

International Colloquium Biology of the Soricidae IV

Poznań, Poland, 11-14 September 2016

Programme & Abstract Book



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International Colloquium
Biology of the Soricidae IV
Poznań, Poland, 11-14 September 2016

organised by

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

with help of

Institute of Biology, Faculty of Biology and Chemistry
University of Białystok, Poland

Programme & Abstract Book

edited by

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Poznań, 2016

Logo of the conference – caravanning in *Crocidura leucodon*.

Graphics by MARK KLINGLER; artwork by NANCY PERKINS; modified by LESZEK RYCHLIK

Photos on the cover

LESZEK RYCHLIK (front), MARC MOUNIER (back)

Technical Editor

TOMASZ MAGOWSKI

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Department of Systematic Zoology, Institute of Environmental Biology,
Faculty of Biology Adam Mickiewicz University, Poznań 2016
Kontekst Publishing House, Poznań 2016

ISBN 978-83-65275-23-3

Printed in Poland

Kontekst Publishing House
kontekst2@o2.pl
www.wkn.com.pl

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Programme of the International Colloquium – Biology of the Soricidae IV Poznań, Poland, 11-14 September 2016

Day 1: Sunday, 11 Sep. 2016

- 16:00-19:00 *Registration*
19:00-19:15 Agnieszka Ludwików: Dean's welcome
19:15-19:45 Sara Churchfield & Joseph Merritt: Opening speech
19:45-21:00 *Welcome part*

Day 2: Monday, 12 Sep. 2016

- 08:00-09:00 *Registration*
09:00-09:40 PLENARY 1
Jeremy Searle: Shrews, chromosomes and speciation
09:40-09:50 *Short break*

Session 1

Chromosomal & molecular diversity – Chair: Dina Dechmann

- 09:50-10:10 Nikolay Shchipanov: The common shrew story in Russia: postglacial recolonization of the area and current distribution of chromosomal races
10:10-10:30 Jan M. Wójcik: New data on the phylogeography of the pygmy shrew (*Sorex minutus*) from Poland and Ukraine support a widespread lineage in Europe
10:30-10:50 Hasmahzaiti Omar: Genetic relationships of the house shrew in peninsular Malaysia inferred from cytochrome *b* sequences
10:50-11:10 Andrew Hope: Genetic diversity, endoparasite richness, and co-evolutionary history of the endemic Pribilof Islands shrew (*Sorex pribilofensis*)
11:10-11:40 *Long coffee break*

Session 2

Morphological diversity & paleobiology – Chair: Joseph Merritt

- 11:40-12:00 Alina Mishta: The role of skull and mandible shape in intra- and interspecific differentiation of *Neomys* (Mammalia: Eulipotyphla): first results
- 12:00-12:20 Moritz Hertel: Seasonal bone dynamics in shrews (Soricidae)
- 12:20-12:40 Javier Lazaro: Seasonal individual shrinking and regrowth of the braincase in recaptured common shrews
- 12:40-13:00 Marc Furió: New data on the Plio-Pleistocene extinction of shrews in Europe
- 13:00-13:20 Raquel Moya Costa: Paleobiology of the shrews of the Early-Middle Pleistocene of Gran Dolina site (Burgos, Spain)

13:20-14:20 *Lunch*

14:20-15:00 PLENARY 2

Satoshi D. Ohdachi: Phylogeography of a wide-ranged shrew (*Sorex minutissimus* – *S. yukonicus* complex) in the holarctic region and a species endemic to Japan (*Crocidura dsinezumi*)

Session 3

Phylogeography & zoogeography – Chair: Maria da Luz Mathias

- 15:00-15:20 Violaine Nicolas Colin: Phylogeography and evolutionary history of the *Crocidura hildegardae* complex (Mammalia, Soricomorpha)
- 15:20-15:40 Joaquim Torres Tapisso: Integrating phylogeography and niche modelling to unveil the spatio-temporal distribution pattern of the Mediterranean water shrew (*Neomys anomalus*)
- 15:40-16:00 Alina Mishta: Bioclimatic modelling of the distribution of three *Neomys* species in Eurasia
- 16:00-16:20 Sirma Asenova Zidarova: Craniometric variability of common species of shrews (Soricidae: *Crocidura*, *Neomys*, *Sorex*): comparison between central and southeast Europe
- 16:20-16:40 *Short coffe break*
- 16:40-17:40 Round table 1
Diversity, evolution & phylogeography of shrews – Leaders: J. Searle & S. Ohdachi
- 17:40-19:10 POSTER SESSION 1

Day 3: Tuesday, 13 Sep. 2016

09:00-09:40 PLENARY 3

Dina Dechmann: Evolution of Dehnel's Phenomenon

09:40-09:50 *Short break*

Session 4

Ecology & physiology – Chair: Maria da Luz Mathias

- 09:50-10:10 Saikat Ray: Understanding the smallest mammalian brain
10:10-10:30 Paul Schaeffer: Daily patterns of energy metabolism in *Sorex araneus*
10:30-10:50 Joseph Merritt: Social thermoregulation in least shrews (*Cryptotis parva*)
10:50-11:10 Krzysztof Kowalski: Toxic activity of venom of the water shrew (*Neomys fodiens*)
- 11:10-11:40 *Long coffee break*

Session 5

Ecology – Chair: Sara Churchfield

- 11:40-12:00 Allan McDevitt: The untamed shrew: origins, impacts and evolution of the invading greater white-toothed shrew (*Crocidura russula*) population in Ireland
12:00-12:20 Leszek Rychlik: Factors influencing population sizes and overlap of trophic niches of water shrews, *Neomys anomalus* and *N. fodiens*
12:20-12:40 Boris Sheftel: Collapse of cyclic dynamics and changes in structure of shrew communities in central Siberia. Analysis of 40 years observations
12:40-13:00 Yakov Volpert: Population adaptations of the shrews (Soricidae) on the Northern periphery of the range
13:00-13:20 Nadezhda Poddubnaya: Shrews in the diet of carnivorous birds and mammals
- 13:20-14:20 *Lunch*

14:20-15:00 PLENARY 4

Nikolay Shchipanov: Ecological and behavioural studies of shrews in Russia. Past decade

Session 6

Ecology & behaviour – Chair: Sara Churchfield

- 15:00-15:20 Sophie von Merten: Better be bold? The relationship between life-history strategy and personality differences in European shrew species
15:20-15:40 Paweł Kardynia: Interspecific differences influencing seasonal changes in food hoarding and consumption in shrews
15:40-16:00 Flávio Oliveira: Do shrews use daily torpor to reduce risk exposure?
16:00-16:20 Hiroaki Saito: Can non-semi-aquatic Soricidae species swim and/or dive?
16:20-16:40 Dieter Köhler: Diving in the Eurasian water shrew (*Neomys fodiens*)
- 16:40-17:00 *Short coffee break*
- 17:00-18:00 Round table 2
Ecology, behaviour & physiology of shrews – Leaders: D. Dechman & N. Shchipanov
- 18:00-19:00 POSTER SESSION 2
- 20:00-22:00 *Banquet*

09:00-09:30 **PLENARY 5**
Vasyl Tkach: Evolution of hymenolepidid cestodes of insectivores: a history of host switching and geographic expansions

Session 7

Parasites & diseases – Chair: Leszek Rychlik

09:30-09:50 Subha Bhasu: Transcriptomics of filarial infected shrews: Insights on transcriptional level
09:50-10:10 Tomáš Týmł: Parasites of European shrews: cnidarians thrive in livers of terrestrial mammals

10:10-10:30 *Short coffee break*

10:30-10:50 Rasa Binkienė: Helminthes fauna of the common shrew (*Sorex araneus*) in Baltic states
10:50-11:10 Bob K. Rose: Shrews (*Blarina* spp.) and the Lyme disease cycle: exploring their role as a reservoir host for *Borrelia burgdorferi* in southeastern Virginia, USA.

11:10-11:50 Round table 3
Parasites & diseases – Leaders: V. Tkach & R.K. Rose

11:50-12:00 Leszek Rychlik & Host of the next Colloquim: Closing speech

12:15-13:15 *Lunch*

14:00 Depart for excursion

PLENARY LECTURES

Evolution of Dehnel's Phenomenon

Dina Dechmann

Max Planck Institute for Ornithology, Am Obstberg 1, 78315 Radolfzell, Germany, email: ddechmann@orn.mpg.de

With their extreme adaptations to a fast-paced, high-metabolic lifestyle, shrews are a fascinating mammalian taxon anyway. In addition, red-toothed shrews show a profound seasonal and reversible individual change in mass, the size of many major organs including the brain and skull: Dehnel's Phenomenon. Even almost 70 years after its discovery Dehnel's Phenomenon remains poorly understood yet it continues to mystify us. In my talk I will review the literature as well as four years of research on Dehnel's Phenomenon in our group in an attempt to better understand the evolution of such incredible post-natal individual flexibility.

Phylogeography of a wide-ranged shrew (*Sorex minutissimus*
– *S. yukonicus* complex) in the holarctic region and a species
endemic to Japan (*Crocidura dsinezumi*)

Satoshi D. Ohdachi

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In Japan, there are two contrasting shrew (Soricidae) species as to distribution range: one is *Sorex minutissimus* (Soricinae) and the other is *Crocidura dsinezumi* (Crocidurinae). *Sorex minutissimus* occurs only in Hokkaido, northernmost Japan but demonstrates holarctic range from Alaska, via Siberia, to Norway, whereas *C. dsinezumi* occurs fundamentally in Japan (and Jeju Island, South Korea). Thus, the comparison of the phylogeography of these two shrew species is fascinating to get deep insight into the nature of range expansion among shrew species.

Intraspecific phylogeny was estimated based on mitochondrial genes and (only for *C. dsinezumi*) nuclear ApoB gene sequences. The *S. minutissimus* – *S. yukonicus* complex was divided into 2 main groups, Eastern and Western Eurasian Clades. *Sorex yukonicus* was included in eastern Eurasian clade. Monophyly of shrews from Hokkaido-Sakhalin, Primorye, Mongolia-Transbaikalia, south-eastern Finland was strongly supported respectively. Shrews from western and central Siberia were included in the clade of south-eastern Finland. Also, most shrews from central-northern Finland and Norway made a clade close to but different from the south-eastern Finland clade. Nucleotide diversity of shrews from Cisbaikalia-western Siberia and Fennoscandia had high nucleotide diversity. This finding suggests that Fennoscandian shrews might consist of individuals which were re-colonised from various refugia after the Last Glacial Maximum. In the phylogenetic trees of *C. dsinezumi*, two haplogroups (Eastern and Western Clades) were recognized and the demarcation line between them existed in central Honshu without overlapping area. The estimated divergence time indicated that the Eastern and Western Clades could have diverged prior to the geologic division of the regions where these clades are currently found. It was also confirmed that populations in Hokkaido (Japan) and Jeju (South Korea), were recently introduced by humans from north-eastern Honshu and Kyushu, respectively.

