ticks collected from small mammals (voles and mice) trapped in agricultural areas surrounding rural settlements in several regions of Romania. Ticks were collected from small mammals ($n = 1001$, 12 host species, 16 regions) and identified according to morphological keys. Four species of ticks were detected and used for DNA extraction and analyzed for the presence of *Rickettsia* spp. and *Anaplasma* spp, using generic primers. We found 5 species of zoonotic *Rickettsia* (*R. helvetica*, *R. monacensis*, *R. mongolitimonae*, *R. raoultii* and *R. slovaca*) and *Anaplasma phagocytophilum* and *Babesia* spp. Using GLM we investigated the importance of host ecology and distribution in determining the prevalence and abundance of ticks and tick-borne disease.

Maze runners: common voles (*Microtus arvalis*) in T-maze trials for identifying repelling or attracting substances

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Common voles as a major European rodent pest species can cause severe agricultural damage. An integrated, sustainable and ecological management is urgently needed. We combined methods to establish a barrier between cultivated areas and the adjacent refuges of voles. Those methods could include baited traps or repellents both requiring appropriate attractive or deterrent substances. Appealing compounds to rodents can be sweet, fatty or familiar substances but little is known about the favorite bait base for common voles. A selection of compounds smelling sweet, fatty compounds or agents familiar to the vole was tested with eight voles in a T-maze. The distal T-maze tunnels ended at live traps where either an attractant or water was presented on cotton wool. The time until each vole entered the trap with the attractant or the trap with water (control) was measured. Three attractive substances were identified and further tested in semi-natural enclosures regarding catch success and bait intake. Repelling substances are already used in rodent management but scientific research of vole repellents is limited. Compounds as well as single substances of repelling essential oils avoided by rodents were tested in T-maze trials with eight voles per treatment. The distal T-maze tunnels ended at boxes where the tested substance or water (control box) was offered on cotton wool. Each vole stayed 30 min in the maze and its presence in the boxes was registered by an antenna recognizing the vole's PIT tag. Results of these T-maze trials will be presented and discussed.

On the determination of personality traits in the common vole

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In the last two decades a lot of papers demonstrated that animals display consistent intraspecific behavioural differences stable more or less over time and across situations. We investigated the behavioural stability/repeatability of exploratory behaviour in the common vole (*Microtus arvalis*). Under laboratory conditions 61 individuals were tested in an Open Field (OF) test. The test lasted 3 min and was carried out five times with an interval of two months between tests. We evaluated changes of single behavioural elements (locomotion, immobility, freezing, rearing, grooming and jumping) as well as synthetic variables created by Principal Component Analysis (PCA). The repeatability of exploratory activity was evaluated as an intraclass correlation coefficient (ICC). ICC ranged from 0.25 to 0.38. Data based on these relatively long-term laboratory experiment were compared with data obtained by the capture-mark-recapture (CMR) method. Wild individuals were caught in their natural habitat, immediately tested in the laboratory and then released at the capture site. Using the last mentioned procedure, the ICC ranged from 0.53 to 0.75. Generally, the CMR values were markedly higher than the data from long-term laboratory experiment. The difference of exploratory activity between the second and the first captures/tests was negatively correlated with the time (in days) between the captures/tests ($r = -0.718$, $p = 0.019$). Based on this relationship it was possible to assess theoretically the interval for the second capture/test of exploratory activity that shows the same activity values as the first one. This interval reducing habituation takes 3–4 weeks. Under the long-term laboratory experiment the comparative interval exceeded 10 weeks.

Phylogeography and taxonomy of the northern three-toed jerboa (*Dipus sagitta* Pallas, 1773) species complex

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The history of the fauna and the dynamics of geographic ranges of mammals of arid areas of Palearctic are not studied well enough. The key object for studies of rodent phylogeography in the Great Palearctic Desert Belt is the autochthonous family Dipodidae. *Dipus sagitta* is one of the most wide-spread species of jerboas (distributed from North Caucasus to north-eastern China), demonstrating pronounced morphological variability (12–15 subspecies grouped in two or three large groups). Data on mitochondrial and structural DNA sequences (cytb (213 sequences), IRBP and BRCA1 (68 sequences) from Mongolia, China, Zaisan Basin, Balkhash, Kyzylkum Desert, and North Caucasus) indicate the complexity of geographical variability. Geographic variabilities of mitochondrial DNA, structural DNA and sub-specific structure based on morphological data are only partially consistent with one another. The level of divergence between some phylo-groups potentially corresponds to the species. The most isolated position occupied by populations of a) Tarim Basin, southern and western Qaidam and b) central, southern and eastern Mongolia, Alashan, Ordos and northern Qaidam, while between-population differences for the most parts of Central Asia are relatively small. The Dzungarian Basin, NW Mongolia, East Kazakhstan and Turan regions are characterized by a high level of divergence between populations inhabiting isolated sand massifs (Dzungarian Basin – Zaisan hollow – south Balkhash – Kyzylkum – Daghestan), what corresponds to the expectations based on the more strong specialization to sandy habitats in the Middle Asian forms of *Dipus*. Populations of NW Mongolia and Tuva seem to bear footprints of an ancient hybridization during the secondary contact of two divergent phylogenetic lineages.

Effect of social environment on female reproduction in the Zaisan mole-vole, *Ellobius tancrei*

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Mole-voles (genus *Ellobius*) are highly social rodents specialized for a subterranean lifestyle. Singular breeding has been reported for most studied species and populations, but nothing is known about the proximate mechanisms of the reproductive monopolization. We examined the effect of social conditions on female survival and reproductive success in the Zaisan mole-vole, *Ellobius tancrei*. In Experiment 1, young females were housed with a strange male ($n = 10$) or with a strange male and a dam ($n = 9$). By the end of a 6-mo period, all monogamous females were alive, while 4 daughters and one dam died in polygynous groups. Seven of 10 young monogamous females and 6 of 8 survived dams in polygynous groups delivered and weaned at least one litter. To the contrast, only one daughter housed in trio gave birth; and her pups died on the first day. In Experiment 2, we compared vaginal conditions of young females housed with their natal family ($n = 10$) or living with a male sibling ($n = 9$). The focal females in both treatments had no contact with any strange male. The average proportion of days with an open vaginal orifice was significantly higher in females housed with a brother than in those housed with parents (73% and 18%, respectively). In addition, our preliminary data suggest that breeding in sire–daughter, dam–son and brother–sister pairs is not uncommon. From these results, social inhibition rather than strong incest-taboo appears to be involved in the female reproductive suppression in this species. The research was supported by the RFBR project 16-04-00479.

Did climatic changes trapped Ctenodactylidae species on Sahara–Sahel mountains and shaped intraspecific genetic variation?

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The Sahara-Sahel is composed of a mosaic of habitats that are strongly shaped by climatic oscillations, defining both species distribution and within species genetic structure. Within the region, mountains display areas retaining humidity that allow the formation of variable habitats, often surrounded by hyper-arid and arid zone. This variability potentially reinforces isolation and constrains distribution of local biota, like Ctenodactylidae rodents of mountains and rocky outcrops of North Africa. Previous ecological analysis suggested that Ctenodactylidae distributions can be constrained by habitat types related to increased humidity, suggesting that mountains could form climatic-traps for the species-group during hyper-arid stages within Sahara-Sahel. We reconstructed phylogenetic relationships between extant members of Ctenodactylidae family and assessed biogeography of North Western Africa endemic, *Felovia vae*. Primarily non-invasive samples were sequenced for partial cytochrome b ($N = 100$; 700 bp) and growth hormone factor receptor genes ($N = 24$; 362 bp). Topoclimatic factors related to occurrence of *Felovia vae* were identified for present conditions and projected into the past environmental conditions. Phylogenetic results showed that diversification of the family occurred during Miocene and coincided with major geologic and climatic events in the region. Biogeographic analyzes of *Felovia vae* showed that dry and wide sandy valleys and permanent rivers are important landscape barriers, during dry and humid periods respectively, but savannah like habitats might have allowed dispersal during opposed climatic stages. Species demographic expansion is apparently related with more humid periods, while arid phases restricted the species distribution to mountains. This study highlights past connectivity between putatively isolated contemporary populations, suggesting dynamic histories for the regional biota shaped by climatic fluctuations.

Population size estimates for *Apodemus* spp., *Myodes glareolus*, *Glis glis* and *Muscardinus avellanarius* inhabiting a deciduous forests in Zonguldak Province

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Population size estimates are one of the most important components of demographic, conservation, management and ecological studies. In this study, we determined the population sizes of rodent species inhabiting a selected deciduous forest area in Zonguldak Province, Turkey using the marking method between December 2011 and November 2012. A total of 130 live traps were placed at 10-meter intervals according to a grid method in a 250 m × 40 m area (1 ha) in five rows. We calculated the population size of *Apodemus* spp., *Myodes glareolus*, *Glis glis* and *Muscardinus avellanarius* to be 689, 97, 68 and 3 individuals/ha, respectively; we calculated the super population sizes of *Apodemus* spp., *Myodes glareolus* and *Glis glis* to be 1166, 283 and 98 individuals/ha, respectively. The monthly population size of *Apodemus* spp. was the smallest in January (7 individuals/ha) and the largest in June (119 individuals/ha), the population of *Myodes glareolus* was the smallest in September (1 individual/ha) and the largest in May (20 individuals/ha), and the population of *Glis glis* was the smallest in June (4 individuals/ha) and the largest in September (20 individuals/ha). Our findings provide a base for comparative studies in future, and data on populations of rodents in a selected area in Turkey for the first time. This study was supported by the Research fund of Bülent Ecevit University (Project no. 2012-10-06-04 and 2012-10-06-05).

Gene–environment interaction in the bank vole (*Clethrionomys glareolus*)

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Bank vole (*Clethrionomys glareolus*) currently represents important model species for promising field of adaptive phylogeography. Two bank vole populations that successively colonized Great Britain after end of the last glaciation differ not only in their mtDNA but also in the type of haemoglobin they carry. These two variants are distinguished by single amino acid substitution of serine for cysteine in two paralogous beta globin coding genes and this variability is demonstrably functional. Presence of extra cysteine in the haemoglobin carried by the second colonizing population increases the antioxidant capacity of the red blood cells and it thus may have had a role in determining the adaptive advantage over the first colonists, promoting the population replacement. Further research revealed that in continental Europe the extra cysteine might have played similarly important role. Both the serine and cysteine alleles are widely dispersed, however there is clear geographical pattern and each of the alleles is exhibiting association with a different phylogeographic lineage of the bank vole (as defined by mtDNA). Some populations also segregate both variants. Since the phylogeographic lineages originated in different glacial refugia, this association and the well-defined geographical distribution of the cysteine allele points to a possible adaptation of the different populations to specific climatic conditions. In my talk I will present the newest insights regarding this possible interaction between the haemoglobin genotype and environmental conditions we gained from analyses including PCA, Spearman's Rho and spatial analysis. Our results support the hypothesis of functional divergence (and hence selection) being important in determining which glacial refugia were ultimately successful in populating current species distributions.

Light or temperature; that is the question. Circadian rhythms of the silvery mole-rat (*Heliophobius argenteocinereus*)

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Strictly subterranean mammals are a suitable model to study factors determining circadian activity patterns in mammals because they live in a stable and monotonous environment with a neglected influence of some potentially confounding factors. Although the influence of light on their activity was demonstrated repeatedly during laboratory experiments, there is growing evidence that free-living subterranean mammals may adjust their activity to the course of the ambient (soil) temperature. More specifically, radio-tracking studies on African mole-rats (Bathyergidae, Rodentia) revealed that solitary or small social species increase their activity with the increase of the soil temperature during a cold season probably as a mean of behavioural thermoregulation. However, such data do not provide convincing evidence about the role of the soil temperature as a zeitgeber of the circadian activity. To test if the soil temperature acts as a zeitgeber, we designed a long-term experiment studying the locomotor activity of a solitary bathyergid, the silvery mole-rat (*Heliophobius argenteocinereus*) in artificial burrows with respect to changes of the ambient temperature and light cycles. Mole-rats increased their activity with the increase of the temperature under constant darkness and while an artificial circadian temperature cycle was maintained, but preferred to be active during the light phase of a day in the experiment with a constant temperature of 24 °C. Importantly, tested mole-rats shifted their activity during a day according to the six hour shift of both factors. Although the test was designed to reveal whether both factors act as a zeitgeber, it did not provide conclusive results. It seems that even 45 days of the test phase is still not enough to stabilise circadian rhythms in this species.

A recent outbreak of Dobrava-Belgrade hantavirus in a population of wild rodents in northern Italy: causes and implications

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Dobrava-Belgrade hantavirus (DOBV) is an infection carried by wild yellow-necked mice (*Apodemus flavicollis*) that may cause serious zoonoses in humans, with a case fatality rate of 12%. The prevalence of antibodies to DOBV in a wild population of *Apodemus flavicollis* in the Province of Trento (northern Italy) from 2000–2013, ranged from 0% to 12.5%, with an abrupt increase from 2010. Over the 14-year study period, 2189 animals were live-trapped and mean hantavirus seroprevalence was 3.15% (SE = 0.3%). Climatic (temperature and precipitation) and host (population density; individual body mass and sex; and larval tick burden) variables were analyzed with Generalized Linear Models, giving indications that mean annual precipitation, annual maximum temperature and individual body mass have a positive effect on DOBV seroprevalence. We then analyzed the transmission dynamics of the recent outbreak of this virus using a computational model that accounts for territorial behavior and seasonal changes of the host population. This model underlined the high stochastic fadeout of DOBV, due to natural population drops associated to seasonal mating and winter mortality. DOBV established an endemic infection in the rodent population under study, and the predicted increase in rodent seroprevalence implies a possible higher risk of spillover to humans in the future. Continued surveillance on the rodent population is recommended to monitor future trends.

