



18th to 21st
September 2017
Greifswald

91st ANNUAL MEETING DEUTSCHE GESELLSCHAFT FÜR SÄUGETIERKUNDE (DGS)



Welcome note

Dear colleagues,

It is a great pleasure to welcome you this year to Greifswald for the 91st Annual Meeting of the German Society for Mammalian Biology (DGS). This year's meeting has been organized by the Friedrich-Loeffler-Institut and the University of Greifswald, Zoological Institute and Museum Greifswald, the OZEANEUM Stralsund, the Tierpark Greifswald and the Zoo Stralsund.

We are sure that the city of Greifswald, with its rich history as a former member of the Hanseatic League, combined with the modern amenities it offers as a university town and its superb location on the Baltic Sea will be a perfect setting to create a stimulating atmosphere of exciting talks, inspiring discussions, and scientific curiosity.

In order to help create just this kind of exciting and interdisciplinary scientific environment, we have set up an exhilarating conference program for you this year. This will include a public lecture to be held by Prof. William B. Karesh (New York) as well as plenary lectures by Prof. Barbara König (Zurich), and Prof. Gerald Heckel (Bern). These are of course in addition to the numerous other state-of-the-art presentations being held by experts in the wide range of research fields represented by the society, including mammalian biology and ecology, as well as veterinary and human medicine.

Additionally, we have several informal get-togethers planned as part of this year's meeting, which we hope will further facilitate scientific exchange between the invited speakers and participants in order to establish new contacts and collaborations. The social program includes guided tours of the Friedrich-Loeffler-Institut on the Insel Riems and to the OZEANEUM aquarium in Stralsund. Furthermore, the Tierpark in Greifswald and the Zoo in Stralsund will be pleased to welcome you for a visit.

Once again, welcome to Greifswald, and we wish you a successful and stimulating conference!

Yours sincerely,

Rainer G. Ulrich
Friedrich-Loeffler-Institut

Gerald Kerth
University Greifswald,
Zoological Institute and Museum

Harald Benke
OZEANEUM Stralsund

Heidi Schönherr
Tierpark Greifswald

Christoph Langner
Zoo Stralsund

Content

Program	6
Plenary Lectures	12
Topic 1: Small mammals and their pathogens	18
Oral presentations	18
Poster	42
Topic 2: Hibernation and torpor	78
Oral presentations	78
Poster	90
Topic 3: Free Topics	100
Oral presentations	100
Poster	124

Program

Monday, September 18th, 2017

Venue: Alfried Krupp Wissenschaftskolleg Greifswald

- 18:00-20:00 **Plenary lecture: One Health in the 21st Century**
William B. Karesh, New York, USA
Introduced by Thomas C. Mettenleiter, Greifswald - Insel Riems, Germany
- 20:00-22:00 Get-together

Tuesday, September 19th, 2017

Venue: University Greifswald, Campus Loefflerstraße,
Ernst-Lohmeyer-Platz 6 / Friedrich-Loeffler-Straße 23
17489 Greifswald

- 09:00-09:30 **Opening of the conference**
Werner Weitschies
Dean of the Faculty of Mathematics and Natural Sciences,
University of Greifswald, Greifswald, Germany
Sabine Begall
President of the Deutsche Gesellschaft für Säugetierkunde,
Essen, Germany
- 09:30-10:30 **Plenary lecture: Space, time and pathogens in the fastest radiation of mammals**
Gerald Heckel, Bern, Switzerland
Introduced by Rainer G. Ulrich, Greifswald - Insel Riems, Germany
- 10:30-11:00 Coffee break

Topic 1, Part 1: Small mammals and their pathogens

Chair: Gerald Heckel

- 11:00 Anchored phylogenomics resolves the most successful late Miocene radiation of African rodents (tribe Arvicanthini)
Josef Bryja, Brno, Czech Republic
- 11:15 Isotopic signatures in small mammals, sharing limited territory of a seasonally flooded meadow
Linas Balčiauskas, Vilnius, Lithuania
- 11:30 Rodent outbreaks: patterns and prediction of population dynamics
Jens Jacob, Münster, Germany
- 11:45 Is social dominance a part of animal personality? How dominance rank affects space use and fitness in social voles
Jana Eccard, Potsdam, Germany
- 12:00 Group-level differences in a transport task emerge from individual differences in personality: a study in the mound-building mouse
Heiko G. Rödel, Paris, France
- 12:15 Thyroid hormones in a subterranean rodent - testing physiological implications for a life underground
Yoshiyuki Henning, Essen, Germany
- 12:30-16:00 **Poster session (including Lunch)**