Hence, Japanese (Hokkaido) population of *S. minutissimus* was included into Eastern Eurasian Clade, which also includes *S. yukonicus* in Alaska. Especially, Hokkaido population is genetically closed to those in Sakhalin and Primorye, suggesting they were diverged recently (ca. last glacial age or so). On the other hand, *C. dsinezumi* was genetically clearly divided into two haplogroups in central Japan without clear geographic barrier and they were estimated to be diverged in old time (about 0.5-1 million years ago). Nonetheless, *C. dsinezumi* were immigrated overseas by humans to Hokkaido and Jeju Island (South Korea). Therefore, Japanese shrew fauna consist of species which have unique biogeographic history.

Shrews, chromosomes and speciation

Jeremy Searle

Department of Ecology and Evolutionary Biology, Cornell University, Ithaca, NY 14853, USA, email: jeremy.searle@cornell.edu

The norm for species of mammals is that there is an invariant karyotype. The common shrew (*Sorex araneus*) is utterly extraordinary for the level of chromosomal variation that it displays. This variation reflects the occurrence of whole-arm rearrangements (Robertsonian fusions and fissions and whole-arm reciprocal translocations). The variation within the species relates to the autosomes, but even the sex chromosomes are atypical: the common shrew 'X chromosome' is the product of a tandem fusion between the true X chromosome and an autosome, and there are two 'Y chromosomes' (the true Y = Y1 and the unattached autosome = Y2). This means that males have one more chromosome than females and the chromosome number varies between 20/21 and 30/31 because there are ten autosomes which may be present as unattached acrocentrics or joined together at the centromere as metacentrics. The ten variable autosomes may be fused in different ways as 47 types of metacentrics and different combinations of these metacentrics and unattached acrocentrics define 74 different chromosome races over the large Eurasian distribution of the common shrew. Some of these races have very narrow distributions, others cover a vast area. Their origin is recent, but they differ in such a way that it might be expected that they may become reproductively isolated from one another. Large chromosomal differences between hybridising races have the potential to cause meiotic difficulties and reduce fertility. The shrew races have, therefore, become an important model for the role of chromosomes in speciation. I will review the large body of work examining meiosis and hybridisation in common shrews and show that the unfitness of hybrids may lead to a situation where there is a reduced chance of speciation rather than an enhanced one.

Ecological and behavioural studies of shrews in Russia. Past decade

Nikolay A. Shchipanov

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Applied value of *Sorex* is more than we used to think. They are regarded the hosts of tick-borne diseases, play a relevant role in natural ecosystems directly and as dispersers of spores of microscopic fungi. Understanding of population dynamics implies the developing of a holistic model which should be based on studying of interspecies competition, revealing of a type of population dynamics, and understanding of environmental and demographic causes of fluctuations in reproduction and mortality rates. Although a new model of population dynamics and a number of data on differences in demographic patterns related to population density have appeared, the understanding of general processes that drive population is still not comprehensive. One may find incongruence both between results of study and reasoning of the authors. A disagreement could be related to a technique of collecting of the primary data. Results obtained with using mark-recapture technique may show significantly different population dynamics, demographic and behavioural patterns as compared to results obtained with using pitfall trapping. Distribution in space is not entirely corresponding to expectation of spatial isolation of individuals. Even under the least population density an individual visited about 1/3 of traps together with his neighbours. Observations in captivity do not give evidences of territorial behaviour. One could anticipate that social interactions in shrews are rather complex. I intend to discuss a number of recent studies devoted to these issues. Also some studies on olfactory reactions of the common shrews and its possible application to search of appropriate home range are discussed.

The study was supported by RFBR grant #15-04-04759.

Evolution of hymenolepidid cestodes of insectivores: a history of host switching and geographic expansions

Vasyl V. Tkach¹, Stephen E. Greiman², Svetlana Kornienko³, Andrew G. Hope⁴

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Insectivores, especially shrews, harbor a highly speciose cestode fauna. While very diverse at species and genus levels, the overwhelming majority of insectivore tapeworms belong to a single family, Hymenolepididae. Hymenolepidids of shrews are characterized by broad geographic distribution and great diversity of morphological characters and host associations. Their life cycles may involve aquatic or terrestrial

invertebrates. Their strobilae may consist of hundreds of proglottids or just a few segments with maturation being gradual, serial or involving hyperapolyosis. The scolex of shrew hymenolepidids may be armed with hooks or unarmed, with or without rostellum or its rudiment. Representatives of several shrew hymenolepidid genera demonstrate various egg-protecting structures. This diversity creates difficulties in understanding of the character evolution, their homology and relative systematic/phylogenetic value. Rather little is currently known about the phylogenetic interrelationships and evolution of shrew cestodes. The present study uses sequences of nuclear 28S rRNA gene and includes a broad selection of shrew hymenolepidids collected from numerous locations on four continents, as well as cestodes parasitic in other mammalian hosts. Our analysis indicated non-monophyly of some of currently recognized hymenolepidid taxa and revealed major trends in the evolution of these parasites. It demonstrated multiple host switching events that occurred in the course of evolution of shrew hymenolepidids. Geographic expansion, especially in North America, was another important driving factor of diversification among shrew cestodes. Evolution of some other morphological and biological traits, such as scolex armament and type of life cycle, is also analyzed. Our analysis showed multiple secondary losses of scolex armature among shrew cestodes and a secondary transition to aquatic life cycles from terrestrial circulation typical of the majority of mammalian hymenolepidids.

Transcriptomics of filarial infected shrews: Insights on transcriptional level

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Shrew can be categorized into a number of different species belonging to different families and genera. Some shrew species has been used as animal models in research. For example, the house musk shrew (*Suncus murinus*) has been used as a model for emetic research since it is one of a few mammalian species that vomits in response to emetic drugs. Recently, it has been identified as a model species for studies of nutritional regulation of reproduction. Its abundance, its early description by Linnaeus and its association with human make it an important insectivorous study species. Besides that, tree shrew (*Tupaia belangeri*, family Tupaiidae) has been used as a model for study of influenza H1N1 virus. Tree shrews are classified as separate order of mammals (Scandetia) that diverged approximately 85 million years ago. Tree shrews are much more phylogenetically related to human which make them useful as model to study human viral disease. In this study, we would like to explore the use of RNA seq approach to understand the response of tree shrews (Scandetia) towards filarial infection and gain more knowledge on differential pathways allows new novel ideas for future studies.

Helminthes fauna of the common shrew (*Sorex araneus*) in Baltic states

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Sorex araneus were collected in Estonia, Latvia and Lithuania during 2000-2015. Digestive tracts of 261 shrews have been examined; 95% of shrews were infected with helminthes (97% in Estonia, 98% in Latvia and 93 % in Lithuania), 27 species of adult helminthes have been found: *Neoglyphae sobolevi*, *Brachylaima fulvum*, *Rubensstrema exasperatum*, *R. opisthovitellinus*, *Pseudoleucochloridium soricis*, *Neoskrjabinolepis schaldybini*, *N. singularis*, *N. fertilis*, *Vigisolepis spinulosa*, *Ditestolepis diaphana*, *Gulyaevolepis tripartita*, *Spasskylepis ovaluteri*, *Pseudobothriolepis mathevossianae*, *Staphylocystis furcata*, *Staphylocystoides stefanskii*,

Soricinia infirma, *Urocystis prolifera*, *Lineolepis scutigera*, *Monocercus arionis*, *Hepatocestus hepaticus*, *Longistriata* spp. (at least two species), *Parastrongyloides winchesi*, *Liniscus incrassatus*, *Aonchotheca kutori*, *Calodium soricicola*, *Eucoleus oesophagicola*. The lowest number of helminth species was recorded in Estonia, where *P. mathevossianae*, *U. prolifera* and *A. kutori* were not detected. However, *H. hepaticus* was found there, but not found in Latvia. *Rubinstrema opisthovitellinus*, *S. infirma* and *C. soricicola* were found only in Lithuania. The most abundant helminth in the shrews from Lithuania and Latvia was *U. prolifera*. The number of helminth species in common shrews from the Baltic is lower than in those from Poland and Belarus, but in Lithuania there are more helminth species than in Karelia and Finland. This shows that toward the north, the quantity of helminth species decreases. The detection of less helminth species in Latvia and Estonia than in the north of Europe probably is due to small shrew samples (50 in Latvia and 34 in Estonia), which did not allow to find rare species like as *R. opisthovitellinus* and *S. infirma*.

The study was funded by the Research Council of Lithuania (grant No. MIP-43/2015).

Phylogeography and evolutionary history of the *Crocidura hildegardeae* complex (Mammalia, Soricomorpha)

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Within the *Crocidura hildegardeae* complex, three species are actually recognized (*C. denti*, *C. attila* and *C. hildegardeae*), but the validity of these species, their phylogenetic relationships and geographical distributions are unclear. To clarify these aspects, and to better understand diversification processes within this complex of species, we performed a phylogeographic study based on the mitochondrial gene for Cytochrome b. Our results show that the complex *C. hildegardeae* is not monophyletic, but clusters with the complex *C. poensis* (comprising the species *C. buettikoferi*, *C. foxi*, *C. nigeriae*, *C. poensis*, *C. theresae*, *C. turba* and *C. wimmeri*). None of the three nominal species of the *C. hildegardeae* complex is monophyletic in our phylogenetic tree. Based on two molecular criteria (monophyly and genetic distance), we propose to recognise three species within this species complex. These three species have allopatric geographical distribution ranges: one is present in west-central Africa (Cameroon, Gabon, Congo, Central African Republic and Democratic Republic of Congo on the right bank of the Congo River), one is present in northern Zambia and southern Democratic Republic of Congo, and one is present in east Africa (Kenya, Tanzania, Burundi, Malawi and Zambia). Additional analyses including type specimens are necessary to verify how our findings relate to the already existing taxonomy for this group. Our findings suggest that climatic fluctuations during

the Pleistocene may explain the observed intra- and inter-specific genetic divergences. While the Sanaga and Ogooué rivers are not identified as barriers to gene flow within this species complex, the eventual role of the Congo and Zambezi rivers as barriers to gene flow needs to be confirmed.

New data on the Plio-Pleistocene extinction of shrews in Europe

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The Early Pliocene (5.3-3.6 Mya) was the “golden-age” of shrews in the Old World. The Pliocene fossil sites from Europe have delivered up to twenty different fossil genera of Soricidae. Many of them overlapped in time, and indeed several – highly specialized – forms could thrive in the same environments. The current situation is quite different, with only four different genera inhabiting the continent. Moreover, as the recent species *Suncus etruscus* is considered a newcomer that arrived to the western and northern Mediterranean coastal areas not too long ago (probably introduced by humans during historical times), the European diversity of soricids is limited to only three “autochthonous” genera: *Sorex*, *Neomys* and *Crocidura*. The decline in the diversity of shrews turned to be a rather rapid event instead of a gradual and progressive loss of Pliocene species. Most of the extirpations recorded in localities from Hungary, Poland and The Netherlands occurred in less than one million years, and close to the Plio-Pleistocene boundary. In the absence of other similar studies, it was assumed that the number of species of Soricidae decimated simultaneously all around Europe. However, new research on the diversity of this group in Spain reveals that the extinction event recorded in central Europe was preceded by a promptly increase of genera coexisting in southern areas. This biogeographic pattern is most likely explained by the forcing action that climatic episodes like the first northern hemisphere glaciations exerted over the distribution of such small homoeothermic animals.