Species-specific response of desert rodents to human-induced landscape change from desert to steppe

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During 22 years we have studied population dynamics of desert rodents under landscape change from desert to steppe caused by the drastic reduction of the livestock in southern Russia after the collapse of the USSR. The population of mesophilic folivorous tamarisk gerbil, *Meriones tamariscinus*, a food and habitat specialist, first quickly increased in numbers and range in response to desert contraction and vegetation recovery, but then, along with further steppe expansion, drastically declined and finally went extinct. On the contrary, the population of a psammophilous granivorous midday gerbil, *Meriones meridianus*, a food and habitat generalist, hasn't showed immediate response and has remained robust to landscape change from desert to steppe for over 10 years, and only then experienced a step-like transition from the high- to low-abundance density-regulated equilibrium, where it stays until now showing no response to increasing grazing. The inertia in response to changing environment shown by *M. meridianus* in contrast to *M. tamariscinus*, corresponds to its ecological generalism, which can enhance a species resilience to exogenous perturbations allowing to cope with changing environment and stay in the same regime until the critical level of change is reached. This is a rare well-documented demonstration of a threshold response of a wild unexploited mammal population to landscape change caused by socio-economic perturbations, which may shed light on the mechanisms of resilience of biological system in a changing world and underlying causes of threshold population dynamics.

The effects of vole population variability on annual productivity of barn owls: testing Jensen's inequality using a predator–prey system

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Environmental variability has long been known to affect ecological processes and individual fitness. The nonlinear responses of organisms to environmental variability are prevalent in biology. As a consequence, their long-term response measured as the average in a long run is inevitably either higher or lower than that measured in a less variable or constant environment. This results from Jensen's inequality stating that for a non-linear function $f(x)$ the average function $\overline{f(x)}$ does not equal to $f(\bar{x})$. Based on this reasoning, life history theory predicts that temporal environmental variability in food resource availability can affect the long-term organism's response (e.g., production of young) negatively if the response function is decelerating (concave down). Birds feeding on small herbivore voles whose population numbers fluctuate greatly in time represent a useful model system to test this theory. We used the system barn owl (*Tyto alba*)–common vole (*Microtus arvalis*) to study the responses of the barn owl annual productivity to common vole population variability in central Europe. This type of response function has been shown to be concave down in white storks or Montagu's harrier. Using the data on productivity (the number of fledglings) of barn owls and vole numbers from the period 2000–2014, we show that the response function is linear, suggesting no effects of vole population variability on a long-term mean in owls' productivity. However, we proved that the precision (e.i., synchrony) of the response did increase with vole population variability.

A monitoring program for the edible dormouse (*Glis glis*) in the Iberian Peninsula

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Biodiversity monitoring programs represent a useful tool to understand the status of the natural systems and to evaluate the causes of the changes in our territory. The edible dormouse (*Glis glis*), is a small arboreal mammal whose populations undergo awesome variations at both temporal and spatial scales related to the availability of food resources (i.e. energy-rich seeds). This species can be used as a bioindicator of environmental change owing its strong association with deciduous forests, and knowing that climate warming is producing its habitat retreat. There are many studies about this species in Europe, but knowledge about status and distribution of Iberian populations is limited due to the lack of specific sampling methods. As a tree-dwelling species, the edible dormouse is rarely captured with traditional trapping methods (Sherman, Longworth, etc.) set at ground level; on the contrary, this small mammal rapidly accepts nest boxes placed on trees. Around this situation, in 2004 we settled the basis of the first monitoring program using specific nest boxes for arboreal mammals in Catalonia (NE Spain). This monitoring protocol has continued to date with a significant increase of sampling stations (66 active from a total of 83) due to the involvement of volunteers ($n = 14$) around Catalonia, Andorra, Basque Country and Galicia. The sampling units are plots (20 boxes per grid) or lines (6 nest boxes), checked from a minimum of two times a year (one per month), to a maximum of every two weeks during the active period (summer and autumn) and one time during the inactive period (box cleaning). The aim of this protocol is offering a flexible methodology to be able to include both professionals and volunteers in order to obtain robust information from quantitative data (capture-recapture) combined with qualitative (presence-absence) data without needing dormice handling.

A monitoring protocol for the Spanish small mammal biodiversity (SEMICE) in the light of environmental change

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Biodiversity monitoring programs have been implemented worldwide as a source of information on human-induced environmental change. However, controversy concerning the indicators that should be monitored, and the development of adequate monitoring protocols for multi-species communities still hamper such implementation, especially in the case of small mammals. We present the protocol and results of the Spanish small mammal monitoring scheme (SEMICE, acronym of SEguimiento de MICromamíferos Comunes de Espana) for the period 2008–2016. This program is based on monitoring common small mammal species—those which are important in ecosystem functioning (i.e., food webs and seed dispersal)—but also rely on the “citizen science” contribution, that is, by including volunteers in the development of the scheme. The monitoring protocol was started in Catalonia (NE Spain) and has continued until date with a significant increase due to involvement of non-professional people (a total of 75 stations and more than 100 volunteers in Spain). The protocol follows a compromise between sampling effort and results obtained, trying to reduce plot size and sampling duration to a minimum affordable by volunteers. The sampling design consists on a 36 grid of Sherman/Longworth traps, set for three consecutive nights, and two sampling sessions a year (spring and fall). During the study period, we captured 6,568 small mammals of 23 species. The most frequent species was *Apodemus sylvaticus* (50%), followed by *Crocidura russula* (18%), *Mus spretus* (10%), and *Myodes glareolus* (8%). The other 19 species showed frequencies lower than 3%. High detectability of common small mammal species by the sampling methods used would allow the establishment of robust monitoring programs for the involved species, owing their important function in the terrestrial ecosystems. (With financial support of Fundación Biodiversidad from Ministerio de Agricultura, Alimentación y Medio Ambiente de Espana.)

Viral pathogens in exotic and indigenous squirrels, Central Europe

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The network “Rodent-borne pathogens” is investigating different zoonotic pathogens in rodent reservoirs, and has been involved in the discovery of novel rodent-specific viruses. For the identification and characterization of novel pathogens a work-flow was developed based on initial open-view methods such as necropsy, histopathology, next-generation sequencing and subsequent real-time and conventional (RT-)PCR-based detection methods. In 2013, a novel squirrel associated adenovirus has been found in a red squirrel (*Sciurus vulgaris*) from Germany which suffered from acute diffuse catarrhal enteritis. Furthermore, a novel zoonotic bornavirus was identified in a variegated squirrel (*Sciurus variegatoides*) in a private holding; the variegated squirrel 1 bornavirus (VSBV-1) has caused lethal encephalitis in three squirrel breeders in Germany. An ongoing investigation of squirrels of different subfamilies by PCR-screening and sequence determination revealed additional VSBV-1 positive variegated squirrels, but also Prevost’s squirrels (*Callosciurus prevostii*) in several holdings in Germany and the Netherlands. All infected animals were clinically healthy, but high genome loads were detected in brain, kidney and skin. During the 2015/2016 winter-season, a disease outbreak was observed in red squirrels at rescue centres for wildlife in different regions of Germany with high mortality in young animals. By using a novel real-time PCR targeting the adenoviral polymerase gene, viral DNA was detected predominantly in the intestine, but also in liver, lung and kidney samples of affected animals. In conclusion, the recent disease outbreak in red squirrels indicates a broad distribution of squirrel adenovirus and highlights the necessity of continuous wildlife surveillance. The multiple detection of VSBV-1 in variegated squirrels and Prevost’s squirrels underlines the urgent need for a broader search on the origin of this novel virus and to develop public health measures.

Rethinking omnivory in rodents

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The diets of animals reflect their evolutionary adaptations and ecological roles. Mammals have been studied intensively, but the criteria used to define discrete diet classes are inconsistent. Although all rodents share a conserved suite of craniodental features that form a mechanical complex for gnawing, they are highly diversified from an ecological viewpoint. Classifications of rodent diets condense data on stomach or cheek-pouch contents, the contents of food caches, behavioural observations, or faecal analysis. The most common approach has been to designate species as herbivorous, carnivorous or omnivorous, in which omnivores consume both plant and animal matter. A more meaningful classification should consider the ecomorphological and evolutionary implications of consuming different food items. This work describes how recent studies have defined splits within herbivorous and carnivorous taxa. Biologically-relevant categories reflect the adaptive implications of consuming fibrous plant parts, nonfibrous plant parts, soft-bodied invertebrates, small vertebrates, or chitinous invertebrates. With some exceptions, most rodents are generalized herbivores that consume various nonfibrous plant parts (fruits, seeds, gum, nectar), and will opportunistically consume animal matter, lichens, or fungi. These generalized herbivores are by definition omnivorous, so an additional category is redundant and will introduce biases if it is used in studies that use categorical variables, such as discriminant analyses or state-dependent models of speciation and extinction rates.

Spatial patterns of activity in the giant root-rat (*Tachyoryctes macrocephalus*), a fossorial rodent endemic to the Bale Mountains, Ethiopia

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The spatial organization of individuals is one of the principal aspects of species' ecology providing important information about social organization, territorial behavior and habitat use. Fossorial rodents are characterized by limited mobility confined to their self-constructed underground burrow systems. Despite the limited mobility, their spatial organization is neither random nor stable, but is affected primarily by seasonal changes in ecological conditions. A solitary fossorial rodent, the giant root-rat, inhabits grasslands in afro-alpine zone of Bale Mountains in Ethiopia. It lives under relatively high population densities (60 individuals/ha) which is surprising with respect to both body size (weight exceeding 1 kg) and relatively low food supply in the afro-alpine ecosystem, especially in the dry season. Our aim was to reveal root-rats' home range dynamics and factors which affect it using radio-telemetry. In total, 28 individuals were radio-collared and their spatial movements monitored in two periods corresponding with the early dry season with relatively accessible food and late dry season with lower food supply. Our results show that size of home-ranges changed seasonally according to sex. While the average size of females' home-range slightly increased in the late dry season (from $89 \pm 22 \text{ m}^2$ to $96 \pm 22 \text{ m}^2$), males' home-ranges markedly decreased in size (from $98 \pm 29 \text{ m}^2$ to $63 \pm 21 \text{ m}^2$). This trend could imply that males exploited bigger space in order to search for females in the early dry season. Spatial activity differed also individually in relation to food supply and contrary to our expectations, individuals with higher food supply had bigger home-ranges in the late dry season. We also revealed that root-rats whose home ranges were located in the stripe along the periodic wetland and offered more food in the late dry season were significantly bigger than other individuals from the study population. This can indicate a strong competition for space.

Geographical physiological adaptation in energy and water metabolism in Mongolian gerbils (*Meriones unguiculatus*)

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Mongolian gerbils (*Meriones unguiculatus*) have a large-scale distribution in Inner Mongolian of China, Mongolia and the Baikal region of Russia. Precipitation decreases from east to west along this geographic gradient, and the landscape consequently transitions from typical steppe to desert steppe to desert. Precipitation and primary productivity are considerable environmental variables to affect animal survival and distribution in this area. Geographic physiological variations which related to energy and water metabolism are critical to animals' local adaptation and distribution. Gerbils in desert population had lower resting metabolic rate (RMR) and total evaporative water loss (TEWL) than mesic population. Serum metabolomics revealed that concentrations of five tricarboxylic acid cycle intermediates (citrate, cis-aconitate, α -ketoglutarate, fumarate and malate) were lower in desert population than mesic population. Gastrocnemius metabolomics and citrate synthase activity analysis showed a lower concentration of citrate and lower citrate synthase activity in desert population. The relative medullary thickness (RMT) serum osmolality, vasopressin concentration, and renal expression of AQP2 did not detected geographic variations, but showed phenotypic flexibility in renal morphology and osmoregulation when faced seasonal environmental variations. Further, under extreme water scarcity condition, Mongolian gerbils could have high efficiency in urinal, fecal and evaporative water loss, and up-regulate renal AQP2 protein.

Poster presentations



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Comparative phylogeography of the Somali-Maasai savanna in eastern Africa using small rodents as a model

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Somali-Maasai savanna is one of the least known African regional centre of endemism and information about genetic structure within species or alternatively, among closely related species is thus almost entirely missing. The lack of empirical data precludes to assess which historical climatic factors and geomorphological barriers have influenced the evolution of savanna biota in this part of Eastern Africa. Relevant information from model species can be useful also for understanding the history of our own species, because many crucial fossil(?) localities in context of human evolution are located in the Somali-Maasai region. Small mammals, and especially rodents, are very suitable model for phylogeographic reconstructions, because they are tightly linked to particular habitat type, they have low dispersal ability and high substitution rate of mitochondrial DNA. In the present study we analyzed genetic structure of three African rodent genera (*Acomys*, *Arvicanthis* and *Gerbilliscus*), which are common faunal element in the Somali-Maasai savanna. With fully Bayesian framework (*MrBayes*, *BPP*, *BEAST*) we identified new genetic lineages corresponding to putative new species requiring further taxonomic revision. Using combination of detailed distributional data with divergence dating, we propose the scenario of historical changes in the Somali-Maasai region identifying the most important barriers of gene flow in (e.g. mountain chains, large rivers or paleo-lakes in the Rift Valley), which have played important role in the evolution of savanna ecosystems in Eastern Africa during Plio-Pleistocene.

Comparison of neural stem cell activity in the adult brain of “lab” and “wild” mice

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The most widely used experimental animal is the “lab mouse” that derives from the western house mouse subspecies, *Mus musculus domesticus* (Rodentia: Muridae). Previous research has shown that stress and exercise can induce proliferation of adult brain Neural Stem Cells (NSCs). The aim of our study was to compare NSC activity in the brain of “lab” and “wild” mice; the former kept in controlled conditions of no stress and of limited external stimuli and the latter exposed to constant stress and physical activity due to predators, the search for food and complex intra- and interspecific interactions. Although the “lab mouse” has a diploid chromosome number of $2n = 40$, the “wild mouse” karyotype is characterized by the appearance of Robertsonian fusions: the joining of unpaired chromosomes at their centromeres, leading to the formation of bivalent chromosomes and causing a reduction in the chromosome number from the typical $2n = 40$ down to 22. Here, we compared the levels of proliferation and the appearance of progenitors of neuronal commitment (neuroblasts) in the major NSC niche of the adult mouse brain, located at the subependymal zone of the lateral wall of the lateral ventricles in “lab mice” and in three populations of Greek “wild mice” ($2n = 40$, 37 and 30) captured in N Peloponnese and SW Sterea Ellada. We found that “wild mice”, irrespective of karyotype, differed significantly from “lab mice”, showing increased density of total cells, of proliferating cells and of neuroblasts. These results indicate that levels of NSC activity in “lab mice” are sub-natural, probably due to their maintenance in controlled lab conditions and they raise concerns as to whether we can extrapolate research findings in pharmaceutical or clinical applications. Finally, we also found significant differences between the $2n = 30$ and both the $2n = 40$ and $2n = 37$ wild populations, suggesting an effect of either their chromosomal constitution or their narrow geographical collection region on neurogenic activity.

Preliminary results on the cytogenetic study of wild populations of the blind mole rat (*Nannospalax*, Spalacinae, Rodentia) in Greece

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Many mammalian species are characterized by a rather impressive chromosomal diversity, which is the result of chromosomal rearrangements. Such diversity can possibly hamper genetic flow between chromosomally different populations and even initiate speciation events. The blind mole rat species of the genus *Nannospalax* are a typical example of such chromosomal diversity, with dozens of distinct chromosomal races that have been described throughout Europe and Asia. Nevertheless, in Greece, despite the extended range of occurrence of the genus, only a handful of old cytogenetic studies exist based on conventional staining techniques. Those few studies have revealed the existence of three different chromosomal races, attributed to *Nannospalax leucodon*, each from a different part of mainland Greece and characterized by $2n = 52/NF = 86$, $2n = 56/NF = 84$ and $2n = 58/NF = 88$, respectively. Moreover, Lesvos Island, E Aegean region, has been found to possess $2n = 38/NF = 74$, a karyotype similar to those of Asia Minor populations of *N. xanthodon*. Even though these little data predispose for a very interesting and complex case of chromosomal diversity in Greece, most of the *Nannospalax* wild populations still remain unstudied. Therefore, this study aims at investigating in detail the chromosomal diversity of the populations of the genus in Greece, both insular and continental, with the use of G-banding, C-banding and Ag-NOR staining techniques. Based on our results, we will try to uncover the chromosomal evolution of the different races of the genus *Nannospalax* in Greece, as well as their relationship to the other European races. Until now, our preliminary results include data from Lemnos Island, E Aegean region, where the mole rats seem to be characterized by $2n = 38/NF = 74$, which allocates the respective population to *N. xanthodon*, along with the population from Lesvos island. This result is rather unsurprising, based on the zoogeographical relation of these two islands with Asia Minor.

Reduction of body size in field vole (*Microtus agrestis*)

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A number of studies have shown that the body sizes of many species decline in response to climate change. To assess such a change, it is necessary to evaluate the geographic component (Bergmann's rule), as animals become larger (or smaller in some shrew species) to the north. Using museum and recently trapped specimens, we studied temporal and latitudinal trends in body and skull size of the field vole (*Microtus agrestis*). Our sample consisted of nearly 300 individuals trapped in 1968–1996 and 2014–2015 in Lithuania and over 100 individuals trapped in Estonia in 1980–1994. We tested if differences in body and skull character size were present and, if so, whether these differences were associated with latitude (53.9–56.3°N in Lithuania and 57.7–59.5°N in Estonia) or time (trapping period). We used 23 skull characters and five body measurements. Body condition was evaluated as an index based on the ratio of body weight and body length. ANOVA analysis showed that differences in the sizes of voles trapped in the same time period in Lithuania and Estonia were not significant. However, voles became smaller in Lithuania in the last decades (Tukey HSD test, $p = 0.005$). Nine skull characters were significantly reduced in size, among them condylobasal length of the skull (25.1 ± 0.13 vs. 24.0 ± 0.28 mm, $F_{1,157} = 11.54$, $p < 0.001$), length of mandibula excluding incisors (12.7 ± 0.07 vs. 12.4 ± 0.10 mm, $p < 0.05$), zygomatic skull width (13.5 ± 0.08 vs. 13.2 ± 0.11 mm, $p < 0.04$) and height of the braincase (9.7 ± 0.04 vs. 9.3 ± 0.12 mm, $p < 0.001$). A decrease in body mass (29.4 ± 0.64 vs. 24.9 ± 0.98 g, $F_{1,274} = 11.19$, $p < 0.001$), body length (100.1 ± 0.85 vs. 93.3 ± 1.40 mm, $p < 0.001$) and ear length ($p < 0.05$) was also observed. An increase was only found in body condition (2.88 ± 0.03 vs. 3.05 ± 0.05 , $p < 0.01$). We agree with other authors attributing such changes to climate warming, but habitat conversion and pollution could have an influence.

Matrilysin (MMP-7) immunodetection in the seminal vesicle of the Libyan jird (*Meriones libycus*) during the seasonal reproductive cycle and after orchiectomy

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An immunohistochemical study of matrilysin (MMP-7) using the indirect method with streptavidin-biotin-peroxydase was carried out on the vesicle seminal of a nocturnal Saharan rodent, the Libyan jird (*Meriones libycus*) in order to investigate their involvement in the physiology of this organ and in the seasonal reproductive cycle. The animals were collected from their natural habitat (Béni Abbès, Algerian Sahara) during the breeding period (spring and early summer) and the resting phase (late of summer, autumn and late of winter) of the seasonal sexual cycle. The castration was performed in the spring after ether anesthesia and castrated *Meriones* were euthanized a month later. In the breeding period, the immunohistochemical signal of the MMP-7 was intense and essentially localized in the epithelial cells and smooth muscle cells with no immuno-response in the extracellular matrix and the secretion that abundantly fills the seminal vesicle lumen. In the quiescence phase and after castration the same profile of immunostaining was observed. In the castrated animals the epithelial fold axis was enlarged and show a slight dispersed immunoreaction. Similar results were obtained by Filonzi et al. (2007) and Cardoso et al. (2010) in rat vas deferens. MMP-7 have a physiologic function in the Libyan jird seminal vesicle and may be involved in the tissue remodeling associated to the seasonal reproductive cycle as has been demonstrated for Siberian hamster ovaries (Shahed et al., 2015). MMP-7 could also be related to the fertilization process as it was postulated by Ferrer et al. (2012, 2016) which have demonstrated an MMP-2 presence in the inner acrosomal membrane at the moment of acrosome reaction.

Hyperhomocysteinemia, oxydative stress and remodeling of epididymis of Wistar rat

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Hyperhomocysteinemia, defined by elevated plasma homocysteine (Hcy) level, is associated with many diseases affecting various organs structure (Heart, Kidney, Liver, Uterus...). The oxidative stress seems involved in these tissular changes. The tissue response to the injury includes the activation of matrix metalloproteinases (MMPs) and remodeling of the extracellular matrix. The aim of the study was therefore to investigate whether Hhcy involve a oxidative stress and has an effect on the extracellular matrix of the epididymis of Wistar rat. Wistar rats divided into two: a Control group, which received diet standard and tap water; the Experimental group received the same diet and water supplemented with solution of L-methionine (1 g/Kg body weight/day) for 1 month. Plasma homocysteine was measured. We quantified the MDA, product of lipid peroxydation and activity of catalase. The metalloproteinases (2 and 9) in the epididymis was estimated by zymography completed by densitometric analysis. The excess of methionine does not seem effecter the body weight as well as the weight relative and absolved from the epididymis. Methionine supplementation caused a significant increase in the plasma homocysteine levels. In the proximal and distal epididymis of hyperhomocysteinemic rats, an oxidizing stress marked by an increase of the MDA associated with a decrease of the activity of the catalase was observed. Our results reveal, in the group Met, an increase of the expression of the MMP2 (56 at 62%) and the low expression of MMP9 and proMMP9 characterizes the remodeling of extracellular matrix of epididyme. Hyperhomocysteinemia leads a oxidative stress and remodeling of the extracellular matrix of epididymis in Wistar rat.

Pancreatic response to a hyperhomocysteinemia to the sand Rat, *Psammomys obesus*

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The sand rat, *Psammomys obesus*, diurnal rodent which lives in the south east of the Algerian Sahara is an excellent animal model for research (atherosclerosis, diabetes, obesity...). Hyperhomocysteinemia (Hhcy), defined by elevated plasma homocysteine level, is associated with many diseases affecting various organs (heart, vessels, liver...). The aim of the study was to investigate whether Hhcy has an effect on the pancreas of sand rats (*Psammomys obesus*). The *Psammomys obesus* were divided into two groups: a Control group received their natural diet with halophile plant of the Chenopodiaceae family (*Suaeda mollis*,) and a Experimental group received the same diet and methionine at the rate of 150 mg/Kg of body weight/day during 6 months. Blood samples obtained from retro-orbital sinus were used for the estimation for homocysteine by Fluorescence Polarization Immunoassay (Abbott AxSYM system). A histological and histochemical analysis of the pancreas of the sand rat was completed by a morphometric study. The excess of methionine led to a hyperhomocysteinemia at *Psammomys obesus*. We observed at the pancreas of the hyperhomocysteinemic sand rats, matrix, cellular and vascular changes. The changes of the extracellular matrix are marked by an accumulation of fibrillars collagens and glycoproteins leading to a fibrosis. This accumulation is observed in the in islets of Langerhans and in the exocrine pancreas (intertitial tissue, around blood vessels and channels excretors). A phenotypic modulation of endothelial cells, a disorganization of the vascular wall and a steatosis micro- and macrovesicular are also observed in the pancreas of hyperhomocysteinemic *Psammomys obesus*. The hyperhomocystéinémie generated by the excess of méthionine leads to a remodeling of the pancreatic extracellular matrix of *Psammomys obesus*.

Microsatellite-based genetic diversity of Turkish yellow-necked fieldmouse (*Apodemus flavicollis*) populations

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Habitat barriers (human-induced or natural) are considered to be an important environmental factor leading to the local reduction of genetic diversity by dividing a population into smaller parts and hindering gene flow among them. Located at a crossroads between Europe and Asia, Turkey's land mass contains various habitat barriers such as Bosphorus and Dardanelles between two continents or mountain chains. The aim of the present study is to detect the role of habitat barriers in developing the genetic structure of yellow-necked fieldmouse (Melchior, 1834) populations in Turkey. For this purpose, within and among population genetic diversity in 17 populations from Anatolia and Thrace were analyzed based on 7 microsatellite loci. Various statistical methods (Analysis of Molecular Variation, Neighbour-Joining tree construction, Factorial Correspondence Analysis (FCA), Structure Analysis and BAPS Analysis) were employed. Results revealed that genetic diversity is high within and among populations. According to NJ, FCA, Structure and BAPS analysis, Anatolian and Thrace populations were differentiated genetically by the barrier effect of Bosphorus and Dardanelles. On the other hand, the determination of similar haplotypes from different localities of Anatolia and the mixed groupings of Anatolian haplotypes in NJ tree and FCA graph revealed the inefficiency of terrestrial barriers (mountains) and human induced barriers (motorways, railways) to prevent gene flow between *A. flavicollis* populations, as the yellow-necked fieldmouse is a highly mobile species that can cross the terrestrial barriers easily to maintain local genetic variation. This study was supported by the Scientific Research Project Office (No: 12B4240013) of Ankara University.

European beaver (*Castor fiber*) on the south-eastern Slovakia: first evidence of new migration route from Hungary

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From 06 to 10 June 2016, during fieldwork, the first records of the European beaver (*Castor fiber*) in south-eastern Slovakia were recorded. Beavers are nocturnal animals, and as such, they are rarely observed, therefore the monitoring of their population was mostly indirect. It was based on searching for harmed trees. The southern part of Košická kotlina basin from Kosice city down and surrounding villages in Hungary had been controlled. We found isolated location of beavers by harmed trees in the vicinity of Slovakia/Hungary state border (Milhost' village, 48°31'47.3"N, 21°17'15.8"E, 156 m a.s.l.). The harmed trees were found on the coast of the lake water (Kechnecké štrkovisko), as well as in the confluence of two streams (Szartos patak and Sokoliansky potok) from Hungary and Slovakia. Based on the number of harmed trees and their average size (Djakov 1975), we estimated the number of beavers on 3 individuals, which corresponds to one family. According to local fishermen, the first occurrence was observed in autumn/winter 2014/2015. Therefore, we assume that this isolated occurrence at the state border represents the beginning of the spread of probably over Hornád river.

Social transmission of food preferences in wild *Mus spretus*

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Social information plays a major role in many of the animals' decision-making processes. When it comes to food choices, a trial-and-error strategy can often end up being a deadly one, making social learning of food preferences an important alternative. Knowing that, changing animals' food habits using social transmission could be an important tool for in-situ management of endangered species. Using an experimental paradigm of social transmission of food preferences, with an already validated methodology performed in laboratory rats and house mice, we developed an experiment with wild Algerian mice (*Mus spretus*), to understand whether wild animals are similarly influenced by their conspecifics' food preferences. By developing a horizontal transmission test, we were able to demonstrate that preference for a novel food was transmitted after social interaction with a conspecific that had eaten that food. Additionally, mice maintained the acquired preference after a 30-days period without contacting with the food, suggesting preference has a long-term persistence and will probably be maintained over time. Currently we are carrying an additional experiment – vertical transmission test, to determine if preference for a novel food is transmitted from mother to offspring during pregnancy and nursing. Using wild *Mus spretus* as a case study, we hope to create a new management tool that could eventually be applied to species conservation. Our aim is to show that knowledge about the social transmission of food preferences in rodents could be used to change and hence control the feeding habitats of these species in the wild. This method can potentially represent a reduction in costs, while promoting the use of alternative and less invasive methods.