Seasonal bone dynamics in shrews (Soricidae)

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August Dehnel first described the seasonal shrinkage and regrowth of shrews decades ago, ever since this is referred to as Dehnel’s Phenomenon. However, up to date very little is known how those changes in bone structure actually happen on a histological level. Here we show, together with our collaboration

partners from the University Hospital in Göttingen, that these changes are not caused by the well described osteoblasts and osteoclasts, cell populations active e.g. after a bone fracture. Instead it seems the lesser known osteocytes, cells which reside within the bone matter, are responsible for reorganization of the bone material including the changes in density and length. This observation resembles very well changes that are observed in human osteoporetic bone. This might make shrews an interesting model for osteoporosis since here we observe a controlled regrowth in spring after bone structure was degraded during the winter.

Genetic diversity, endoparasite richness, and co-evolutionary history of the endemic Pribilof Islands shrew (*Sorex pribilofensis*)

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St. Paul Island in the Bering Strait between Alaska and Far-East Siberia supports one native mammal species, the Pribilof Islands shrew, isolated there following fragmentation of the Bering Land Bridge (~16,000 ya). This shrew is the only species in the subgenus *Otisorrex* that is listed as endangered (IUCN red list), although this status largely reflects a deficiency of data. To better understand challenges facing management of this small isolated population under rapidly changing environmental conditions, we investigated both genetic and parasite diversity associated with this mammal species. We addressed three hypotheses: 1) that this population exhibits very low genetic diversity due to both prolonged isolation and phylogeographic history; 2) that parasite richness is low due to faunal relaxation; and 3) that associated endoparasites reflect a Nearctic origin of this shrew (i.e. coevolution) rather than acquisition of new parasite taxa as shrews shifted their historic distribution. We assessed mtDNA diversity within a population of 22 specimens donated by the Native Aleut Tribe of St. Paul, and used molecular and morphological methods to identify endoparasite taxa. Both host and parasite genetic sequences were compared with mainland taxa from the Palearctic and Nearctic using tree-based methods. Our results tentatively support all three hypotheses. Only one shrew parasite species was discovered although parasite loads were often extremely high. In combination with very low genetic diversity, high parasite loads and rapid climate change, the shrew population of St. Paul Island should be carefully monitored into the future. This case study demonstrates a valuable new direction for investigating sorcid evolutionary ecology.

Interspecific differences influencing seasonal changes in food hoarding and consumption in shrews

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Winter is a critical time for homeotherms as it takes more energy to compensate the heat loss and maintain their stable body temperature than in summer. Shrews, with their relatively high metabolic rate and large surface-area-to-volume ratio, are particularly prone to low temperatures. Our aim was to investigate how this predicament influences shrew foraging behavior. Namely, we analyzed how the interspecific differences in shrew's body size, metabolic rate and foraging mode affect their food consumption and food hoarding. Using cafeteria tests performed in summer and winter, we compared foraging behavior of 3 shrew species: the pygmy shrew (*Sorex minutus*; body mass 3.0 g, highest BMR, feeds mainly on epigeal invertebrates), the common shrew (*S. araneus*; 8.0 g, medium BMR, hunts underground) and the Eurasian water shrew (*Neomys fodiens*; 14.4 g, lowest BMR, preys on aquatic invertebrates).

Analyzing the food consumed per capita and per unit of body mass, we found two patterns. The two smaller species with higher metabolic rate, *S. araneus* and *S. minutus*, increased their food intake in winter. In contrast, the large *N. fodiens* with lowest metabolic rate adopted a reverse strategy by significantly reducing the consumption in winter. All three shrews species performed food hoarding in both seasons. However, the seasonal differences occurred only in *N. fodiens* and *S. araneus*: both species hoarded significantly more food (per capita and per unit of body mass) in winter than in summer. This suggests that food hoarding is a strategy specially aimed at winter survival for these two species. Meanwhile, *S. minutus* hoarded food equally intensively in both seasons.

Diving in the Eurasian water shrew (*Neomys fodiens*)

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For better understanding of the effectiveness of *Neomys fodiens* in underwater foraging, its diving behaviour and adaptations were analysed in individuals kept in captivity and tested in aquaria of different size (from 68 × 30 × 30 to 145 × 32 × 26 cm, water depth 120-350 mm) and in an outdoor enclosure with a small artificial brook. Spontaneous diving or diving of trained shrews was filmed or photographed. All shrews were familiar to their keeping conditions for a long time. The submerged *Neomys* has a silvery appearance caused by total reflection of the trapped air in its fur. An important property of the pelage is its water-repellency, which prevents wetting. The water-repellence was a main subject to illustrate by the photographs. Other interesting details observed in diving water shrews are queues of small bubbles in the vibrissae-area. These bubbles may prevent hypothermia of the sensitive tactile receptors. The water shrews breath out small bubbles therefore nostrils are always open in submerged swimming.

Toxic activity of venom of the water shrew (*Neomys fodiens*)

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It is believed that the water shrew (*Neomys fodiens*) employs its venom (injected with saliva) to hunt on large prey. However, the composition, properties and activity of its venom are unknown. Therefore, we analyzed the cardio-, neuro- and miotropic properties of the saliva of the water shrew and the common shrew *Sorex araneus* (control tests) *in vitro* in physiological experiments carried out on two model organisms: beetles and frogs. The saliva was obtained from the submandibular salivary glands of shrews. The protein concentration was measured by spectrophotometry and the final samples were prepared (1 µg proteins / 1 µl saline). Cardioactivity of saliva was determined in the semi-isolated hearts of beetles and frogs and the contractile activity of hearts was recorded. Neuroactivity was determined on the isolated sciatic nerves of frogs and the nerve conduction velocity was measured. Mioactivity was determined on the isolated calf muscles of frogs and the contraction force of muscle was recorded.

The contractile activity of beetle and frog hearts decreased significantly more in reaction to the water shrew venom (beetle heart: 8.12%, n=16, U=200.0, p=0.003; frog heart: 1.73%, n=30, t=6.16, df=29, p<0.0001) than to the common shrew saliva (beetle heart: 0.62%, n=40, t=1.52, df=39, p=0.12; frog heart: 1.50%, n=30, t=-0.71, df=29, p=0.48). Neuroactivity of frog nerve decreased significantly more after application of the water shrew venom (20.4%, n=32, t=4.18, df=31, p=0.0002) than the common shrew saliva (3.4% increase, n=30, t=-3.22, df=29, p=0.003). Similarly, mioactivity of frog muscle dropped significantly more in reaction to the water shrew saliva (10.6%, n=30, t=2.28, df=29, p=0.03) than to common shrew saliva (1.0%, n=30, t=0.03, df=29, p=0.97). Our results show that the water shrew venom possesses stronger neuro- and miotropic properties than cardiotropic activity. We confirm that the common shrew is not a venomous mammal.

Seasonal individual shrinking and regrowth of the braincase in recaptured common shrews

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Organisms inhabiting temperate regions have evolved diverse adaptations to seasonal fluctuations in climate and resources. Small mammals, which have high energy demands and are unable to migrate away from harsh conditions, have developed seasonal strategies based on great phenotypic flexibility that involve

changes in anatomy, physiology and behaviour. One of the most outstanding but poorly known examples is the profound seasonal morphological transformation of soricine shrews, which includes a de- and then re-increases in body mass and size as well as the size of the brain and braincase, i.e. Dehnel's Phenomenon. However, these changes in braincase have never been described at the individual level since previous studies were based on post-mortem skulls, providing a single data point per individual. Using time series of x-ray images we show for the first time that individual free-ranging common shrews (*Sorex araneus*) shrink their braincases by an average -15.3% (individual maximum -20.1%). Thereafter, during winter and spring, individual shrews re-grow their braincases by +9.3% (individual maximum +13.2%). These data match measurements of post-mortem skulls. This variation is thus not caused by seasonal size dependent mortality, but reflects profound individual changes in bone anatomy. The observed braincase and correlated brain size changes are hypothesized to translate into large energetic savings that strongly influence individual winter survival in these high-metabolic animals. Shrews therefore offer a unique model for the evolution of coping strategies as well as the study of the underlying mechanisms causing reversible size changes of bone and organs, including the brain and the correlated physiology.

The untamed shrew: origins, impacts and evolution of the invading greater white-toothed shrew (*Crocidura russula*) population in Ireland

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The greater white-toothed shrew was discovered in Ireland in 2007 and has been expanding its range rapidly. The species is already having a significant negative impact and is associated with the local extinction of the pygmy shrew. I will discuss the likely origin of the invasive population inferred from molecular and morphometric data, as well as the distribution, spread and impacts of the invasive shrew. Populations such as these also represent ideal opportunities for studying the effects of range expansions/invasions on the evolution of both genotype and phenotype. Next-generation sequencing was applied to identify single nucleotide polymorphisms (SNPs). SNPs were identified as being under selection in regions associated with immunological, physiological and cellular processes. We also investigated if phenotypic traits (body size, weight and foot length) are evolving towards the range edge. Such changes are indicative that invasions can generate strong selective pressures, even during its early stages.

Social thermoregulation in least shrews (*Cryptotis parva*)

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Cryptotis parva exhibits a geographic range and ecological requirements unique among North American soricines: it possesses a latitudinal distribution, metabolism and communal nesting pattern more like the crocidurines of the eastern hemisphere. We utilized oxygen consumption (VO_2) techniques to examine metabolic shifts and video to document activity patterns and dynamics of solitary and group nesting *C. parva*. Between ambient temperatures of 4°C and 34°C, solitary *C. parva* demonstrated an inverse relationship between ambient temperature (T_a) and resting metabolic rate (RMR); thermal neutral zone (TNZ) was very narrow, between a T_a of 34°C and 36°C. VO_2 was measured in groups ranging in size from one to eight at T_a s of 4°C, 14°C, 24°C and 34°C. The group size had a significant effect on the median RMR and median predicted Kleiber value and was more effective at reducing metabolic cost at a lower T_a . In a second experiment designed to assess the effects of huddling group size and incubator T_a on the T_a of the nest chamber, both had significant effects. Group size had significant effects on the T_a of the nest chamber at incubator temperatures of 5°C, 10°C, 15°C, and 32°C, but not at 25°C. We found no behavioral or physiologic evidence of heterothermy.