Effect of acorn crops on populations of yellow-necked mouse (*Apodemus flavicollis*) and bank vole (*Clethrionomys glareolus*) in the South of Moravia between 2002 and 2012

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Yellow-necked mouse *Apodemus flavicollis* – AF) and bank vole (*Clethrionomys glareolus* – CG) are usually the most frequent rodent species in Central European forests. Their populations were monitored with crops of acorns at three sites in southern Moravia (south-east of the Czech Republic) for 11 years (2002–2012). Major acorn crops were found in 2003, 2006 and 2009; minor crops were in 2010 and 2011; crops were none or minimal in the remaining years. An extension of regular breeding period until winter after the major crop in 2006 was found in both species. In some cases, the average body size (weight and length) of both species changed significantly after the acorn crops. The reaction to acorn crops among populations of both species was significant but statistically different. Relative abundance of the AF had a wider amplitude and its linkage to acorn crops was more conclusive than in the CG. A statistically significant increase in the relative abundances of AF was recorded in 2004 and 2007, i.e. a year after major crops. Within series of minor crops, AF abundance either remained unchanged (2012), or even fell (2011). Consecutive acorn crops in 2009–2011 did not result in infestation or proportional increase in AF abundance, but in stagnation of population during the following years. Dominance of the AF in all areas gradually decreased in favour of the CG. In a floodplain forest, this process was the fastest: CG was the most dominant rodent species from March 2010 until the end of the monitoring. Among two remaining sites, the AF stayed the most dominant species but its superiority was significantly lower at the end of the monitoring than at the beginning. We can only speculate about the cause of such phenomenon. It can be associated to more frequent but less intensive acorn crops, or to rainfall deficiency across the whole region in recent years.

Genetic structure of *Allactaga* (Mammalia: Rodentia) species distributed in Turkey inferred from the partial cytb gene

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Habitat barriers (human-induced or natural) are considered to be a genus *Allactaga*, also known as the jerboa, is presented by 3 species as *A. williamsi*, *A. elater* and *A. euphratica* in Turkey. Although the relationships among these species were identified morphologically, the validity of the species and subspecies of this genus have not been precisely clarified by the molecular data. The aim of the present study is to survey the genetic structure and the validity of *Allactaga* populations distributed in Turkey inferred from 458 bp of the mitochondrial DNA cytochrome b (Cytb) gene. In this study Mega v.7 was used to generate phylogenetic trees. DnaSP v.5.1 was used to estimate the haplotype and nucleotide diversities, and the mismatch distributions. The relationships among haplotypes were detected using the median-joining method (Network v.4.6). Arlequin v.3 was also operated to compute the neutrality analysis as Tajima's D, Fu's Fs and also AMOVA. Our results reveal the existence of 3 species of *Allactaga* in Turkey supporting the morphological data. On the other hand, subspecies of *A. williamsi* is complicated that *A. w. shmidtii* grouped both *A. w. williamsi* and *A. w. laticeps*. Thus the validity of *shmidtii* has become problematic and might be denied. Further studies including genomic data could be clear up the subspecies of *A. williamsi*. This study was supported by The Scientific and Technological Research Council of Turkey (TUBITAK Project no: 114Z941).

Phylogenetic relationships among Gliridae (Mammalia: Rodentia) species in Turkey and the Balkan Peninsula inferred from mitochondrial CO1 gene

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The family Gliridae is represented by 9 genera and 28 species. The aims of the present study are to determine the phylogenetic relationships among the investigated species of the family Gliridae inhabiting Anatolia and the southeastern part of Balkan Peninsula, and to study the phylogeographic relationships among populations of investigated species. Mitochondrial CO1 region of 139 specimens belonging to *Glis glis*, *Dryomys nitedula*, *Dryomys laniger*, *Myomimus roachi* and *Muscardinus avellanarius* from 24 localities of Turkey and Bulgaria were examined. In order to determine the phylogenetic relationships of species, Neighbour-Joining (NJ), Maximum Likelihood (ML) Maximum Parsimony (MP) and Median-Joining (MJ) analyses were conducted. Forty-nine haplotypes were detected. The results of our analysis revealed no apparent genetic difference among *D. nitedula* populations of the southeastern part of the Balkan Peninsula and Anatolia. We found similar results about the genetic relationships for the populations of *G. glis*. The results we obtained as a whole contributed significantly to our understanding of the phylogeographic relationships between populations of investigated species. This study was supported by The Scientific and Technological Research Council of Turkey (TUBITAK) and Bulgarian Academy of Sciences, Sofia (Project no: 113Z822).

Renal gene expression of the long-haired mouse *Abrothrix hirta* (Sigmodontinae) in contrasting environments of southern South America

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Here I present results of a comparative analysis of renal gene expression of specimens of the long-haired mouse *Abrothrix hirta* from natural populations exposed to contrasting levels of water availability (i.e., forests and steppes). An RNA-seq approach conducted on 40 specimens identified genes and genetic pathways involved in renal water homeostasis. Financial support: FONDECYT 1141055

Population dynamics of common voles in a semi-natural, constant environment at an airport in eastern Germany

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Small mammals at the premises of airports can pose a risk because they can attract predatory birds that may collide with landing and starting airplanes. The population dynamics of small mammals were studied at airfield greens at Leipzig-Halle International Airport to identify specific times of increased bird strike risk. From 2012 to 2014 the population dynamics of small mammals were investigated by capture-recapture. In each of 6 evenly distributed plots (0.10–0.14 ha) small mammals were trapped once a month (Mar–Oct/Nov) for 2½ days in a grid of 49 live traps with 10 × 10-m spacing. Animals ≥10 g were PIT tagged and lighter individuals were marked with individually numbered ear tags. As expected, common voles were always highly dominant in numbers (87–99% of trapped animals, $n = 2,267$ common voles). The population dynamics showed several typical phases of the common vole cycle including an outbreak in 2012 when the entire region (Thuringia, Saxony Anhalt, Saxony and Brandenburg) experienced high common vole abundance. In 2013, the population crashed and slowly recolonized some of the plots. In 2014 all plots were recolonized by June with exponential population growth afterwards to up to 1,800 ind./ha. Although all plots appeared homogenous due to identical pasture management there were marked differences in the dynamics of recolonization and the following population growth (including reproduction). At the airfield greens common vole populations follow a similar pattern as voles in the surrounding agricultural habitats. During population outbreaks (2012, 2014) the high densities of common voles had to be regarded as critical and have warranted management action, because they may attract high numbers of birds of prey to the airport that can pose a risk to air traffic.

Seasonal effects on the gonadal steroids receptors expression in the seminal vesicles of the Libyan jird: *Meriones libycus*

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The Libyan jird (*Meriones libycus*) is a nocturnal Saharan rodent. The male shows a period of total testicular regression in autumn followed by a maximum regrowth in spring. The aim of the present study was to localize the androgen receptors (AR) and the estrogen receptors (ER α and ER β) during the seasons in the seminal vesicles of Saharan rodent, *Meriones libycus*. Adult males were caught in their natural environment (region of Beni Abbes (30°7'N, 2°10'W)) during two periods of the annual reproduction cycle. Immunohistochemistry was carried out on paraffin-embedded tissues using a rabbit polyclonal IgG antibody as the primary antibody and a biotinylated antibody as the secondary antibody. Avidin-biotin-peroxidase complex was then applied followed by diaminobenzidine. Our study demonstrates variations in the distribution of Androgens receptors (ARs) and estrogens receptors (ER α and ER β) in the seminal vesicles as well as changes in immunostaining levels during two periods. ARs are localized in glandular epithelium and stroma. Although, ER α expression is usually localised in the stromal cells. However, ER β is mainly expressed in the epithelium. Androgens and oestrogens are thus involved in homeostasis and the physiology of this gland. They shall participate certainly in the success of the reproduction of this rodent.

Searching for signatures of genetic adaptation to climate in microtine mammals

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Temperature and patterns of precipitation are changing on a global scale. This has strong effects on many existing species, influencing the physiology, behavior and range of many populations. In contrast to these ecological effects of climate change, evolutionary responses to climate change are less well studied. With ongoing climate change, adaptation has recently become the focus of much ecological genomic research. Differences in climatic variables between environments influence the spatial distribution of phenotypic and genetic variation across a meta-population which can lead to local adaptation. Thus, the detection of climate-mediated evolutionary responses can potentially shed light on the genetic basis of adaptation to climate change. Up until now, most studies have been restricted to livestock, model species, or species with a fully sequenced genome. But little research has been done on microtine mammals like voles, despite the fact that they are widespread and encounter many contrasting climates. Therefore, the aim of this study is to uncover signatures of genetic adaptations to climatic variables among natural populations of voles. Voles are small rodents; they are widespread throughout Europe where they inhabit farmland or forest habitats from sea level up to 2000 m. altitude in the Alps. They are characterized by very large levels of genetic variation and relatively strong genetic differentiation across Europe. To find signatures of genetic adaptation to local climate we will be searching for co-variation between genetic loci and different climatic variables over different gradients. We will scan the genome for SNP variability among different populations using a RADseq approach using pools of individuals. A variety of tests will be used to analyse the data based on differentiation of SNPs and co-variation between genomic and climatic variables. First results will be presented.

Non-invasive fluorescent technology for monitoring of rodents

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Methods of monitoring of rodent spatial activity must cope with nocturnal activity and hidden way of rodent life. Many techniques rely on indirect signs of rodent activity such as presence of droppings, urine, footprints and gnawed food/materials. Despite the above mentioned simple methods, various fluorescence-based methods (e.g. dusts) were also applied for rodent detection. However, most of these methods are time consuming, expensive and require a capture of the animal. The recently developed fluorescent commercial bait brings new possibilities for simple rodent monitoring. After ingestion of the fluorescent bait, rodents produce brightly fluorescent faeces that are easily detectable by pocket ultraviolet torch. Since the bait is non-toxic, it may be employed by both pest control operators and ecologists/ethologists in their field studies. We tested palatability of this fluorescent non-toxic bait in a wild population of commensal house mice (*Mus musculus*) in laboratory conditions. Using two-choice feeding tests with fluorescent non-toxic bait as one choice, the mice were offered wheat or barley grain as an alternative food source. The results showed that the tested mice preferred to consume fluorescent bait over both types of introduced grains. It indicated good palatability of the tested bait that should ensure the bait consumption by commensal and wild mice populations even in environments where alternative food is abundant.

Prevalence of zoonotic pathogens in common vole (*Microtus arvalis*) during a demographic explosion

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There are several rodent-borne zoonoses of public health concern. For some of these, rodents play a key role as a source for humans and transmission risk may be density-dependent. The common vole (*Microtus arvalis*) was originally restricted to mountainous areas of northern Spain but the species has completely colonized the Spanish Northern Plateau during the last 30 years. Common vole populations experience cyclic demographic explosions that relate to increasing incidence of vole-borne zoonoses in coexisting humans, e.g. tularaemia. However, there is scarce information on other zoonotic pathogens circulating in common vole populations and coexisting wildlife, and consequently on the risk that sudden demographic changes pose to human health. In this study, 276 spleen samples collected from common voles ($n = 253$, 92.3%) and coexisting wild rodents, wood mouse *Apodemus sylvaticus* ($n = 19$, 6.9%) and greater white-toothed shrew *Crocidura russula* ($n = 3$, 1.1%) were analysed for zoonotic pathogens. Wild rodents included in this study were captured in 2014 from a population experiencing demographic explosion. Spleen samples were screened for the presence of *C. burnetii* – the causal agent of animal and human Q fever, *Leishmania* spp. and *Borrelia* spp. by PCR. Pathogen DNA was not detected in spleen samples from coexisting wood mice and greater white-toothed shrews, perhaps due to low sample size. In voles, prevalences of *C. burnetii*, *Leishmania* spp. and *Borrelia* spp. were 12.2%, 1.2% and 0.0%, respectively. *Coxiella burnetii* prevalence was slightly higher than that found in the same population 2 years before (8.0%), suggesting that perhaps increasing vole density increases *C. burnetii* transmission and therefore the risk of transmission to other animals and humans. Future risk factor analyses on pathogen prevalence data would clarify if density-dependent effects modulate the rate of *C. burnetii* transmission in common vole populations.

Molecular phylogeny of African striped grass mice (genus *Lemniscomys*)

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Murine rodents form one of the most diverse, evolutionary successful as well as important group of extant mammals, due to the significant role as vectors and reservoirs of zoonoses or agricultural pests. The fast and relatively young diversification impede our understanding of phylogenetic relationships and species delimitations of many murine taxa. The striped grass mice (genus *Lemniscomys*) are distributed throughout Africa in 11 currently recognized species. These are separated in three morphological groups characterized by different shape and numbers of stripes on the back: a) group *L. barbarus* (*L. barbarus*, *L. zebra* and *L. hoogstraali*) with several continuous pale longitudinal stripes; b) group *L. striatus* (*L. striatus*, *L. macculus*, *L. bellieri* and *L. mittendorfi*) with pale stripes diffused into short lines or dots; and c) group *L. griselda* (*L. griselda*, *L. rosalia*, *L. roseveari* and *L. linulus*) with a single mid-dorsal black stripe. We describe phylogenetic relationships between *Lemniscomys* species using mitochondrial and nuclear markers (cytochrome b and IRPB, respectively) by combining new and already published sequences of nine species. The results show four main lineages which do not always correspond to the phenotypic groups: a) *L. striatus*; b) *L. griselda* and *L. rosalia*; c) *L. bellieri*, *L. macculus* and *L. linulus*; and d) *L. mittendorfi*, *L. zebra* and *L. barbarus*. The species *L. zebra* is paraphyletic and includes *L. barbarus* as an internal lineage. Our results present the most comprehensive molecular phylogeny of the genus *Lemniscomys* to date and suggest the need of further taxonomic investigation and reconsideration of current species. The research was funded by GACR project No. 15-20229S.