Bioclimatic modeling of the distribution of three *Neomys* species in Eurasia

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Ecological niche modelling has been used to estimate the potential distributional area for three shrew species of the genus *Neomys* (i.e. *Neomys anomalus*, *N. fodiens*, *N. teres*) using models based on range distribution data. Despite the fact that water shrews fill very similar ecological niches which often overlapped, it was revealed that each species has specific set of factors limiting their distribution. For *N. fodiens* the most deterrent factors are a dryness index (precipitation of driest season) and a temperature dominated variable; for *N. anomalus* – primarily a temperature dominated variable (minimal temperatures of the coldest season, etc.) and then a dryness index; for *N. teres* – a temperature dominated variable and a wetness index (highest weekly moisture and precipitation). The peculiarities of *N. anomalus* and *N. fodiens* areas formation in the past as well as trends of their changes in future are discussed. As for *N. anomalus*, the expanding of the range to the north and east has been observed during last decade that can be linked to global warming. Modelling performed for *N. fodiens*, using further climatic conditions predicted for the year 2050, shows that the disjunction of the species' home range in Eastern Siberia will remain. In general, areas of suitable habitat under predicted climate change, particularly

in Europe, as previously will hold the largest portion of “excellent” habitat, however may turn out to be relocated. In Ukraine, due to the continentality of the climate, changes may be more pronounced than elsewhere in Europe and areas of “excellent” habitat are predicted to be reduced by 38% and seem to be shifting westwards, whereas “low” habitat suitability will increase by 6%.

The role of skull and mandible shape in intra- and interspecific differentiation of *Neomys* (Mammalia: Eulipotyphla): first results

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Geographic variation in shape of the skull and mandible in three species of water shrews (*Neomys anomalus*, *N. fodiens* and *N. teres*) was studied using geometric morphometric methods. We recorded 25 landmarks on the ventral view of the skull and 16 landmarks on the labial view of the mandible. Analyses included 760 specimens of *N. fodiens* (188 localities, 25 countries), 568 specimens of *N. anomalus* (122 localities, 17 countries) and 28 specimens of *N. teres* (10 localities, 5 countries). In cases where a locality was represented by a small number of specimens, samples were pooled on the basis of geographical proximity. For all species no significant differences between males and females were found. The shape of the mandible turned out to be more important for diagnostics of the three *Neomys* species, than the shape of the skull. At the same time both the skull and mandible shape in *N. anomalus* and *N. fodiens* demonstrated high plasticity and tendency to a high level of adaptation to local environments. For *N. anomalus* and *N. fodiens* a clear morphometric distinction between geographically isolated Iberian populations and populations from the other parts of their range was characteristic. At the same time allopatric populations of *N. fodiens* and *N. anomalus* also demonstrated their disparateness. In areas where ranges of the above mentioned species overlapped, the phenomenon of character displacement has been observed. Environmental correlates of geographical variation in the skull and mandible shape as well as their influence on separation of southern populations are discussed.

Paleobiology of the shrews of the Early-Middle Pleistocene of Gran Dolina site (Burgos, Spain)

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The Gran Dolina (TD) site (Burgos, Spain) is a cave deposit belonging to the Sierra de Atapuerca localities with one of the most complete succession of small-vertebrates of Early-Middle Pleistocene age. Soricines are characterised by living in humid habitats and having ferruginous enamel, probably due to their metabolism and diet. Here we describe the distribution of soricids along the sequence of TD linked to environmental changes and start the study of fossil soricines enamel in relation to this environment. Early (TD4, TD5, TD6) and Middle Pleistocene levels (TD10) were studied. Small-vertebrates were obtained by washing and sieving sediments. Their associations were used to infer palaeoenvironmental changes through the sequence. Two incisors of *Sorex* sp. and *Dolinasorex glyphodon* respectively were cut and analysed with SEM and TEM.

The Early Pleistocene soricids are Crocidurinae indet., *Sorex* sp. and *D. glyphodon*, and in Middle Pleistocene *Sorex* sp., *Sorex minutus* and *Neomys* sp. Between the Early and Middle Pleistocene the abundance of soricids decreased as the environment became harsher, the main change in this transition. In the enamel of both soricines teeth, three layers with zones can be distinguished. The highest quantities of iron are located in internal zones forming nanocrystals of oxides or hydroxides cumulated between the prisms of apatite. The precise implications of this disposition will be further studied.

The study was supported by MINECO/FEDER Projects CGL2012-38434-C03-01, CGL2015-65387-C3-2-P and CGL2013-46169-C2-1-P. RMC has a grant from the MEC (FPU14/05528) and JG and CNL of the DGA. JR has a Marie Curie Fellowship (MCA-IEF FP7/2007-2013 Project n°629604).

Do shrews use daily torpor to reduce risk exposure?

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Daily torpor is a state of decreased physiological activity used by some species of birds and mammals to save energy during periods of food shortage. Recent evidence has suggested that this behaviour may reduce mortality by decreasing the amount of time animals are exposed to risks such as predators or anthropogenic disturbances.

We tested if torpor can be used as a direct reaction to these risks using *Crocidura russula*, a white-toothed shrew known to enter daily torpor, as a model. We predicted shrews would reduce their activity and either stay inside the nest more often or focus their time outside the nest more on feeding behaviour when exposed to these risks. Shrews were captured in Sintra, Portugal, and brought to the facilities of the University of Lisbon. After an acclimation period of three days, shrews were tested during four non-consecutive nights in an arena provided with a controlled amount of food and a nest with an affixed datalogger to record nest temperature. Each individual was exposed to four types of sound, one per night: silence and white noise (negative and positive controls, respectively), tawny owl calls and traffic noise. Shrews were video-recorded from 20:00 to 10:00 (lights on at 08:00). Shrews' activity, food intake and nest temperatures were compared between sound treatment groups. Contrary to our main predictions, preliminary results show no evidence of torpor in response to any sound treatment. However, food consumption appears to be larger and more variable in shrews exposed to white noise and tawny owl calls.

Genetic relationships of the house shrew in peninsular Malaysia inferred from cytochrome *b* sequences

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The large Crocidurinae shrews from Malaysia have been poorly studied and their distributions records remain incomplete. Consequently, their taxonomic status is still debated and most large shrews encountered previously were recorded under the species name: *Suncus murinus*, a widespread species that occurs throughout Southeast Asia. In this study we used partial sequences of the mitochondrial cytochrome *b* gene to investigate the genetic relationships between the Malaysian *S. murinus* and the geographically restricted subspecies, and to clarify the taxonomic status of *S. murinus* in Malaysia. Our data showed a similarity of *S. murinus* from west coast of Peninsular Malaysia (Ulu Gombak, Chemor, Lumut and Bukit Katil) to *S. murinus caerulescens* from Colombo (0.5% K2P distance in cytochrome *b* sequences) and demonstrate its intra-specific status to *S. m. murinus* from Anuradhapura. However, the morphological analyses (based on 23 skull characters) of *S. m. caerulescens* (Malaysia and Sri Lanka) presented certain characters have significant variations. In Peninsular Malaysia, sample collected at the edge of forest (Ulu Gombak and Lumut) demonstrate slightly smaller skull than urban area (Chemor and Bukit Katil), but larger when compare them with *S. m. caerulescens* from Sri Lanka. These variations might be caused by different geographical conditions between Malaysia (mainland) and Sri Lanka (island) that contribute to the difference in morphological size of *S. m. caerulescens*. Therefore, broader geographical sampling, particularly from Thailand and Indonesia, of both morphological and genetic characters should help to resolve the relationships of the *S. murinus* species complex across the Sundaland region.

The common shrew story in Russia: postglacial recolonization of the area and current distribution of chromosomal races

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The common shrew (*Sorex araneus*) inhabits a huge area across Eurasia and subdivided into 74 chromosomal races; 24 of them are distributed in Russia. Using data on 1964 karyotypes from 216 localities we mapped a range of each Russian race in detail and found that the ranges in the north-west and south-east are smaller in size whereas the races in central area have larger ranges. In most cases, interracial borders are not attributed to wide rivers or mountains but a race itself may limit distribution of other races. Four main groups of chromosomally relative races were assumed. The western and central parts are occupied by relative Ilomantsi, Moscow-Kirillov and Sok racial lines whereas the separate Baikal line inhabits in the eastern part of the species range. We supposed two distinct centers (western and eastern) of the formation of chromosome diversity of *S. araneus* within Russia. The appearance and further fixation of new metacentrics in the western center is hypothetically attributed to the edge zone of ice-sheet and occurred at the end of the Last Glacial Transition when small isolated shrew populations could survived in available patches of habitats near river valleys. Those habitats were separated by areas of severe aridization. The area of modern inhabited range of *S. araneus* was recolonized in opposite directions; the western fluxes have advanced further to the east, and met the eastern flux near the Ob and the Yenisei rivers.

This study was supported by the RFBR (15-04-04759) and President Grant for Russian Distinguished Young Scientists MK-4496.2015.4.

Shrews in the diet of carnivorous birds and mammals

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Shrews are predators but they sometimes fall prey to larger animals. We have studied the contents of the 5055 mustelid excrements and 334 eagle owl pellets and food elements from the Sikhote-Alin (Russian Far East), as well as 852 canine and mustelid excrements, 249 pellets of 7 raptor species and 9 owl species and 38 items of food of hooded crows from the Vologda region. Carnivorous animals ate 9 species of shrews, of which 98% were the most common species: *Sorex caecutiens* and *S. unguiculatus* in the Sikhote-Alin and *S. araneus* and *S. caecutiens* in the Vologda region. Carnivorous birds and mammals ate shrews more frequently in the Vologda region than in the Far East. This is due to the fact that the population density of rodents – favorite food of many predators – is much lower in the Vologda region than in the south of the

Russian Far East. Thus, the occurrence of shrews in the faeces of sable, Siberian weasel, American mink and badger was 1.5, 2.8, 2.8 and 3.5% respectively, and in the faeces of mustelids of the Vologda region – from 3% in otter to 18% in raccoon dog. Badger, raccoon dog, red fox, and mink consume more shrews than stoat, common weasel and otter. The occurrence of shrews was 6.8% in pellets of raptors, 7% in pellets of owls and 1% in food items of hooded crows. Shrews were consumed by carnivorous animals more frequently in early spring and autumn than in the summer. In general, the composition of diet of carnivorous animals living in areas close to the northern border of distribution is more various than their diet in the south. These results support our earlier suggestion that the species have broad ecological niche in the high latitudes where diversity of shrew species is low (Kolomiitsev & Poddubnaya, in pres.).

Understanding the smallest mammalian brain

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The Etruscan shrew (*Suncus etruscus*) brain is the smallest among terrestrial mammals. At ~60 mg, its volume is ~15% of the mouse brain. Its cortex is extremely thin with an average thickness of ~500 microns, going down to 200 microns in parts. The low cortical thickness and spread makes it an ideal option to study cortex-wide neurophysiology at a cellular resolution using two-photon microscopy. Additionally, the low volume makes it an attractive choice to establish the first comprehensive wiring diagram of a mammalian brain at electron microscopy resolution. Anatomical analysis and physiological mapping has revealed a cortical organization similar to larger mammals, and current efforts to develop an atlas would comprehensively map the cytoarchitectonic organization of the shrew brain. Despite its remarkably small size, the Etruscan shrew exhibits a repertoire of fascinating behaviour. Attacking prey about the same size as itself, and making changes in attack trajectory on timescales of ~50 ms, makes it a natural candidate for the study of different aspects of sensory and motor processing and decision making on neuronal timescales. Its wide variety of physiological states, from extremely fast heart (1500 bpm) and respiration (900 bpm) rates to suspended hibernation-like torpor states make it an excellent candidate to investigate brain centers involved in regulating respiration rates and temperature control. Efforts to generate a whole genome sequence and induced pluripotent stem cells are aimed at increasing genetic access to the shrews and understanding specializations in cellular physiology and architecture which generate the smallest terrestrial mammal.

Shrews (*Blarina* spp.) and the Lyme disease cycle: exploring their role as a reservoir host for *Borrelia burgdorferi* in southeastern Virginia, USA

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Lyme disease incidence is on the rise in the United States, and Virginia is one of the current hotspots with dramatic increases since 2007. The classic understanding of the ecological maintenance of *Borrelia burgdorferi*, the causative agent of Lyme disease, is that the primary reservoir host is the white-footed mouse (*Peromyscus leucopus*). While this rodent is present in Virginia, our preliminary findings indicate that the *Blarina* spp. shrews play a larger role in the ecological system in southeastern Virginia. These shrews are hosts for the immature life stages of the ticks of the region that vector these pathogens, *Ixodes scapularis* and *Ixodes affinis*. Of the seventy shrews trapped in the past five years, 41 had at least one *Ixodes* spp. tick feeding on it. Tissue samples were taken from 63 of these shrews, and all five of the initial samples screened were positive for *B. burgdorferi*. Results of the remaining samples will be presented. These initial findings indicate that more research is needed to better understand the role of *Blarina* spp. in the Lyme disease cycle in southeastern Virginia, USA.

Factors influencing population sizes and overlap of trophic niches of water shrews, *Neomys anomalus* and *N. fodiens*

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Factors influencing population sizes and ecological niches within shrew communities are still poorly understood, especially in coexisting semi-aquatic species. We aimed to test some hypotheses about the influence of certain abiotic and biotic factors on the dietary composition, niche overlap and population numbers of *Neomys anomalus* and *N. fodiens* coexisting under changing habitat conditions. Thus, we analysed data on population sizes (estimated from live-trapping of shrews), monthly mean temperature and sum of rainfall, depth of the stream, availability of terrestrial and aquatic prey, and water shrew diets (based on faecal analysis) collected on a study plot in Białowieża Forest (E Poland) between 1979 and 2004.

Contrary to our prediction, the number of *N. anomalus* increased with rising numbers of its main competitors, *N. fodiens* and *Sorex araneus*. The numbers of all species increased with mean monthly

temperature and decreased with the sum of rainfall. Consistent with our predictions, numbers of *N. anomalus* and *S. araneus* tended to decrease with increasing stream depth, whereas numbers of *N. fodiens* tended to increase. The number of both *Neomys* species tended to increase with increasing numbers of aquatic prey (which was the highest under medium stream depths), whereas the number of *Sorex araneus* tended to decrease. The proportion of aquatic prey in the diets of *N. anomalus* and *N. fodiens* decreased with decreasing stream depth but *N. fodiens* always ate more typically aquatic prey than *N. anomalus*. Interspecific differences in consumption of some terrestrial prey decreased under dry conditions. Contrary to prediction, niche overlap tended to increase with increasing population densities of water shrews. However, as we expected, the overlap decreased with the increase of prey availability (especially terrestrial prey). The results suggest that the population size and diet of the subdominant *N. anomalus* were under a stronger influence of prey availability and abiotic factors than interspecific competition.

Can non-semi-aquatic Soricidae species swim and/or dive?

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The family Soricidae contains a multitude of species occupying various ecological niches and modes of life: such as terrestrial, fossorial and semi-aquatic. Even among those, amphibian soricids (water shrews) have specified life-style rely on riparian region because they feeds primarily on the aquatic preys. Their swimming and foraging behavior are reported in some previous studies, and some characters were discussed as evidences of adaptation for aquatic environment. However, relationship between these behavioral characters and phylogenetical, ecological characters were not known because swimming behavior of most other soricids were not yet studied. We studied swimming behavior and its motion in 10 soricids (7 species of 4 Soricinae genera and 3 species of 2 Crocidurinae genera) from Japan, Taiwan and United States of America during 2014-2016. All individuals were video captured their movements in clear cage with water and rocks, and compared the motions among species. Our result showed that the species in the same genus shared many locomotor features, however, the species in different genera employed different locomotor styles: almost soricids started swimming behavior by themselves and did not drown except for *Suncus murinus* and *Anourosorex yamashinai*. On the other hand, diving behavior was shown only at 2 genera. These genera species checked underwater objects using tip of nose and enter the underwater gaps when they found it. These results suggest that difference in swimming behavior among soricids is united in each genera.

Daily patterns of energy metabolism in *Sorex araneus*

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Pronounced circadian rhythms in activity and energy use are a common feature of mammals under most conditions. Given that shrews possess such an exceptionally high rate of energy demand, they cannot remain inactive for half of any given day. It is suggested that common shrews must refuel approximately every 1.5 hours, thus we predicted that they would display ultradian rhythms across each day. Further, we explored the potential effects of life history on any energetic/activity rhythms by comparing shrews captured during the beginning and near the end of their life cycle. To our surprise, while some shrews exhibited very clear ultradian rhythms, others maintained activity and high energy expenditure throughout the day while others were surprisingly inactive. This flexibility in activity cycles may be important for these animals to respond to changing environmental conditions. We saw very little effect of life cycle stage, but will investigate animals captured in the winter (at the peak of size reduction/Dehnel's effect) in future studies.

Collapse of cyclic dynamics and changes in structure of shrew communities in central Siberia. Analysis of 40 years observations

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We analyzed the long-term dynamics of red-tooth shrew society at the biological station Mirnoe (middle Yenisei taiga, central Siberia) for 44 years of observations. Eight species of shrews from genus *Sorex* inhabit this area: *S. araneus*, *S. caecutiens*, *S. daphaenodon*, *S. isodon*, *S. minutissimus*, *S. minutus*, *S. roboratus*, *S. tundrensis*. The observations were divided into two periods. The first one was done from 1973 till 1994 years, the second one continued from 2007 till 2016 years. The clear 4-years cyclic dynamics was registered for the first period with up to 100 times fluctuations in animal number between peak and depression years. For the second period of observations it was shown that the numerical dynamics of shrew society changed its character to acyclic type with the small number increases shifted by shallow recessions. These multiplicity fluctuations did not exceed 2-3 times. It is important to notice that the long-term average number of shrews was similar for both observation periods. During first period *S. araneus* and *S. caecutiens* dominated, especially in years of peak and before it, while at the years of depression the number of *S. minutus* increased. The similar patterns of dynamic changes were observed for all cycles. At the beginning of the second observation period the number of *S. araneus* was very high for a few years, then this species practically disappeared at the left bank of the Yenisei River and was replaced by *S. roboratus* as dominant species. In previous years *S. roboratus* was one of the most rare species in this shrew society. Thus, in the second period of observations the shrew

society with non-cyclic dynamics had variable species composition which changed from year to year. We analysed and discussed the main reasons of the changes in dynamics characteristics and species composition of shrew society in the middle Siberia.

Integrating phylogeography and niche modelling to unveil the spatio-temporal distribution pattern of the Mediterranean water shrew (*Neomys anomalus*)

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The Mediterranean water shrew (*Neomys anomalus*) is a semi-aquatic species with a wide but fragmented distribution across southern and central Europe and Asia Minor. It is still unclear what are the major factors determining the range fragmentation of this species. The present work intended to better understand the influence of climate and other ecological factors on the distribution of the Mediterranean water shrew by following a time-scaled multidisciplinary approach, that included: 1) the study of the evolutionary history of the species; 2) the analysis of ecological aspects determining its current niche space; and 3) the determination of the effects of future climate changes on the species' distribution. Two factors were identified as significantly contributing to the current distribution pattern of *N. anomalus*: severe climatic alterations, that were extremely important in the evolutionary history of the species and that are also projected to have a significant impact in its future distribution, and the interspecific competition with a congeneric species (*Neomys fodiens*), which is one of the main factors regulating the current habitat preferences of *N. anomalus*. The followed multidisciplinary and time-scaled approach provided relevant insights on the ecological factors determining the presence of the Mediterranean water shrew, ultimately defining its geographical distribution. It also highlighted the need to clarify the taxonomic status of the Iberian populations of this species. The detection of a unique genetic lineage in this region makes the reported findings highly relevant from an evolutionary perspective, and extremely significant for its conservation.

Parasites of European shrews: cnidarians thrive in livers of terrestrial mammals

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A wide range of parasite groups have been recorded from shrews in Europe. Arthropods (fleas, mites and ticks) commonly occur as ectoparasites. Several species of helminths (especially cestodes and trematodes) inhabit the shrew intestine and others (e.g., the nematode *Calodium hepaticum*) the liver. A coccidian parasite (*Sarcocystis* sp.) is often present in muscles, where it produces intramuscular cysts. Recently, the list of shrew parasites has expanded by a rather unexpected group of parasites, Myxosporea (Cnidaria: Myxozoa). Myxosporea are common parasites of fish and, rarely, other aquatic vertebrates (amphibians, turtles, ducks), whereas sexual phase of their life cycle usually occurs in annelids. The first finding of a myxosporean in mammals, including presence of plasmodium and mature spores, was that of *Soricimyxum fegati* Prunescu, Prunescu et Lom, 2007 in *Sorex araneus* from the Białowieża Primeval Forest, Poland. Other hosts (*Sorex minutus*, *Crocidura suaveolens*) and other localities of *S. fegati* in the Czech Republic and Hungary were reported thereafter. Most recently, Székely et al. have described *Soricimyxum minuti* Székely, Cech, Atkinson, Molnár, Egyed et Gubányi, 2015. *Soricimyxum* is a unique myxosporean genus, the only one known to have left the aquatic environment and parasitize mammalian hosts. Development of species of *Soricimyxum* probably alternates between two hosts, i.e., shrew and supposedly earthworm, the complete life cycle, however, is unknown. A further study to determine the supposed alternate host and to describe the complete life cycle is desirable for understanding the myxosporean (cnidarian in general) evolution.

Population adaptations of the shrews (Soricidae) on the northern periphery of the range

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Adaptations to the northern conditions (short warm season, low winter temperatures) by tradition are studied mainly in small rodents. At the same time, shrews infiltrate high latitudes as far as to Arctic tundra, and studies of their species on the northern periphery of their geographic range are of great interest. According to our observations, the changes in biology of shrew species are mainly expressed in diversification of their trophic spectra and intensification of reproduction. Within the taiga zone trophic specialization intensifies northward, which allows 5-6 species to coexist using relatively limited food resources. In the north-eastern direction from the species optimum, the range of food items widens to 4-5 taxa of invertebrates. Further

north, in forest-tundra subzone specialization attenuates, which is explained by the lower species diversity of insectivores: two species (*Sorex caecutiens* and *S. tundrensis*) comprise 95.5% of the community. These species have different biotope preferences, so despite the similar body size they can avoid intense competition even without separate food resources. In addition, on the northern periphery of the range, intensification of reproduction can be observed in small mammal populations, which is achieved by somewhat different means in rodents and insectivores. For rodents it is more characteristic to shift the onset of reproduction to earlier phenological stages and to increase fertility. Shrews are characterized by faster rates of sexual development in juveniles and, to a lesser extent, by increased fertility. In certain years in Yakutia the bulk of juvenile shrews of first generations (up to 100%) reproduce in the year they were born. At the same time it is known that in more favourable conditions juveniles do not reproduce at all or their participation in reproduction does not exceed 2-10%. The aforementioned mechanisms allow shrews to counterbalance the pressure of abiotic factors and populate high latitudes.