Rodent food quality and its relation to crops and other environmental and population parameters in an agricultural landscape

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The diet, its quality and quantity considerably influence population parameters of rodents. In this study, we used NIRS methods for estimation of nitrogen content in stomachs of rodent populations. The study was carried out in diverse arable landscape in South Moravia, Czech Republic. Rodents were sampled in cultural crops (alfalfa, barley, wheat, sunflower, maize and rape) as well as in fallow habitats (herbal set-aside and old orchard). Influence of habitat, date, year, individual parameters (body length, sex, breeding and age), and relative abundance on quality of consumed food was studied. Under conditions of higher population density, dominant species (wood mouse *Apodemus sylvaticus* and common vole *Microtus arvalis*) consumed food richer in nitrogen. Also the strong effect of crop and date (season) was found in both species. There was no significant effect of the other parameters studied on food quality (N-content).

Tula virus in the common voles (*Microtus arvalis*) in the Czech Republic

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Populations of the common vole were investigated for the presence of TULV antigen using ELISA set Hantagnost. In total 1615 individuals in 19 localities were examined. The prevalence in this host species was 10.6%. Heavier individuals were more often hantavirus antigen positive. In all positive voles ($n = 170$), the females were dominant (65%). The highest number of TULV antigen positive voles was found in forage and winter crops in highly agricultural landscape, followed by grasslands. The prevalence of TULV antigen increases with its population numbers. As the population of the common vole, which is an important pest species in central Europe, regularly fluctuates, attention should be paid by farmers also from the epidemiological point of view.

Structure of small mammal communities on clearings in managed Central European forests

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Clear-cutting followed by direct planting currently remains the predominant forest management practice in managed forests in Central Europe. However, this practice may have a pronounced negative effect on the biodiversity of forest ecosystems including small mammals. In this study we investigated the effect of a range of environmental variables on diversity and structure of the small mammal community in relatively small-sized clear-cuts. During 2007–2010 the structure of small mammal communities was assessed at 198 small-sized clearings (up to 2 ha) in 11 areas of managed forest in the Czech Republic. The complete trapping effort was 75,072 trap-nights. Overall 8,542 small mammals belonging to 17 species were caught, including forest species as well as species of open habitats. The diversity and relative abundance of small mammal communities in these small clearings was comparable to that described in the literature for old mature forests. Differences in structure of small mammal communities in our study clearings were mostly influenced by habitat structure, primarily the structure of the herb layer, and partially by altitude (climatic conditions) and size of the clearing. No effect of geographic location (latitudinal and/or longitudinal effect) on small mammal community structure or diversity was detected. Our results indicate that the practice of felling within relatively small-sized clearings may help preserve the diversity of small mammal community in managed forests and might assist in maintaining forest biodiversity by comparison to the more widespread current practice of larger clear-cuts. Re-forestation using small-sized clearings would thus offer a compromise between economic and ecological approaches to forest management, protecting a higher biodiversity of forest ecosystems.

Genes involved in intragenomic conflict and their copy number variations in wild-derived house mice

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Strong intragenomic conflict between X- and Y-linked genetic elements in the house mouse genome has been supported by multiple studies. Work with laboratory strains revealed that multicopy genes (present in >10 copies per chromosome) are involved in this “sex battle”. Here, we focus on three such genes, X-linked Slx, Slx11 and Y-linked Sly. All have been reported to be locked in intragenomic conflict, where the ratio between the numbers of Slx & Slx11 vs. Sly copies seems to be crucial. Studies have shown that changes in functional copy numbers (CN) are accompanied by male sterility, segregation distortion and shifts in offspring sex ratio. The 2500 km long hybrid zone (HZ) between two house mouse subspecies, *Mus musculus domesticus* and *M. m. musculus*, is a natural laboratory for studying the outcome of such conflicts because, in areas along the HZ, asymmetrical unidirectional introgression of the *musculus* Y has been detected. To explore the potential of this system we estimated CN of these three genes in inbred strains derived from mice of both subspecies. We found considerable CN variation. *M. m. musculus* mice tend to carry higher CN for all three genes. It is interesting to speculate whether it is this “superiority in numbers” which has facilitated *musculus* Y introgression. To address such questions we plan to analyze Slx/y CN in wild mice from the Czech–Bavaria transect. In this area extreme introgression of the *musculus* Y chromosome has been detected, accompanied by reduction of female-biased distortion in the census sex ratio compared to the surrounding regions. This study was supported by GA15-13265S (SJEB, MM) & ESF CZ.1.07/2.3.00/20.0303 (ZH, AY, SJEB). We are very grateful to Prof. D. Tautz and N. Thomsen from Max Planck IEB for their help and guidance.

Influence of the habitat fragmentation on *Microtus oeconomus* performance in the Pannonian area where it has a status of the protected species

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The Pannonian root vole, *Microtus oeconomus mehelyi* (Éhik, 1928), is a glacial relict inhabiting wetland areas in Central Europe. Many of its populations seem to be endangered by habitat fragmentation or habitat loss. Draining of wetlands, building of ditches, damming or redirecting the rivers causes the loss of suitable habitats resulting in limited migration which increases the likelihood of extinction. Habitat fragmentation interferes with such important population parameters as immigration, emigration and effective population size. Therefore it is important for an appropriate conservation management to estimate the degree of population isolation at a genetic and ecological level. We lack knowledge of *M. oeconomus mehelyi*'s overall genetic condition in its current range of distribution in the Pannonian basin. In this research we intended to determine the genetic diversity and to reconstruct the genetic structure of *M. oeconomus mehelyi*. We genotyped samples from Slovakia (3 sampling sites, $n = 84$), Austria ($n = 24$) and Hungary ($n = 24$) using 14 microsatellites. Each sampling site represented one cluster with the exception of Hungarian samples from Szigetköz near Danube river. Individuals from this site obtained high membership probabilities to more than one cluster. Presumably, the river banks of Danube branches with hydrophilous vegetation improve the migration and regular floods within this area might increase spread of individuals by the passive transport. We found the inbreeding coefficient ($F_{is} = 0.211$) to be the highest and the allelic richness ($Ar = 5.543$) to be the lowest on the Slovakian site north of the Danube. The presence of a water dam in this region reduced migration resulting in high F_{is} and low Ar . The existence of barriers and migration corridors resulted in the specific genetic structure where genetic distances were not explainable by geographic distances (Mantel test, $r = 0.445$, $P = 0.190$). Acknowledgements: Research supported by LIFE 08 NAT/SK/000239

The reconstruction of the phylogeography of an invasive species: tracing invasions routes of Norway rat (*Rattus norvegicus*) using mtDNA control region

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The Norway rat, *Rattus norvegicus*, is a cosmopolite invasive species that moves especially following human routes and it is considered one of the worst pest, overall for native species, agriculture and foodstuff. This species reached Europe during XVIII century from Far East, but little is known concerning its invasion history and population structure in this area. Here we used the mtDNA control region to study pattern of invasion of *Rattus norvegicus* by a phylogeographic approach. We used 404 rat sequences, 193 collected from 55 localities from Europe, Africa, Middle East and Far East and 211 from 23 localities retrieved from GenBank. Despite the very recent invasion of Europe, the results show an unexpected high genetic diversity. Twenty-six haplotypes were recognized and we built a Statistical Parsimony (SP) network to identify the relationship between them and their geographical distribution. In the SP network, two groups show a star-like structure that suggest a populations expansion. This structure, corroborated by mismatch distribution, Tajima's D and Fu's Fs neutrality indices, suggest a recent sudden expansion of the populations in Europe, Africa and Middle East. In addition, the different geographical distribution of the haplotypes suggests the occurrence of two different invasion events in Europe possibly along two different colonization routes: an African route and a Middle East one. Furthermore, some haplotypes are shared between Europe and other invasive areas. This suggests to consider Europe as a possible new source area for *Rattus norvegicus*. For 117 specimens, 18 selected from our samples and 99 retrieved from GenBank, we performed an additional phylogeographic analysis using the cytochrome b as molecular marker. We built a network to identify the geographical distribution of the haplotypes again according to the SP method. The structure of the cytb network supports the hypothesis of at least two separate routes of colonization of Europe.

Revisited phylogeography of the yellow-necked mouse, *Apodemus flavicollis* (Melchior, 1834)

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Previous phylogeographic studies showed that southern European peninsulas served as refugial areas from where the recolonization of European environments started. We studied the phylogeography of the yellow-necked mouse, *Apodemus flavicollis*, covering its entire range in Europe, with higher number of samples from Balkan peninsula. The aims of the study were to re-examine the main haplotype groups and define respective Balkan refugia from Pleistocene glaciations. Haplotype analysis was performed on 299 nucleotide long sequence of cytochrome b gene, by median-joining network algorithm followed by maximum parsimony analysis. 192 sequences found at GenBank were aligned together with 27 sequences from new samples of *A. flavicollis* from Serbia, Montenegro, Romania, Turkey, and Russia. Haplotypes from Balkan peninsula segregated in several groups. The resulting haplotype network revealed possibility of numerous previously undefined refugia within Balkan peninsula and near Black Sea, and gave more insights into directions of recolonization processes.

Preliminary surveys of the small mammal fauna of the Natma Taung National Park (Mount Victoria) in Myanmar

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This study was conducted to clarify the characteristics of small mammal community and establish baseline data of small mammal fauna of the Natma Taung National Park in Myanmar during the dry seasons of 2014–2015 and the rainy season of 2015. Data from 184 individuals of 14 small mammal species were recorded at five study stations. *Apodemus lastronum*) was the most dominant species in study area. Most captured small mammal showed higher adult proportion and similar sex ratio. In this study, population of small mammals was not stable. Further researches is required to collect additional ecological data of small mammals for conservation and proper management plans for the biodiversity of the Natma Taung National Park.

Does maternal size affect size of eggs and offspring in fleas?

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To test for the relationships between maternal size, egg size and new offspring size, we studied (a) the effect of maternal size on egg size and number and maternal survival after oviposition in three species and (b) the effect of egg size on duration of development and new imago size in three species of fleas (host and habitat generalist *Xenopsylla ramesis*, host generalist but habitat specialist *Synosternus cleopatrae* and host and habitat specialist *Parapulex chephrenis*) parasitic on rodents. In general, the number and size of eggs appeared to be independent of maternal body size. No trade-off between egg number and size was found as well. However, female body size was related to their ability of survival after oviposition with larger females survived after oviposition longer than smaller females. In addition, female *X. ramesis* (but not the two other species) that produced more eggs died after oviposition. There were no significant size differences between eggs that succeeded to develop into new imagoes and eggs that did not survive as well as between male and female eggs (although new adult females were significantly larger than new adult males). Significant relationships between egg size and duration of preimaginal development were found in female but not in male fleas of all three species with larger eggs developing faster than smaller eggs. In *X. ramesis* and *S. cleopatrae*, faster developing eggs developed into larger new imagoes. We conclude that the patterns found in this study were to a great extent consistent among the three flea species suggesting that they result from the same mechanisms and are weakly affected by the level of ecological specialization of a given species.

Population genetic structure of the Northern mole vole, *Ellobius talpinus*, in the Novosibirsk region

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The Northern mole-vole, *Ellobius talpinus*, is a highly social subterranean rodent widespread in grasslands of Eurasia. The population genetic structure and dispersal strategies of any *Ellobius* species are poorly studied. We investigated the genetic structure of the *E. talpinus* population in the Novosibirsk region. A 482-base pair fragment of mitochondrial control region and gene of proline transfer RNA was sequenced for 50 individuals from 3 subpopulations. In total, 4 haplotypes were found and 27 nucleotide positions ($S = 5.6\%$) were variable. Two most common haplotypes displayed the highest divergence. As a result, both haplotype and nucleotide diversities were high (0.71 and 0.028, respectively). An analysis of molecular variance (AMOVA) showed strong genetic differentiation among subpopulations on high geographic scale (~100 km; $F_{st} = 0.32$) and the absence of differentiation on low scale (~10 km; $F_{st} = -0.01$). In some social groups, adult females had different haplotypes. This finding does not support the hypothesis about matrilineal structure. AMOVA analyses were conducted for 18 social groups, separately for two sexes. Males had large proportion of haplotype variation among groups (71.8%) and low proportion within groups (28.2%), while females had the opposite pattern (8.6% and 91.4%, respectively). These results suggest that male Northern mole-voles tend either to be philopatric or to disperse as kin groups. The research was supported by the RFBR (projects 16-04-00479 and 16-04-00888).

One, two, or six? Rethinking fossil muskrat taxonomy using molar morphology

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The muskrat lineage, presently represented by a single species, *Ondatra zibethicus*, is traditionally aligned into as many as six species, and recently, as few as one due to a multitude of species concepts and different interpretations of lower first molar morphology. Muskrats are semiaquatic and herbivorous rodents that are also the largest member of subfamily Arvicolinae. Remains have been found across North America dating back to 3.75 Ma, and have come to be described as one of the best examples of anagenetic evolution. This analysis tests these assertions about the taxonomy and evolution of the lineage using both qualitative and quantitative traits of the lower first molar. Data from modern and fossil muskrat molars were tested with analysis of variance, analysis of covariance, and regression to examine levels of intra- and interspecific variation. Molar characters used to distinguish species of *Microtus* aided in determining interspecific variation for arvicoline rodents, such as triangle number, dentine tract height, and cement. Examination of muskrat lower first molars suggested that the previously accepted number of six species should be condensed into only two, and that only a single genus exists. Our findings suggest that the modern *Ondatra zibethicus* should also comprise the fossil *O. nebracensis* and *O. annectens* species, while both species of *Pliopotamys* should be assimilated into *O. idahoensis*. Number of triangles was found as the most discriminating trait of the muskrat molar, showing little intraspecific variation in modern samples, and providing a natural break between the two newly designated fossil species. Cement amount and dentine tract height were highly variable traits and were found to be of limited value for discriminating between fossil muskrat species. Data plots revealed a variable rate of size change and allowed an improved view of the tempo of muskrat evolution.