Better be bold? The relationship between life-history strategy and personality differences in European shrew species

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Some animals are bold and active, others shy and inactive. If such behavioural patterns are consistent they are referred to as personality. It has been suggested that such consistent behavioural differences are related with life-history strategy. Animals with a fast life-history strategy often have also a higher metabolism and are likely forced to more fixed patterns of behaviour by their higher energetic needs. We thus hypothesise that fast-living species will show less behavioural variance than slow-lived ones, both on the individual and on the species level. Shrews are a perfect model to verify our hypotheses: Two phylogenetic groups of shrews, which differ tremendously in life-history strategy and metabolism, occur sympatrically in many places of the Palaearctic. We aim to understand how the behavioural variance is partitioned between individuals, populations and species. We measured boldness and aggression of over 150 wild-caught individuals from five species of shrews (*Crocidura russula*, *C. suaveolens*, *Neomys fodiens*, *Sorex araneus*, *S. minutus*) from five different locations across Europe (in Poland, Germany and Portugal). We found that most of the variance in our data lies between species and between individuals. Nearly no variance existed between the populations, i.e. between the geographic regions of one species. These results suggest that the life-history strategy and phylogenetic background play a stronger role in shaping a species' personality than its current geographic location. In the next step, we will analyse if the variability between individuals is higher in those species with a slower life-history strategy and a lower metabolism, namely the two *Crocidura* species as opposed to the two *Sorex* species.

New data on the phylogeography of the pygmy shrew (*Sorex minutus*) from Poland and Ukraine support a widespread lineage in Europe

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In this study we analyzed 124 new mtDNA sequences of cytochrome *b* of pygmy shrews (*Sorex minutus*) from Poland and Ukraine. Our data filled a gap in the area of central and eastern Europe, where the pygmy shrew was sporadically sampled in previous studies. This allowed us to re-investigate the phylogeography of this species in Europe using cytochrome *b* sequences. We analyzed the new sequences together with 312 published sequences available in GenBank. We identified six mtDNA lineages of pygmy shrews in Europe using Maximum Likelihood and Median Joining Network analysis. The new sequences from Poland and Ukraine belonged to the previously described Northern lineage, which has the most extensive range across Europe. Additionally, we found that the Western and Northern lineages showed evidence of recent (postglacial) population expansion, which was calculated on around 9,000 and 11,000 years before present, respectively.

Craniometric variability of common species of shrews (Soricidae: *Crocidura*, *Neomys*, *Sorex*): comparison between central and southeast Europe

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The morphometric variability of the skull and the lower jaw of 6 species of shrews (*Crocidura leucodon*, *C. suaveolens* sensu lato, *Neomys anomalus*, *N. fodiens*, *Sorex araneus* and *S. minutus*) was analyzed. By using a large number of measurements an attempt to characterize the morphology of the skull maximally comprehensive was made. Principal component analysis (PCA) was conducted within each genus in order

to condense the information, contained in the initial data sets. In order to analyze the structure of the multivariate data set, consisting of the principal component scores, unsupervised model-based clustering was employed. PCA and model-based clustering revealed clearly expressed morphometric differences between central European and southeastern European populations of both *Crocidura* species. The geographic variability was poorly exhibited in *N. anomalus* and *N. fodiens* and was almost missing in *S. minutus* and *S. araneus*. The obtained results provided a morphological confirmation of the recent molecular data, which indicate that the former subspecies *C. s. mimula* and *C. s. suaveolens* could be treated as separate species. The differences of a similar scale between central and southeastern European populations of *C. leucodon* set the question whether these geographic groups correspond to separate forms, which also deserve a taxonomic differentiation.

Invasions and extinctions in real-time: determining the causes of the local extinction of the pygmy shrew in the face of the invading greater white-toothed shrew in Ireland

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The greater white-toothed shrew (*Crocidura russula*) was discovered in Ireland in 2007 and has already been implicated in the rapid disappearance of the island's only resident shrew species, the pygmy shrew. The means by which the invasive shrew is displacing the resident shrew are unknown. This system provides us with a unique opportunity to understand the mechanisms by which invaders can quickly impact insular populations as it is occurring in real-time at the onset of a well-defined invasion. In order to examine resource competition between these insectivores, we will apply next-generation DNA metabarcoding to study dietary competition between them as the invasion progresses to determine if the invasive shrew is outcompeting the resident shrew. Complementary to this, we will also implement geometric morphometrics of pygmy shrew mandibles to study dietary adaptation to determine if the Irish population is particularly susceptible to a new competitor. In addition to examining resource competition, we will screen both species for pathogens using morphological and molecular techniques to determine if the invasive shrew has introduced novel pathogens to the island which could be detrimentally impacting the resident shrew. This multi-disciplinary study has important implications for potentially predicting the immediate impacts of successful invaders as they rapidly spread.

Influence of vertical gradient of environment on the abundance of common shrews (*Sorex araneus*) in relation to forest habitats

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Based on available data from the years 2006–2011, the abundance of common shrew (*Sorex araneus*) was evaluated depending on vertical gradient of environment (lowlands 173–233 m, uplands 450–660 m, mountains 640–1200 m a.s.l.) and different forest habitats (adult forests, plantations of young trees). The data were obtained on experimental plots in the Czech Republic (South Moravia lowlands, Dražanská vrchovina Upland, Kelečská pahorkatina Upland, Moravskoslezské Beskydy Mts and the Hrubý Jeseník Mts). Based on the results of statistical evaluation of abundance the importance of these areas and habitats for existence of the population of that species was assessed. A total of 200 individuals were included in the study. The traps were exposed for 4 days (i.e. 3 nights) and checked every following morning. Statistical evaluation (One-way ANOVA, Tukey's honest significance test, t-test) was carried out by means of the Statistica v.12 programme. Significant differences in abundance of the common shrew among the individual forest habitats were found. The abundance was changed either depending on the altitude (growing with altitude) or with regard to the type of forest habitat. The populations of shrew in plantations of young trees were demonstrably larger than in adult forests (at all levels – mountains, uplands and lowlands). The plantations in the mountains and the mountain forests with dense herb layer proved to be the most suitable habitat for *Sorex araneus*, while adults forest in the areas of uplands as the least appropriate.

Morphotypical variability of the lower teeth of *Sorex* shrews (Lipotyphla, Soricidae)

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In order to recognize possible species of shrews by their isolated teeth, morphotypical analysis of the lower teeth was performed for large-sized shrews of genus *Sorex* (*S. araneus*, *S. daphaenodon*, *S. isodon*, *S. roboratus*, *S. tundrensis*). Recent collections of shrews (of subadult age) from the territories of Pre-Urals, Polar Urals, Siberia and the Far East were studied.

For lower incisors (i), the morphotypes were distinguished by the location of anterior and posterior edges of the incisor (buccal side), the ratio of the depths in the recesses between the apexes, pigmentation of buccal and lingual sides. Anterior edge is approximately at the same level as the incisor's posterior edge in *S. isodon*, *S. daphaenodon*. The recess between the first and second apexes is equal to or deeper than the recess between the third and fourth apexes in *S. daphaenodon*. The strongest pigmentation is characteristic

of incisors in *S. daphaenodon*, *S. tundrensis*. For the antemolar (a1) morphotypes are distinguished by the shape of the first apex, the pigmentation of the second apex. In *S. daphaenodon* the first apex is rounded, the others are pointed. Pigmentation of the second apex is typical for all species except for *S. isodon*. For a premolar tooth (p4), the coefficient of the length-to-height ratio and the degree of the postlingual fossa depth were identified. For all species, except for *S. tundrensis*, the tooth length is greater than its height. The postlingual fossa is deep (up to 2/3 of the tooth height) in *S. tundrensis* and *S. araneus*. The first molar (m1) was considered on the basis of the following morphological features: pigmentation, cingulum shape from the buccal side, the ratio of the lengths of trigonid and talonid. Morphotypes where the pigmented part is smaller than half of the tooth height, are typical only of *S. isodon* and *S. roboratus*. The concave shape of cingulum is found only in *S. roboratus*, *S. tundrensis* and *S. araneus*. The trigonid length is lower than or equal to the length of talonid in *S. daphaenodon*.

This study was supported by RFBR nr. 15-04-03882.

Co-circulation of soricid- and talpid-borne hantaviruses in Poland

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Previously, we reported the discovery of a genetically distinct hantavirus, designated Boginia virus (BOGV), in the Eurasian water shrew (*Neomys fodiens*), as well as the detection of Seewis virus (SWSV) in the Eurasian common shrew (*Sorex araneus*), in central Poland. In this expanded study of 133 shrews and 69 moles captured during 2010–2013 in central and southeastern Poland, we demonstrate the co-circulation of BOGV in the Eurasian water shrew and SWSV in the Eurasian common shrew, Eurasian pygmy shrew (*Sorex minutus*) and Mediterranean water shrew (*Neomys anomalus*). In addition, we found high prevalence of Nova virus (NVAV) infection in the European mole (*Talpa europaea*), with evidence of NVAV RNA in heart, lung, liver, kidney, spleen and intestine. The nucleotide and amino acid sequence variation of the L segment among the SWSV strains was 0–18.8% and 0–5.4%, respectively. And for the 38 NVAV strains from European moles captured in Huta Dłutowska, the L-segment genetic similarity ranged from 94.1–100% at the nucleotide level and 96.3–100% at the amino acid level. Phylogenetic analyses showed geographic-specific lineages of SWSV and NVAV in Poland, not unlike that of rodent-borne hantaviruses, suggesting long-standing host-specific adaptation. The co-circulation and distribution of BOGV, SWSV and NVAV in Poland parallels findings of multiple hantavirus species co-existing in their respective rodent reservoir species elsewhere in Europe. Also, the detection of SWSV in three syntopic shrew species resembles spill-over events observed among some rodent-borne hantaviruses.

Isolation of a highly divergent hantavirus from the European mole (*Talpa europaea*) in Poland

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Persistent uncertainties in hantavirus taxonomy result from the paucity of full-length genomes and the dearth of hantavirus isolates. Although referred to as novel viruses, nearly all of the more than 30 hantaviruses (family Bunyaviridae, genus *Hantavirus*) identified recently in shrews and moles (order Eulipotyphla) and insectivorous bats (order Chiroptera) exist only as viral sequences. Because Nova virus (NVAV), harboured by the European mole (*Talpa europaea*), represents a highly divergent hantavirus lineage which is widespread across Europe, its isolation has been a highly-priority. Lung tissue homogenates, prepared from four NVAV-infected European moles captured in Huta Dłutowska in central Poland in 2013, were inoculated onto Vero E6 cell monolayers, then subcultured at two- to four week intervals, at which time cells and culture media were analysed for NVAV RNA by RT-PCR. After several failed attempts NVAV RNA was detected in cells and culture media at 34 days after inoculation with tissues from one of four European moles. Subsequently, NVAV RNA was detected following inoculation of fresh Vero E6 cells with culture supernatant, indicating virus replication, and typical hantavirus-like particles, measuring 80-120 nm in diameter, were found by transmission electron microscopy. Genomic sequences of the isolate, designated NVAV strain Te34, were identical to that amplified from the original lung tissue, and phylogenetic analysis of the full-length L, M and S segments, using maximum-likelihood and Bayesian methods, showed identical topologies, with NVAV clustering with the highly divergent bat-borne hantaviruses. Infant Swiss Webster mice, inoculated with NVAV by the intraperitoneal route, developed weight loss and hyperactivity, beginning at 16 days, followed by hind-limb paralysis and death. NVAV RNA was detected in lung, liver, kidney, spleen and brain tissues by conventional and quantitative real-time RT-PCR. The long-awaited isolation of NVAV, as the first mole-borne hantavirus, will accelerate the acquisition of new knowledge about its evolutionary origin, phylogeography and pathogenicity.

Mercury in organs of common shrews (*Sorex araneus*) from Cherepovets (Vologda region, Russia)

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Mercury and its compounds are among the most toxic substances for living organisms. In Cherepovets, Vologda region, there are large industrial enterprises which are the sources of mercury in the environment.

We need to know the level of mercury pollution of the environment. The aim of the study was to determine the level of mercury in the bodies of the common shrew from the forest park Green Grove in Cherepovets (59°3'44"N 37°51'2"E). During the period of study (2008-2010, 2015) 409 samples from 111 individuals were analyzed. The mercury content in samples were determined on a mercury analyzer (PA-915+ with PYRO device, Lumex®). The results were processed in the software package STATGRAPHICS Plus 2.1. A high mercury content was found in kidneys and liver (0.386 and 0.101 mg / kg fresh mass, respectively) and a low – in muscles and brain (0.069 and 0.068 mg / kg fresh mass, respectively). Such a ratio of mercury was observed in all studied individuals. Comparison of the data from the 2008-2010 and 2015 showed an increase in the average level of mercury in kidneys by almost two times (0.248 and 0.524 mg / kg wet mass, respectively). Perhaps this increase is caused by weather factors – high moisture content in 2015, which lead to increased formation of organic mercury compounds. Shrews occupy the top of the ecological pyramid. Therefore, we compared our data with the content of mercury in organs of the raccoon dog and the pine marten: in the muscle and kidney of shrews and dogs mercury level was about equal, in martens it was 4 and 5 times higher. In the liver of raccoon dogs it was 4 times and martens 6 times higher than in shrews. The mercury content in organs of shrews was significantly higher than in the same organs of herbivorous rodents (Ivanova *et al.* 2015).

On reproductive behaviour of *Neomys fodiens* (Soricidae)

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To learn more about reproductive biology of *Neomys fodiens*, five individuals (2 female, 3 male) were observed in an indoor enclosure of 10 connected cages of different size (overall 2.7 m²). Multiple copulations appeared over a period of about 12 hours. Ten litters with 56 offspring were born and 33 survived. The female gave birth to her latest litter at an age of about 20 month, 2 month later as the end of her natural lifespan. The period of fertility lasted 336 days and is comparable to those of *Crocidura*-species. After successful copulations a copulatory lock was achieved and the female could track her mate. The mating behaviour can be classified as follows: a) male entering female's territory, b) precopulatory chasing, c) approaching of the mates, d) mounting and repeated copulations attempts, e) successful copulation, male slipping down from female's back, f) copulatory lock and resting, g) cleaning sexual organs, h) continuing chasing and further copulations or i) displacing the male and finishing sexual behaviour. Driving off the male from female's territory could last some time. No special calls were uttered in the close context of copulatory behaviour, only the known ones while chasing, some low contact calls inside the nest and aggressive calls while driving off the male.

Cestodes of the Holarctic shrews

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Sorex shrews possess rich cestode fauna including about 90 valid species of 21 genera, almost all of them belonging to the family Hymenolepididae and 5 species – to the family Dilepididae. The majority of species (more than 60) is parasitizing in Palearctic region. Only 19 species from 15 genera are found in Europe shrews and 12 species of them have Transpalearctic spread. North American shrew possesses 12 genera (23 species). There is only one endemic genus for Europe *Vigisolepis* (1 species), two – for Asian part of the Palearctic: *Brachylepis* (4 species) and *Diorchilepis* (1 species) and three – for Nearctic: *Vogelepis* (1 species), *Lockerrauschia* (1 species) and *Protogynella* (1 species). It was considered that the genus *Mathevolepis* is endemic for Asia, however, *M. alpina* – the species belonging to this genus – was found in the alpine shrew (*Sorex alpinus*) (Binkienė & Kontrimavičius 2012). Cestodes of the tribes Lineolepidini (34 species) and Ditestolepidini (23 species) are dominating in the structure of population of Hymenolepididae of Palearctic. Only few cestodes belong to the tribes Skrjabinacanthini (3 species) and Staphylocystini (4 species). The taxonomic structure of the cestodes population of shrews of Palearctic and Nearctic is characterized by a high similarity which is the result of close faunistic contacts between them (Dokuchaev & Gulyaev 2007). Ten genera are common for Holarctic: *Mathevolepis*, *Ecrinolepis*, *Spasskylepis*, *Skrjabinacanthus*, *Lineolepis*, *Staphylocystis*, *Staphylocystoides*, *Neoskrjabinolepis*, *Soricinia*, *Monocercus*. Until recently it was believed that only one species (*Lineolepis pribilofensis*) was shared by Nearctic and Palearctic (Chukotka, Alaska). The last studies have shown two more species with transberingian distribution: *Neoskrjabinolepis fertilis* and *N. hobergi* (Kornienko & Dokuchaev 2012).

Predation by the Eurasian water shrew (*Neomys fodiens*) on prey with different body size

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It is believed that the Eurasian water shrew (*Neomys fodiens*) employs its venom to hunt upon prey. According to the optimal foraging theory, hunting and gathering a large prey reduce the costs of prey handling and maximize energetic profits. It also reduces the predation risk. Thus, we hypothesized that the water shrew uses the venom to hunt mainly on larger and more difficult to handle prey. We predicted that (1) smaller prey (mealworm larvae, beetles) will be eaten by the water shrew immediately; (2) larger and more active prey (such as large earthworms or frogs) will be at first bitten, in order to inject the venom into its body,

and only after immobilization will be eaten or hoarded. We performed behavioural tests in the glass terrarium equipped only with a transparent shelter. A single water shrew or common shrew (*Sorex araneus*; control tests) were placed in the terrarium and after 5 minutes a live prey of the selected type was given. The hunting behaviour of shrews was video-recorded until the prey was killed and eaten, or hoarded in the shelter, or up to 30 minutes, if the shrew did not hunt the prey. According to our predictions small prey was usually eaten immediately by both shrew species. They hoarded mainly earthworms and mealworms. Only the water shrew was able to subdue and kill frogs. However, frogs usually were killed and eaten immediately (it seems they were not paralyzed before). This suggests that the water shrew does not need to employ its venom to hunt on such a large prey.

The method of assessing fine locomotive patterns of the common shrew in the open field behavioural test

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Classical behavioural testing of laboratory mammals, like the open field test, depends on averaging observations over many trials and usually large number of objects tested. This approach is well suited for discerning differences in motivational states and/or traits of personality, provided that selected groups are homogeneous enough and behave consistently. However, in our attempts at applying the test in investigations of shrews we had met some problems. In wild animals, like the common shrew both inter-object and intra-object variability of behaviour is usually high. In the common shrew interweaving short episodes of fast locomotion and non-locomotive behaviour have been observed. Therefore, assumptions of the open field testing that are fitting small rodents may not be applicable to mammals having markedly lower ability of seeing distant objects or very high metabolic rate or different ecology (e.g. predators, not herbivores) such as *Sorex* shrews. We propose some alternatives to commonly used methods of assessment of behaviour in the open field (and other similar experimental environments), specifically applying an in-depth analysis of fine locomotor patterns of individual animals in each trial, instead of observation extension and repetition. The method focuses on duration and distance travelled during each consistent episode of behaviour, applying a range of descriptors. While this approach allows for tracking changes in the aim and motivation of behaviour in real time, some of the parameters such as respective length of consecutive episodes or distance covered during each episode seem to be more individually specific than classically assessed motility or boldness/fear equilibrium.

Understanding the global distribution of the two major Soricidae subfamilies, Soricinae and Crocidurinae

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Environmental changes, especially those originating from human activity, are currently a very important topic, as they are a present and future reality and have been proven to influence species distribution and persistence. The Soricidae family (order Eulipotyphla) is an excellent model group as the life history traits of the members of this family make them considerably susceptible to environmental changes. The two major subfamilies of Soricidae (Soricinae and Crocidurinae) are here analyzed considering three interesting traits: there exists a clear turn-over in the distribution of one subfamily into the other at around the 40th parallel north; Crocidurinae are not present in America; and each subfamily represents a distinct physiological response to climatic extremes. More specifically, Soricinae reduce their body size during winter, while Crocidurinae enter daily torpor. For this study, climate data was obtained from WorldClim and spatial data for each member of the subfamilies, 132 species of Soricidae and 170 of Crocidurinae, were gathered from IUCN Red List. Two distance matrices, one of all the species and other solely of the species present in Eurasia and Africa, based on the three most informative climatic variables were created. An analysis of these matrices indicated that there is a significant influence of climate in the distinct distribution of the subfamilies. However, Species Distribution Modelling using MaxEnt shows that the Soricinae subfamily seems to occupy a bigger climatic niche in America than in Eurasia and Africa, giving rise to the possibility that competitive pressure between both subfamilies also exists.

Intrapopulation skull variability of the common shrew (*Sorex araneus*) in the South Bohemia

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The common shrew (*Sorex araneus*) as a model species has been constantly studied for several decades. Despite this, we have only incomplete knowledge about its morphological variability in the Czech Republic.

Majority of previous studies was focused only on body measurements or condylobasal- and mandibular length. The aim of this study is to analyse intrapopulation morphological variability in the population of the common shrew in the Novohradské hory Mts. (South Bohemia, Czech Republic). We compared four groups – adult males, adult females, juvenile males, and juvenile females. We measured 174 individuals and evaluated seven mandibular and seven cranial variables. Sexual dimorphism was ascertained in the length of the mandibular dental row (taken without first incisor), which was longer both in adult and juvenile females than in the corresponding male groups. The breadth of the cranium was bigger in adult males than in other three evaluated groups. There are differences between age groups as well. Higher values in adults were found in condylobasal length, length of cranium, length of mandible and mandibular height. The most important differences between adults and juveniles were found in height of mandible measured under the first molar where mandibles of adults were significantly thicker in both sexes.