Cross-fostering of *Mus musculus* and *M. spicilegus*: effect on response to species odors

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To determine the role of maternal environment in the development of adult olfactory preference, pups of two species of mice (*Mus musculus* and *M. spicilegus*) were reciprocally cross-fostered shortly after birth. At 30 days of age all pups were individually housed in the cages. At 2 months of age all mice were tested for response to con- and heterospecific urine odors in two-choice experiments (in their home cages by introducing two 35 mm Petri dishes as sources of odors or on neutral territory by introducing two slides). Mice of control (non-fostered) groups investigated urine odors of conspecifics significantly longer in all presented combinations. Cross-fostered *M. musculus* and *M. spicilegus* showed increased preference for heterospecific odor (*M. musculus* weaned at 6 days of age) or showed no preference (*M. musculus* weaned at 3–4 days of age and all *M. spicilegus* regardless of weaning age). These results suggest that adult species-specific odor preferences are learned during the neonatal period. We compare these results with those of other authors. In the future, we plan to explore the value of different forms of learning modifying response to con- and heterospecific odors and neuronal activity of some regions of brain in control and cross-fostered individuals. Supported by Russian Science Foundation (project № 16-14-10269).

New data on the Robertsonian system of the house mouse, *Mus musculus domesticus* (Rodentia: Muridae) from Peloponnese

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Several mammalian species are characterized by a remarkable chromosomal evolution, occasionally with phylogenetic implications. The house mouse, *Mus musculus domesticus*, populations demonstrate extensive fixation of Robertsonian (Rb) fusions in their karyotype from acrocentric chromosomes, causing a reduction of the diploid chromosome number ($2n$) from $2n = 40$ to $2n = 22$. More than 100 Rb fusions have been recorded so far, leading to the formation of Rb races and complex Rb systems. Moreover, Homogenously Staining Regions (HSRs), restricted to chromosome 1 of the karyotype sporadically occur in natural populations of the house mouse. In Greece, 3 Rb systems have been described until today, i.e. in Peloponnese, Ipeiros and E Sterea Ellada. Even though the Rb system of Peloponnese is by far the most well-studied, there still remains a lot to be discovered. With this work, we focused on expanding our knowledge, regarding the true geographical dimensions and attributes of existing Rb races of this system, particularly, GRP1 with $2n = 30$ and GROL, the most widespread Rb race of this Rb system, with $2n = 24$, as well as of the acrocentric population. About 30 individuals from ca. 10 localities of Peloponnese were karyologically studied, following direct bone marrow chromosome preparations and G- and C-banding staining of the chromosome slides. Our results reinforce the idea that the center of GRP1 does not appear to be Patras, as previously thought, but rather the higher altitude areas at its SE outskirts. Regarding GROL, its distribution area seems to extend further inland from the W than previously thought and the acrocentric population appears to be approaching the center of Peloponnese from the E, reaching the outskirts of Tripoli, a major city of central Peloponnese. Notably, several of the studied acrocentric individuals were characterized by HSRs on chromosome 1, even in homozygosity, which constitutes the first report of HSR occurrence in a Greek acrocentric population.

Mammalian keratin as a useful source of high-quality DNA from museum specimens

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DNA derived from museum specimens is proving to be increasingly useful for projects related to phylogeography, systematics, taxonomy, disease, and conservation, among others. In particular, projects utilizing high throughput sequencing have facilitated obtaining large amounts of data from ancient/degraded DNA, thus resulting in a dramatic increase in destructive sampling requests to museums. Due to the destructive nature of sampling museum specimens for DNA extractions, a cost-benefit of loss of valuable specimen material relative to knowledge gained is required for any project utilizing destructive sampling. Variation exists in DNA preservation quality from historical specimens due to age, museum preparation types (e.g. dried, tanned, treated, formalin preserved), and other factors. Thus, it is important to assess DNA yield from different sources of museum specimens when considering the needs of a particular molecular project (e.g. mitochondrial versus nuclear datasets). We tested several common sources of DNA from museum specimens including osteocrusts, bone, skin+hair, and keratin. Analyses were performed on a variety of mammals including the orders Carnivora, Marsupialia, Lagomorpha, and Rodentia. DNA extractions included tests of two techniques (phenol chloroform versus silica-based). We quantified DNA quality by assessing average fragment size (Agilent Bioanalyzer electropherogram images), quantity (Qubit fluorometric quantitation), copy number (qPCR), and whole mitochondrial genome sequence coverage.

Molecular phylogeny of the genus *Praomys* (Rodentia: Murinae) with an emphasis on *P. jacksoni* species complex

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Although murine rodents form a very important group of mammals, they are still one of the least explored vertebrates. This situation is noticeable especially in tropical areas, where the impact of mice on human health and food resources is even more pronounced. One of the most important rodents in sub-Saharan Africa are common and abundant representatives of the *Praomys* genus. There are currently 17 recognized species, but there are indications that the species richness is still underestimated. Further, the taxonomy (e.g. questionable involvement of some lineages in the genus) and species delimitations are very complex and remains insufficiently resolved. Here we present molecular phylogeny of the *Praomys* genus both within the Praomyini tribe (evidence for polyphyly of the genus in its present interpretation) and between the species. In addition we combine published and new mtDNA and nuclear sequences to analyse closer the phylogenetic relationships within the *P. jacksoni* species complex. It consists from six main mtDNA lineages corresponding to the species *P. degraaffi*, *P. mutoni*, *P. sp. B* sensu Nicolas et al. (2012), *P. minor* and two clades of *P. jacksoni*. Their geographical range is presented as well as more detailed structure for some of the main lineages. Gathering together all previously analysed data from various publications and adding numerous unpublished sequences, our main aim is to provide a comprehensive review of contemporary knowledge on *Praomys* phylogeny and diversity as a starting point for further taxonomic, phylogenetic and phylogeographic studies of this prominent group of African rodents. The research (DM, JB and AK) was funded by GACR project No. 15-20229S, the contributions of EV and JK was funded by Fund for Scientific Research – Flanders (FWO). Fieldwork was supported by a Flemish Inter-University Council–University Development Cooperation Own Initiatives Project (VLIR) between the University of Antwerp and University of Kisangani.

Transgelin: a specific molecular marker of physiological reproduction mechanisms from Saharan rodents

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In arid climates, mammals, in particular rodents adapted their reproduction mechanisms to the environmental conditions. The sand rat, *Psammomys obesus*, is a Béni Abbès arid area gerbillinae rodent (30°7'N, 2°10'W) characterized by a seasonal cycle of reproduction. In the seminal vesicles, one major androgen-dependent protein with an apparent molecular weight of 21 kDa is expressed in large amounts in autumn and winter. It is greatly reduced in the beginning of spring and non expressed at the late of spring. The site of synthesis was determined and its peptidic sequence was analyzed. This protein was identified as transgelin. More recently, three major androgen proteins with the same molecular weight were characterized in seminal vesicles from other Saharan rodents: *Meriones libycus*, *Meriones crassus* and *Meriones shawi*. These three species are nocturnal rodents; their reproduction seasonal cycle is characterized by a short period during spring and in the beginning of summer, and a long phase of sexual quiescence from the end of summer until the end of winter. Using polyclonal antibodies directed against transgelin, we demonstrated by immunoblotting, an immunological homology with transgelin. MLVSP21, MCVSP21 and MSVSP21 were localized by immunohistochemistry and identified by applying proteomic approach. The comparative analysis peptidic sequences, from MLVSP21, MSVSP21 and MCVSP21, showed that these three isolated proteins seem to correspond to the same protein: the transgelin. Therefore transgelin can be used as a specific marker to these rodent physiological reproduction mechanisms.

Testing automated sensor traps for mammal field studies

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In mammal studies live traps are often used in field or enclosure settings. In some studies it can be crucial to identify the exact time an animal was captured if the focus is on temporal patterns, samples need to be collected soon after capture or the time animals are contained inside a trap needs to be minimized. Presently there are few suitable systems available that alert the researcher immediately when an individual is trapped. We tested an automated system (ERMINEA Permanent Monitoring System for Rodent Detection) designed to automatically send a signal when an animal is trapped. A sensor (6.8×3.8×6.0 cm) registers movement of a trapped mammal via a passive infrared sensor and sends a signal to a receiving device (pager, computer, mobile phone). Sensors were attached to Ugglan multiple capture traps for capturing small mammals and used under laboratory, outdoor enclosure and field conditions. Generally, the system was reliable, flexible and easy to handle. In enclosure and field trials 100% and 94% of traps recorded captured common voles (*Microtus arvalis*) and bank voles (*Myodes glareolus*) correctly. There were no sensor signals when rodents moved along the outside or in the entrance compartment of the traps. Rodents sitting on the trap door without fully entering the trap did not trigger sensors when traps were baited and bedding (wood wool) was provided. However, without bedding in the traps sensors were triggered in 50% of cases by rodents sitting on the trap door. In laboratory trials, crickets (model insects) triggered the sensor depending on ambient temperature and whether bedding was in the trap. The sensors can be combined with various trapping and monitoring devices. The use of sensors may improve study designs and minimise stress for trapped animals because they can be removed shortly after capture.

Structural niche overlap of two forest dormouse species: effects of imperfect detection on accuracy of estimates

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Small mammal communities in European forests stresses their potential use as bioindicators. However, to effectively study the role of small mammals as bioindicators, an accurate assessment of species detection is crucial, as sampling biases can misrepresent abundance and niche estimates. We explored detection probability and niche overlap in two European arboreal rodents, the common dormouse *Muscardinus avellanarius* and the edible dormouse *Glis glis* in a deciduous forest of the Italian central Apennine. One nest-box and one hair-tube were set up at 83 random sampling sites surveyed by visual encounters four times at 15 days intervals. A total 14 qualitative and quantitative structural characteristics of forest stands were measured within a circle of 13 m radius around sampling sites. We used Generalized Linear Mixed Models (GLMM) and Occupancy Models (OM), which explicitly account for imperfect detection, to estimate the occurrence probabilities of the two species. Niche Equivalency (NET) and Niche Similarity (NST) were then performed on occurrence probabilities predicted by both models. Based on GLMM predictions, both NET and NST were not significant, i.e. the niches of *M. avellanarius* and *G. glis* resulted statistically identical. On the contrary, NET performed on OM probabilities accounting for detection error gave significant outputs, showing that imperfect detection can reduce the accuracy of niche overlap quantification. NET derived from the projection of *G. glis* niche on that of *M. avellanarius* yielded a significant outcome, but not in the opposite direction. Such an asymmetry indicates a narrower niche of *G. glis*, totally included in a marginal fraction of *M. avellanarius*'s niche, suggesting different ecological strategies: specialization in *G. glis* and generalism in *M. avellanarius*. Our framework showed that imperfect detection can reduce the accuracy of niche overlap assessment based on GLMM, leading to a substantial underestimation of the species niche.

Cophylogeny between rodents and their pathogens from genus *Pneumocystis*

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Pneumocystis represents a genus of obligatory parasitic fungi from the phylum Ascomycota, which inhabits mammalian lungs and can cause a respiratory disease – pneumocystosis (species *Pneumocystis jirovecii*, causing pneumonia in immunodeficient individuals, was described in humans). For a long time, only three species – *P. murina*, *P. carinii* and *P. wakefieldae*, occurring in house mouse and rat – were described. Recently, studies have shown the occurrence of *Pneumocystis* parasites in, among others, rabbits (*P. oryctolagi*), bats, and several primates. Our data obtained from a wide spectrum of rodents suggest that almost every species of rodents serve as a host for a specific *Pneumocystis* lineage (= species?). We have sampled the DNA lung tissue from 11 rodent, 1 bathyergid and 1 glirid species and analysed the phylogenetic pattern of cytochrome b sequences. The pattern of *Pneumocystis* closely resembles that one of the hosts. Furthermore, we report the existence of two independent and very divergent evolutionary lineages with parallel phylogenies and co-occurring in several host species. Different scenarios arise on the contact zones of several rodent lineages: for some of them the *Pneumocystis* genetic structure mirror the genetic structure of their hosts but in one case, a single lineage of *Pneumocystis* was detected in the two host lineages. In conclusion, *Pneumocystis* represents a good model for the study of host–parasite interactions and genetic structure of parasitic populations themselves.

A Puumala virus rapid field test for rodents validated for application in Germany

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Puumala virus (PUUV) is widely distributed in Europe. Its reservoir species is the bank vole (*Myodes glareolus*) and transmission to humans can cause mild to moderate courses of hantavirus disease. Detection of the pathogen in its rodent host is essential for estimating the health risk for the human population. A PUUV rapid field test for rodents (Reagenia, Finland), based on a recombinant antigen of a Finish PUUV strain (Sotkamo), has been validated for Germany. Blood samples of bank voles were collected by rodent live-trapping from 2013–2015 in two PUUV endemic regions of Germany (North Rhine-Westphalia and Baden-Wuerttemberg) and immediately analyzed by application of the rapid field test. Test results of the rapid field test were compared to in-house enzyme linked immunosorbent assays (ELISA), which were done using recombinant antigens of PUUV strains from Germany (Bavaria), Sweden (Vranica/Hällnäs) and also Sotkamo strain. Rapid field test efficacy was calculated from sensitivity and specificity in comparison to in-house ELISAs and was 93–95%, largely independent of the origin of the antigens used in ELISA. In ELISAs, reactivity for the German PUUV strain was higher compared to the Swedish strain but not compared to the Finnish strain, which was used for the rapid field test. In conclusion, the use of the rapid field test can facilitate short-term estimation of PUUV seroprevalence in bank vole populations. This can aid health authorities in the future to quickly assess the current risk of human PUUV infection based on PUUV seroprevalence in the rodent reservoir.