The study was supported by the Charles University in Prague, project GA UK No. 40216.

Population dynamics of insectivorous mammals and factors determining them in the southern Sikhote-Alin

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The study was carried out in the mountain forests of southern Sikhote-Alin (Ussuri and Lazovsky reserves). The abundance of shrews was monitored, using traps and polyethylene fences and cones filled with water, in May, July, August, September and October, and in some years in other months as well. The abundance of the large mole (*Mogera robusta*) was estimated by counting their permanent tunnels in the humus layer of the soil, crossing the route accounting, and the use of the index of tunnels/km. We found that the seasonal and multiyear changes in the numbers of large mole and shrews occur synchronously (Poddubnaya 1995). High winter mortality of the large mole and shrews was observed in years when a permanent snow cover was established late, in January-February. In contrast, successful wintering of insectivores was observed in years with a permanent snow cover from November-December. Catastrophic death rate of insectivores in winters with little snow, as was earlier recorded on the plains (Formozov 1946), was not observed in the study area. It is because in a mountain relief there are areas with a relatively stable habitat parameters: rocky placers and oak woods where thickness of leaf litter was about 1 m. The numbers of shrews and the large mole were the highest in the autumn of the year with the least rainfall in the first week of May. At this time, most of the females suckle the young of the first litter and high humidity and frequent frosts affects the survival of young animals. As a result of the successful spring breeding of shrews, the greatest increase of population occurs. This is also because the individuals from the spring generation produce own offspring in August-October. An increase in the numbers of the large mole occurs only as a result of breeding of over-wintering animals. Therefore, the amplitude of the seasonal changes in its numbers is always lower than in shrews.

Survey of discarded bottles more effective than short-term trapping in detection of the diversity of shrews and rodents

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Data gaps in distribution maps of small mammal species, which are crucial for successful conservation, are a common problem. Therefore, methods alternative to trapping (e.g. owl pellets, carnivore guts), especially for broad-scale research of small mammal compositions, have been searching for last years. Effectiveness of two methods, short-term live trapping (more time-consuming, expensive and difficult logistically) and alternative surveying of discarded bottles (non-invasive, quick, cheap), in detection of small mammal diversity was compared. Wooden box live-traps were set during two sessions on two sites (i.e., forest and agriculture) in central Poland (total trapping effort was 2280 trap-hours for each site). The discarded containers without corks (bottles, cans, cardboard and canisters) were collected from the same localities during 1 hr/site. A total of 87 individuals representing 6 species (3 shrews and 3 rodents) were captured in live-traps. In 13 bottles (out of 288 collected containers), 58 small mammals belonging to 10 species (3 shrews and 7 rodents) were found, including 5 species not detected in traps. Shannon-Weiner and Simpson indexes showed higher diversity of the small mammal community revealed by the survey of bottles than by live-trapping. Jaccard and Bray-Curtis indices showed low similarity between both methods. Also Spearman rho correlation coefficient was low with a significant difference of results between live traps and bottles ($p < 0.05$). We recommend the survey of discarded bottles as an efficient complement to traditional scientific methods, which can be performed by both specialist and amateurs, who, at the same time, would collect discarded containers and clean the environment.

Pleistocene shrews of the genus *Sorex* (Soricidae, Lipotyphla) from the Michailovka-5 locality, Russia

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Agadjanyan (2009) described *Sorex araneus* from the Late Neopleistocene, Mikulinsky interval (130-120 kyr BP after Petit et al. 1999), of Michailovka-5 locality (Kursk Region, Russia), but its systematic position and phylogenetic affinities are not firmly settled. The aim of the present study was, through morphometrical

and multivariate analyses, to characterize and allocate the Michailovka-5 locality specimens to Recent chromosome race Neroosa from the same region. The Pleistocene material consisted of the 21 remains of the mandibles, having both the ascending and horizontal ramus. Measurements of specimens were taken according to Zaitsev and Baryshnikov (2002). From the race Neroosa, more or less similar in size, shrews from Michailovka-5 locality differ by having a lesser height of the condyloid process (measurement 7 after Zaitsev & Baryshnikov 2002). Height of condyloid process = 2.50-3.05 (n=20) and 1.75-2.50 mm (n=12), respectively. On this character the shrews from Michailovka-5 locality are similar to *S. runtonensis* and *S. satunini tembotovi* and differ from all the other species of *S. araneus* group. This feature indicates the weak force compression of the jaw adductors (Nikolskii 1990). The diet of these shrews could be less diversified and chiefly consist of smaller invertebrates than diet of Recent *S. araneus*. These Pleistocene shrews are unique in having a great variation of the height of the coronoid process (1.95-2.95 mm, n=21) that is the variation from *S. runtonensis* to Recent *S. araneus* sensu stricto. The Pleistocene shrews from Michailovka-5 locality and Recent *S. araneus* s. str. from the same region are different morphological species. It is probable that this form became extinct in the last Ice Age and in the Early Holocene the Russian Plain was inhabited by the recent race Neroosa. The shrews from Michailovka-5 locality require a special additional studies.

Using geometric morphometry to determine the hierarchical structure of the common shrew

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Common shrew is the species with high chromosomal polymorphism, 74 parapatric chromosomal races are known today (Shchipanov & Pavlova 2016). The study of hierarchical structuring of the species is usually based on analyses of a molecular diversity. Following Polly (2007) we tried to evaluate the possibility of using for this purpose the geometric morphometry methods. We analyzed common shrews of known karyotype (Pavlova et al. 2014) that had been collected from 5 localities with 50 km intervals along the course of Upper Volga, shrews from the place of stationary observations in the Tver region from the localities where molecular diversity has been studied (Shchipanov et al. 2012), and two samples from the banks of the Ob sea in vicinity of Novosibirsk (not karyotyped). Scanned skulls were processed in the package MorphoJ programs (Klingenberg 2011). Centroid size (CS) characterized relative sizes of individuals as the value independent of the shape, and relative wraps (RW) were used as a variable of shape. Morphometric distance was evaluated using Qst (Spitze 1993).

Morphometric distances between populations, both in size and shape are similar to those detected in Polly's (2007) study. Good correlation of RW1 with genetic distances among samples from the Tver station ($r = 0.95$, $p < 0.03$) was found. It is of interest that morphometric distance did not correlate to geographic distance. The minimum geographic distance between the samples significantly different in shape made about 1 km, while samples from another area not differ at a distance of 3 km, similar to results of the molecular study. Morphometric distance for CS did not correlate with genetic distance. Smallest CS was found in a sample from mossy spruce. We assumed that the CS differences reflect principally epigenetic variability. The morphometric structuring was not connected with a race and did not correlate with distance, except

for Novosibirsk samples, which are strongly deviated in all characteristics. These results are consistent with previous studies (Polly 2007, Shchipanov et al. 2014).

The study was sponsored by RFBR (grant 150404759a) and the President of the Russian Federation to grant state support of young Russian scientists (MK-449620154).

Demographic characteristics of the captive population of piebald shrew (*Diplomesodon pulchellum*)

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Since 2008, there is a stable captive population of piebald shrew in the Moscow Zoo. During this time we have got 11 generations and 263 animals (127 females and 136 males). The sex ratio in different generations was close to 1:1, as well as the number of pups per litter did not change in different generations - an average of 2.9 cubs per 1 female live up to 1 month. The maximum size of the litter was 6 cubs. In captivity, piebald shrews kept the breeding season: the maximum success of pairing (50%) was in June, whereas from October to January litters have not been received. Average success of pairing was about 25%. Breeding success of females and males was not associated with the generation number. However, the maximum success of breeding in males (41%) was recorded in the 2 year of their life. In females this effect was not so evident, they have successfully bred on the 2nd and 3rd year of life (about 38%). Life expectancy averaged 465 days, registered maximum was 4 years and 3 months. The average mass of the animals was 11.2 ± 3.1 g. We also observed annual dynamics of body mass, with a maximum in January-March (13.1 g) and a minimum in August-October (9.8 g). In the Moscow Zoo a series of researches of the species have been made, i.e. study of sexual behaviour (Vakhrusheva & Ilchenko 1998), maternal behaviour and ontogeny (Zaytseva et al. 2015), and bioacoustics (Volodin et al. 2015).

New data on distribution of insectivorous mammals on the territory of Yakutia (north-eastern Asia)

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North-eastern Asia is characterized by severe climatic conditions which affects both ecosystem productivity and biodiversity. Up to the end of the 20th century, there were nine registered insectivore species on the

territory of Yakutia: eight species of shrews, including the Eurasian water shrew (*Neomys fodiens*), and the Altai mole (*Talpa altaica*). Our studies in 1979–2014 extended the list to 10 species due to finding *Sorex araneus* in the South-West of Yakutia. New data were obtained, which allowed to expand the geographic range of the Eurasian water shrew, Eurasian pygmy shrew, and taiga shrew. Regional features of fauna and structure of insectivore communities of the southern, western, central and north-eastern Yakutia were revealed. According to the latest data, the northernmost habitable points for *S. araneus* and *S. isodon* in the Lena River valley are N60°44' E114°54' and N64°58' E124°58' respectively. The main way for expanding north for these species is the Lena River valley. The northern most point, where the mole was registered in the Lena-Vilyuy interfluvium area, is N61°47' E113°01'. The Eurasian water shrew was registered in the Lena valley at N60°09' E113°53'. *Sorex minutus* was comparatively abundant in the Lena valley up to N59°27' E112°035'. A single specimens of *S. minutus* and *N. fodiens* were collected in the Lena-Aldan interfluvium area. On the whole, it is worth noting that in conditions of the North, insectivores are one of the most vulnerable groups, which results from, on the one hand, small body size and correspondingly high energy expenditures for maintaining homeostasis, and on the other hand, short summer, which leads to lower species diversity and abundance of the main trophic resource, soil mesofauna. As a consequence, the species that advance north further than others are those most eurytopic: the Laxmann's shrew and tundra shrew. A sharp decrease in species diversity of the insectivores coincides with the line of continuous permafrost.

Bold in the city! Urban shrews show a more bold personality than rural ones

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Urbanisation has a huge impact on many animal species, as urban environments differ in several aspects from natural ones. While some animal species are not able to cope with such changed living conditions, others found ways to adapt. Adaptations can be physiological, morphological and also behavioural. As urban animals are more exposed to anthropogenic disturbances, individuals of urban populations can be expected to be bolder than rural individuals. We are currently testing this hypothesis with shrews of two European species, *Sorex araneus* and *Crocidura russula*. In regions of high abundance (*S. araneus* in central, *C. russula* in southern Europe), populations of these species can also be found in gardens or city parks. We trapped individuals of both species from both rural and urban populations, *S. araneus* in and outside Poznań, Poland, *C. russula* in and outside Lisbon, Portugal. We conducted repeated tests of boldness and aggression to assess the differences in personality between the urban and rural individuals of both species. Our first results show that urban shrews of both species were bolder than rural ones. A more bold personality might be advantageous for animals living close to humans, as the more frequent anthropogenic disturbances might disturb natural daily activities of shy individuals.

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Kontekst Publishing House
ISBN 978-83-65275-23-3