Preliminary results on the architecture and use of burrow systems by Thomas' pine vole, *Microtus thomasi* (Rodentia: Arvicolinae)

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Thomas' pine vole, *Microtus thomasi* (Rodentia: Arvicolinae) is a subterranean rodent, endemic of SE Balkans, which occupies a variety of substrates at different altitudes. Although this species is well-studied for its remarkable chromosomal variation, little has been done on its underground behavior and complexity of its burrow systems. In fact, more than 30 years have passed since the last relevant work. Therefore, this study aims at significantly increasing our knowledge on this particular aspect of the species' biology. Our work includes uncovering several burrow systems in different regions of Achaia Prefecture, NW Peloponnese and taking measurements with the help of a differential GPS device, in an attempt to depict in detail their architecture. Through statistical analyses, we intend to report the conditions that may influence burrowing behavior and document possible differences among the vole's burrow systems. Detailed maps of these systems are being created with the GIS software QGIS (Ver. 2.14), to be followed by the estimation of the fractal dimension, based on the box-counting method, in order to describe their complexity. Soil classification is being carried out in each studied site, including particle size analysis and measurement of calcium carbonate (CaCO₃), total carbon (TC), total organic carbon (TOC), total nitrogen (TN) and total phosphorus (TP) content. Finally, the vegetation type of each excavated region undergoes identification, based on characteristic plant species, in order to detect connections between foraging preferences and burrow architecture. Preliminary results on excavated burrow systems show that the size and possibly the complexity of these systems exceed expected values, in comparison to data from older studies. We also estimate that soil hardness does not seem to limit the vole's capacity to establish underground tunnel systems to the degree previously reported, but rather affects their architecture and complexity.

Chromosomal variation of the house mouse, *Mus musculus domesticus* (Rodentia: Muridae), in E. Sterea Ellada, Greece, due to Robertsonian (Rb) fusions

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Chromosomal variation in natural populations is a rather common genetic trait for many mammalian species. Robertsonian (Rb) fusions, i.e. the combination of uniarmed chromosomes into biarmed ones, is the most commonly occurring type of chromosomal rearrangement. The typical karyotype of the house mouse, *Mus musculus domesticus* (Rodentia: Muridae), is acrocentric with $2n = 40$, however a phenomenon of extensive Rb chromosomal variation has been recorded in many Euro-Mediterranean areas. As a result, the diploid chromosome number is reduced even down to $2n = 22$. Numerous, homozygous Rb populations for specific sets of Rb chromosomes, termed Rb races, exist, organized into complex Rb systems that have been under research for more than half a century. In Greece there are 3 such Rb systems, i.e. in Peloponnese, Ipeiros and E. Sterea Ellada, but the last two have not been sufficiently studied so far. The purpose of this work was to provide more information on the Rb system of E. Sterea Ellada, expanding our knowledge away from the city of Thebes, where most available data comes from. In particular, ca. 25 house mice from 6 localities were karyologically studied, using the G- and C-banding staining techniques. Our results show that what had previously been described as a rather rare Rb population in Thebes with $2n = 26$ (GRT1), appears to be an established Rb race, its easternmost border lying ca 20 km to the W. of that city. A second Rb race (GRT2) with $2n = 28$ (GRT2) comes in contact with GRT1 and seems to approach Thebes from the W. and S. The variable chromosomal constitution of the mice closer to Thebes ($2n = 33\text{--}38$), in combination with previous data denote the existence of a hybrid zone in that area with the acrocentric population, which must approach from the NE. and may stop just a few km away from Thebes. Even though there still remain a lot to be revealed about this Rb system, the new data predispose for a very interesting story of chromosomal evolution that lies behind it.

Landscape factors related with common vole burrow systems abundance in agrosystems of NW Spain

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Common vole (*Microtus arvalis*) is an important rodent pest species in Europe. Landscape traits may be promote vole outbreaks, but little is known about this for the recently settled vole population in agricultural areas of NW Spain. We aim to evaluate which are the main landscape traits related with the number and activity of common vole burrow systems (BS thereafter), a key trait of common vole biology reliably reflecting vole abundance, during a low-abundance year. All BS were counted in 8 circular 12.5 ha plots in spring, summer and autumn in 2012 in two study areas. We measured in each plot the area covered by each type of crop, riverine habitats and road ditches, total length of field margins and Shannon diversity index of type and state of crops. We applied to these landscape variables a Partial Least Square Regression (PLS) using three response variables: total number of BS/ha, total number of burrow openings/ha and total number of active BS/ha. Sampling locality had an important effect on the three response variables studied. BS abundance or activity varied at local scale, reaching the highest and more stable densities in permanent crops (old alfalfa fields). But given that age of alfalfa fields was variable among plots, and burrow abundance is usually low in young alfalfa, the main factor negatively affecting BS abundance/activity was the area occupied by traditional (tilled) cereal. Yearly leguminous crops also seemed to favour higher BS abundance. Area covered by riverine habitats (the main well developed natural herbaceous habitats) negatively correlated with the abundance of total and active BS in the plot. Overall, spatial and temporal arrangement of crops at landscape scale and soil disturbance through tillage may be critical traits affecting the persistence of BS and could be a major factor explaining spatial expansion of common voles in agricultural landscapes. Further data are needed about the role of linear herbaceous habitats.

Stylodipus telum in Ukraine

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One of the main problems in the protection of rare animal species is saving of the species with isolated or disrupted range, especially if this isolation or fragmentation caused by anthropogenic factors. The subspecies *Stylodipus* (= *Scirtopoda*) *telum falz-feini* Brauner (1913) areal was isolated from the species area in the Late Pleistocene (Gromov, 1995). Presently, the distance from western isolated part to main areal of the species is more than 500 km. Morphologically this subspecies significantly differ from other subspecies *S. telum*, the differences coefficient of morphological parameters has higher value than in case of subspecies inhabiting the main species areal. The main characteristics of Ukrainian subspecies are larger body size and limbs (especially metatarsus), elongated facial part of the skull and bright coloring fur (Selyunina, 1995, 2008; Shenbrot, 1991). The emergence of a valid subspecies of *S. t. falz-feini* on the isolated part of the species areal is an example of allopatric speciation caused by geographical isolation. The western part of the areal is bounded by Low Dnieper arenas. In the result of anthropogenic transformation, especially sands afforestation, the *Stylodipus* areal in Ukraine has become mosaic and decreased in 10 times over the past 70 years. For this reasons the Ukrainian subspecies *Stylodipus* is listed in the Red Book of Ukraine. Currently, the area of natural habitats of this subspecies is about 40000 ha, the total number does not exceed 50000 individuals. Anthropogenic and natural abiotic factors are decisive for *S. t. falz-feini* population dynamics in the region of the Black Sea Biosphere Reserve. The population density of *S. t. falz-feini* in the region of our research is relatively stable. The decreasing of number caused by reduction of natural habitats. For the successful conservation of this endemic subspecies it is necessary to extend network of protected areas in the region by creating of steppe reserves with limited nature management.

Natural foci of bartonellosis and rickettsioses with an emphasis on communities of rodents and their ectoparasites

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Results of the five-year monitoring (2011–2015) of the natural foci on four localities in eastern Slovakia with varying degrees of anthropogenic use are presented. Communities of small mammals, their ectoparasites (ticks, mites, fleas), and prevalence of bartonellae and rickettsiae in rodents and parasites were studied. Bacterial pathogens were confirmed at all localities. Altogether 966 specimens of six rodent species were sampled. Three rodent species were dominant: *Apodemus agrarius* (35.9%), *A. flavicollis* (33.2%), and *Myodes glareolus* (28.2%). The prevalence of rickettsiae in all dominant rodent species was very balanced and the differences were statistically insignificant – *A. agrarius* (5.9%), *A. flavicollis* (3.8%) and *M. glareolus* (4.1%). In contrast, the differences in prevalence of bartonellae among rodents were statistically significant ($p = 0.001$): *A. agrarius* (9.0%), *A. flavicollis* (27.8%), and *M. glareolus* (17.8%). Parasite communities on rodents were rich and relatively similar. We confirmed 1048 ticks of two species on *A. agrarius*, 463 fleas of 12 species and 433 mites (Mesostigmata) of 11 species. Dominant species were: *I. ricinus* – tick, *Ctenophthalmus solutus*, *C. agyrtes*, *Megabothris turbidus* – fleas; *Laelaps jettmari* and *L. agilis* – mites. In total, 1090 ticks of two species were collected from *A. flavicollis*, 596 fleas belonging to 10 species and 2,269 parasitic mites of 11 species. Dominant parasites on this host were *I. ricinus*, *C. solutus*, *C. agyrtes*, *M. turbidus*, *L. agilis*. A total of 228 ticks of two species, 532 fleas of eleven species and 126 mites of eight species were infesting *M. glareolus*. Dominant parasite species were – *I. ricinus*, *I. trianguliceps*, *C. agyrtes*, *M. turbidus*, *Peromyscopsylla bidentata*, *Haemogamasus nidi*, *Eulaelaps stibularis*, *Laelaps hylaris*, *L. agilis*. Differences in rodent infestation parameters among monitored sites are discussed. The research was sponsored by the projects: APVV-14-0274, VEGA 2/0059/15, VEGA 1/0196/15.

Hantaviruses in *Microtus* voles

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Different hantaviruses were found in North America and Asia to be associated with the meadow vole (*Microtus pennsylvanicus*), the North American California vole (*Microtus californicus*), the Maximowicz's vole (*Microtus maximowiczii*), the reed vole (*Microtus fortis*) or the root vole (*Microtus oeconomus*). Tula virus (TULV) is widely distributed through Europe and has been detected in several vole species – the common vole (*Microtus arvalis*), the East European vole (*Microtus levis*), the field vole (*Microtus agrestis*), the European pine vole (*Microtus subterraneus*) and the water vole (*Arvicola* spp.). In addition, two TULV-related strains were described – Adler virus in Russia (in the common vole) and Tatenale virus in the UK (in the field vole). Here, we present a study of more than 1,000 voles (*M. arvalis*, *M. agrestis*, *M. oeconomus*, *Arvicola* spp.) from Germany, France, Luxembourg, Czech Republic, Switzerland and Lithuania. Blood samples were investigated by in-house ELISA using recombinant nucleocapsid protein of TULV and for detection of viral RNA, lung samples were screened by RT-PCR. TULV was detected in different parts of Central Europe with varying prevalences. Phylogenetic analyses demonstrated a strong genetic structuring of TULV sequences according to geography and independent of the rodent host species. The RNA prevalence was higher in common voles than the other vole species, indicating the common vole as the preferential host with spillover infections to co-occurring field voles and water voles. In conclusion, our investigations confirm a broad geographical distribution of TULV in Europe. Further studies will have to investigate the role of species barriers for TULV infection in different *Microtus* species. The initial finding of large-scale associations of some TULV clades with different evolutionary lineages of common voles indicates the need for future studies to study potential (co-)evolutionary processes in more detail.

Factors influencing vole bark damage intensity in managed mountain-forest plantations of Central Europe

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We studied the impact of vole bark-gnawing in forest plantations dominated by European beech in two Czech mountain ranges (Jeseník Mts., Beskydy Mts.) with different habitat conditions. Of the two dominant vole species, only the field vole caused significant damage, the impact of the bank vole being inconclusive. Trees in the Jeseníky Mts. suffered significantly higher damage than those in the Beskydy Mts. (13.6% vs. 3.3% damaged seedlings), with degree of damage closely related to the abundance and spatial distribution of voles. Distribution in the Beskydy Mts. was more positively influenced by environmental factors than in the Jeseníky Mts. In both ranges, the key factor determining presence and abundance of voles was presence of grasses. The higher degree of gnawing in the Jeseníky Mts. is probably related to forest character, with poorer food quality, combined with poor-quality habitat surrounding the plantations, resulted in voles from surrounding stands concentrating in the plantations. Our results indicate that artificial beech regeneration is more successful in mixed and spruce forests with rich undergrowth (Beskydy Mts.) than in large spruce stands with reduced herb undergrowth (Jeseníky Mts.).

Murine cytomegalovirus in the European house mouse hybrid zone – from field work to genome characterization

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Murine cytomegalovirus (MCMV) is an enveloped dsDNA virus (family Herpesviridae) which is normally used to model human cytomegalovirus infection. The host species of MCMV is the house mouse in which the virus produces persistent asymptomatic or latent infections. Two taxa of house mice, *Mus musculus musculus* and *Mus musculus domesticus* meet and hybridize along a 2500 km long front stretching from Scandinavia to the Black Sea. At this front the taxa form a narrow hybrid zone, a tension zone species barrier. A preliminary study across a transect in the Bavarian/Bohemian part of the house mouse hybrid zone (HMHZ) showed that each mouse taxon carried different MCMV strains. Therefore the HMHZ may serve as a suitable natural system for studying recombination between divergent viral strains, a potentially important natural evolutionary process allowing strains to overcome the host species barrier and to infect a new host taxon. House mouse tissues (especially saliva and salivary glands) were collected across the Bavarian/Bohemian region of the HMHZ to investigate the prevalence of MCMV and for subsequent isolation and genomic characterization of the different viral strains. Molecular screening of 155 saliva samples revealed a prevalence of 83%. A subset of positive individuals were then used for MCMV reactivation in vitro directly from salivary glands and part of the enriched samples were sequenced using the HiSeq 2500 next generation sequencing technology for to obtain the viral genome of MCMV from *Mus musculus musculus*, not yet available in public database. These data will serve as a basis to study MCMV genomic diversity and recombination in the HMHZ.

Conduction of hibernation of jerboas as a way for successful reproduction

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Keeping and breeding of jerboas which need hibernation is still a problem, there are just few facts of breeding them in captivity, and so many aspects of reproductive biology and behavior of this animals is still unknown. We have some experience in keeping and conduction of hibernation for small five-toed, great jerboas (*Allactaga elater* and *A. major*), thick-tailed pygmy, Kozlov's pygmy jerboas (*Salpingotus crassicauda* and *S. kozlovi*), thick-tailed three-toed jerboa (*Stylodipus telum*). We develop special diets, considering year cycles of the animals. Increasing of amount and nutritional value of food gives good result in autumn for gaining fat. The process is under control by weekly weighing. When weight of an animal stop to increase, that the time to put it into hibernation conditions: quiet place with stable low temperature 2–5 °C. Often speed of weight loss in hibernation are not liner, and significantly less in the end of hibernation. After weight of the animal riches summer value, we end the hibernation, moving animals to normal temperature and daylight. After hibernation diet includes less fat and more juicy feed. Only after successful hibernation it is possible to breed jerboas. We have an experience of breeding *Allactaga* and *Stylodipus* jerboas. After hibernation we put animals into conditions with quiet cold nights (10–15 °C), give them ice, juicy feed, vitamin E. Male need to end hibernation first, and female after. Into these conditions testes in males and vagina in females become clearly visible, and breeding of the animals could be successful. Female become in estrus in one of first 8 days after hibernation. We have got litters from small five-toed and thick-tailed three-toed jerboas, but for five-toed jerboas natural weaning was not successful and so conditions need to be better designed.

The European snow vole (*Chionomys nivalis*) in Portugal: contributions to the species' distribution range and phylogeographic structure

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The European snow vole (*Chionomys nivalis*), a microtine rodent, has a highly fragmented distribution range, mostly associated with the main mountain systems from southern Europe to Turkmenistan. In this study, the occurrence of the snow vole was confirmed for the first time by morphological characteristics, biometrics and genetic analysis of two individuals captured in northeastern Portugal. The species' identity was confirmed by mitochondrial and nuclear genetic markers. The analysis of cytochrome b supports previous conclusions on the snow vole phylogeographic structure, revealing the existence of several distinct lineages, and showing that the Portuguese specimens are closely related to the other Iberian populations. This finding adds new information with regard to the spatial distribution of the snow vole, by redefining the southwestern limits of the species' range and highlighting the need of supplementary accurate surveys and assessments of regional population trends and conservation status.

The postnatal growth and physical development of fat-tailed gerbils *Pachyuromys duprasi* in the laboratory colony)

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Data on postnatal growth and development provide basic information for integrative studies and zoo and laboratory management of animals. In the laboratory colony of fat-tailed gerbils *Pachyuromys duprasi* of Moscow Zoo, we examined 40 (17 male, 23 female) pups from 11 litters from birth to 40 days of age for traits of physical development. For comparison, an independent sample of 20 adults (10 males, 10 females) has been examined by the same variables as pups. Litter size varied from 2 to 6 (average 4.00 ± 1.34) pups. The average neonate body mass (2.58 ± 0.45 g) comprised 4.3% of the average adult body mass (60.0 ± 24.3 g). The average neonate body length was 36.22 ± 1.85 mm, head length 14.06 ± 1.01 mm, tail length 8.84 ± 0.68 mm and foot length 6.17 ± 0.43 mm. The upper incisors erupted at 13.5 ± 1.7 days. At 16 days, pups walked at four feet. The hind leg fingers had separated at 21.4 ± 3.0 days. The eyes had opened at 23.7 ± 0.9 days. The ear channel had opened at 27.2 ± 1.2 days. The average body mass gain was 0.491 g per day in the first 10 days of age, 0.498 g per day between 11 and 20 days of age, and 0.421 g per day between 21 and 40 days of age. At 40 days, pup body mass (20.02 ± 4.7 g) was 33.0% of adult body mass, whereas body length (76.6 ± 3.9 mm) was 79.1% of adult body length. The body mass gain and the physical growth did not differ between sexes. Cross-correlation of body mass and body size values revealed periods of coordinated and uncoordinated growth of different body parts. The body mass gain ($F_{1,147} = 42.5$, $p < 0.001$) and the increase of the length of body ($F_{1,147} = 31.8$, $p < 0.001$), head ($F_{1,147} = 10.5$, $p = 0.001$), tail ($F_{1,147} = 35.0$, $p < 0.001$) and foot ($F_{1,147} = 15.1$, $p < 0.001$) were significantly faster in pups from small litters (2–3 pups, 5 litters) compared to pups from large litters (4–6 pups, 6 litters). Compared to other species of gerbils, development of fat-tailed gerbils goes at slower speed. Support: the Russian Science Foundation, grant 14-14-00237.

Classification of discomfort-related ultrasonic calls in pup and adult fat-tailed gerbils *Pachyuromys duprasi*

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Classification of discomfort-related ultrasonic calls (UCs) is an important prerequisite for their applicability as indicators of emotional arousal in laboratory rodents. We classified spectrographically the UCs collected from 40 individual pups (17 males and 23 females from 11 litters) and 20 adult (10 males and 10 females) fat-tailed gerbils *Pachyuromys duprasi* during 420-s isolation-and-handling tests. As ultrasound emerges in fat-tailed gerbils at 6th day of life, we used recordings of 6–10-day-old pups. The UCs were provided by 22 of 40 pups (782 calls in total) and by 7 (3 male, 4 female) of 20 adults (248 calls in total). The UCs differed in the fundamental frequency contour: Flat, Chevron, Downward, Upward, Short (within 4 ms) and Complex (up-down many times), and in the number of notes (1, 2, 3, many) resulting from up or down frequency jumps over 10 kHz. This variation resulted in the total of 42 UC types. In pups, most frequent were single-note UCs (600 of 782 calls), with either Flat (299 calls) or Chevron (193 calls) contour. Another widespread call type was the three-note UC (in total 96 calls with down-and-up frequency jumps) with Chevron contour. In adults, as in pups, most UCs were single-note (193 of 243 calls) with contours Chevron (57 calls), Flat (40 calls), or Short (35 calls). Compared to adult UCs, the pup UCs were longer (50.0 ± 30.9 ms vs 28.1 ± 97.1 ms) and lower in frequency, with the peak frequency of 47.8 ± 5.8 kHz vs 58.8 ± 8.7 kHz; the maximum fundamental frequency of 52.0 ± 4.8 kHz vs 64.2 ± 11.0 kHz, and the minimum fundamental frequency of 41.8 ± 6.4 kHz vs 50.9 ± 8.8 kHz. Consistent differences between pups and adults were found also for most widespread single-note Flat and single-note Chevron UCs, taken separately from other call types. The ontogenetic pathway of fat-tailed gerbils UCs (towards shorter and higher-frequency calls) resembles those of bats and domestic mice. Support: the Russian Science Foundation, grant 14-14-00237.

The sibling species *Microtus arvalis* Pallas, 1779 and *M. rossiaemeridionalis* Ognev, 1924 in the cities in the Middle Urals: presence, features of distribution, parasite infestation

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The aim of the study was to determine the features of *M. arvalis* and *M. rossiaemeridionalis* distribution in urbanized territories near the north boundary of sympatric zone in the Urals and to estimate parasite infestation of voles in relation to potential epidemiological risk for urban population. The sampling was done in 2009–2014 in two big cities Ekaterinburg and Nizhny Tagil in the Middle Urals. Sibling species were revealed in 17 of 21 plots studied in both cities. *M. arvalis obscurus* and *M. rossiaemeridionalis* identification was made using karyological method. In plots of small size, isolated from other biotopes, and exposed to significant anthropogenic transformation (lawns and patches of ruderal vegetation), only *M. rossiaemeridionalis* was found. In relatively large plots under moderate anthropogenic pressure including those connected with suburb territories (forest parks and road verges), only *M. arvalis obscurus* was captured. The cohabitation of both species in an urban park and in a meadow between urban districts was observed. In the cases of cohabitation the density of *M. arvalis obscurus* was lower in the plots with more intensive anthropogenic influence, while *M. rossiaemeridionalis* were numerous in those habitats. Obtained data are consistent with the suggestion made in similar studies in the main parts of the species ranges, that among sibling species *M. rossiaemeridionalis* is better adapted to conditions of urbanized territories due to tolerance to high population density and significant anthropogenic pressure. The presence of ecto- (fleas, ticks) and endoparasites (helminthes) in voles of both species indicated the highest levels of infestation of animals in the residential areas in central parts of the cities in compared with other localities. Thus, the sibling species inhabiting the territories of the cities may represent a potential epidemiological risk for urban population in the Middle Urals. The study was supported by RFBR № 14-04-00614.

Climate-driven changes in phenology: standardized methods for monitoring of Sciuridae

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Phenological shifts caused by global warming are widely studied in plants and birds, but still little is known about its consequences for mammal biology. Climate-related changes are a challenging subject to study. Firstly, it is not clear to what extent phenotypic plasticity or microevolution are involved. Secondly, cause-and-effect relationships are difficult to distinguish from other correlated anthropogenic disturbances, such as changes in land use or pollution. Moreover, detailed data about different parameters of animal biology needs to be collected for extended periods of time. To face up to these issues we propose a standardized methodology developed for a long-term studies investigating phenological shifts in ground-dwelling North American sciurids: Columbian ground squirrel (*Urocitellus columbianus*) and black-tailed prairie dog (*Cynomys ludovicianus*). Protocols include live-trapping, behavioral observations, genetic data collection and allow to describe life histories of individuals and how they are shaped by climate change via phenotypic plasticity or evolutionary processes. We summarize outcomes of this method applied in wild populations, how they depend on the biology of the species and ecological context. We discuss advantages and problems imposed by using this approach, highlight research perspectives and possibilities for application in different study systems.

Species composition and landscape distribution of micromammalia in North-East Kazakhstan

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North-East Kazakhstan includes 2 zones – Kazakh Uplands and the West Siberian Plain. I. West Siberian part of Kazakhstan. The list of micromammalia includes 9 species: *Sicista subtilis*, *Apodemus agrarius*, *A. uralensis*, *Phodopus sungorus*, *Allocrietulus evermanni*, *Cricetulus barabensis*, *Clethrionomys rutilus*, *Microtus oeconomus*, *Lagurus lagurus*. It was also met shrew of the *Sorex* genus. *C. rutilus*, $48.2 \pm 4.2\%$, *L. lagurus*, $13.3 \pm 2.8\%$, *A. uralensis*, $11.9 \pm 2.7\%$, *S. subtilis*, $7.7 \pm 2.2\%$ were dominant; other species were met sporadically, not exceeding 5%. Landscape distribution of micromammalia shows that *L. lagurus*, $73.1 \pm 8.9\%$ and *S. subtilis*, $71.4 \pm 18.4\%$ dominate in the dry steppe. *C. barabensis*, $45.5 \pm 15.7\%$, dominate in the Baraba steppe. *A. uralensis*, $27.2 \pm 14.1\%$ and *Ph. sungorus*, $18.2 \pm 12.2\%$, were subdominants. *C. rutilus* was sporadic, $9.1 \pm 9.1\%$. *C. rutilus* is absolute dominant in the southern forest, $82 \pm 5.4\%$, and in the floodplain of the Irtysh river, $55.1 \pm 7.1\%$. *A. uralensis*, $16.0 \pm 5.2\%$, and *A. agrarius*, $2.0 \pm 2.0\%$, are met less often. *M. oeconomus*, $16.3 \pm 5.3\%$, and *A. uralensis*, $12.2 \pm 4.7\%$ were subdominant in the floodplain. II. Central Kazakhstan part of Kazakh Uplands. There were 7 species of animals: *S. subtilis*, *A. uralensis*, *Ph. sungorus*, *C. rutilus*, *M. gregalis*, *M. agrestis* and *M. arvalis*; and shrew of *Sorex* with small cumulative share not exceeding 5.8%. *M. arvalis* and *A. uralensis* dominated. Their subdominants were *M. gregalis* and *C. rutilus*. The share of the rest did not exceed 4%. According to the landscape distribution *M. arvalis* dominated in mixed forests of Bayanaul with *C. rutilus* as its subdominant, *M. gregalis* was caught in small amounts. *M. gregalis* and *A. uralensis* dominated in the fescue-feather grass steppe.

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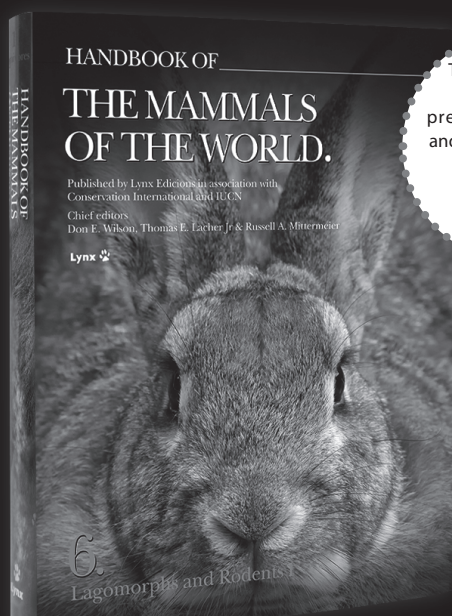
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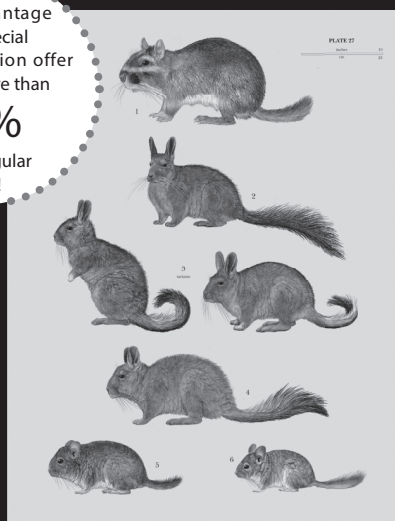
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