Topic 1, Part 2: Small mammals and their pathogens

Chair: Rainer G. Ulrich

- | | |
|-------------|---|
| 16:00 | <p>Origin and impacts of the causative agent of White Nose Disease on hibernating bats</p> <p>Sebastien Puechmaille, Greifswald, Germany</p> |
| 16:15 | <p>When a virus uses another entrance - Immune mechanisms involved in innate anti-lyssavirus immune response in nasal cavity of European bats</p> <p>Bernd Köllner, Greifswald - Insel Riems, Germany</p> |
| 16:30 | <p>Biology of murine cytomegalovirus infection in the European house mouse hybrid zone</p> <p>Jana Těšíková, Brno, Czech Republic</p> |
| 16:45 | <p>Multiple detection of zoonotic variegated squirrel bornavirus 1 in different squirrel species</p> <p>Kore Schlottau, Greifswald - Insel Riems, Germany</p> |
| 17:00 | <p>Seasonal hantavirus dynamics in two rodent reservoir species</p> <p>Christian Imholt, Münster, Germany</p> |
| 17:15 | <p>Bank vole evolutionary lineage association of Puumala virus in Germany</p> <p>Stephan Drewes, Greifswald - Insel Riems, Germany</p> |
| 18:00-22:00 | <p>Visit of the Friedrich-Loeffler-Institut/Insel Riems: Guided tour and Barbecue</p> |

Wednesday, September 20th, 2017

Venue: University Greifswald, Campus Loefflerstraße,
Ernst-Lohmeyer-Platz 6 / Friedrich-Loeffler-Straße 23
17489 Greifswald

09:00-10:00 **Plenary lecture: Social interactions - causes and consequences**

Barbara König, Zurich, Switzerland
Introduced by Gerald Kerth, Greifswald, Germany

10:00-10:30 Coffee break

Topic 2: Hibernation and torpor

Chair: Barbara König

10:30 Early departure from the hibernaculum and its implications on mortality in bats

Christine Reusch, Greifswald, Germany

10:45 The duration of hibernation of indigenous bat species - results of multiannual field research

Karl Kugelschafter, Lohra, Germany

11:00 Extreme flexibility in torpor patterns in a tropical bat (*Hipposideros commersoni*)

Stephanie Reher, Hamburg, Germany

11:15 Stay cool or warm up? Individual variation in energy-saving strategies and the pace-of-life syndrome in eastern chipmunks (*Tamias striatus*)

Melanie Dammhahn, Potsdam, Germany and Montréal, Quebec, Canada

11:30 Seasonal adaptations and inter-specific differences of the energy budgets of two primates (*Lepilemur leucopus* & *L. ruficaudatus*)

Janina Bethge, Hamburg, Germany

11:45 Possible causes and consequences of different hibernation patterns in Malagasy lemurs - Mitovy fatsy sahala

Kathrin Dausmann, Hamburg, Germany

12:00-13:30 Lunch break

Topic 3, Part 1: Free topics

Chair: Peter Giere

- 13:30 Stress assessment in wild ruminants: can we quantify an influence of stress on forest damages by foraging deer?
Jens-Ulrich Polster, Tharandt, Germany
- 13:45 Common leopards and humans: a difficult coexistence?
Sandro Lovari, Siena, Italy
- 14:00 The phylogeny of the hominoids: results from molecular and morphometric data
Udo Rempe, Kiel, Germany
- 14:15 Dark grey gazelles *Gazella* in Arabia: Threatened species or domesticated pet?
Hannes Lerp, Wiesbaden, Germany
- 14:30 External morphology and chondrocranial development in therian mammals
Evelyn Hüppli, Zürich, Switzerland
- 14:45 The lacrimal bone diversity in Cervidae - what size and shape tells us about cervid evolution
Ann-Marie Schilling, Munich, Germany
- 15:00-15:30 Coffee break
- 15:30-17:00 General meeting of the Deutsche Gesellschaft für Säugetierkunde
- 18:00-23:00 Guided tour to the OZEANEUM in Stralsund and Dinner

Thursday, September 21th, 2017

Venue: University Greifswald, Campus Loefflerstraße,
Ernst-Lohmeyer-Platz 6 / Friedrich-Loeffler-Straße 23
17489 Greifswald

Topic 3, Part 2: Free topics

Chair: Gerald Kerth

- 9:00 To fight or not to fight? Behavioural interference between ungulate species
Francesco Ferretti, Siena, Italy
- 9:15 Reproductive strategy in female Alpine mountain hares (*Lepus timidus varronis*): adaptation to different elevation?
Stéphanie Schai-Braun, Vienna, Austria
- 9:30 Seeing clear: New insights on magnetoreception in mammals
Christin Osadnik, Duisburg-Essen, Germany
- 9:45 Species-specific responses to human-induced habitat modifications - A population genetic survey of neotropical bats
Tanja Halczok, Greifswald, Germany
- 10:00 Negligible senescence in mammals? The case of *Myotis bechsteinii*
Toni Fleischer, Rostock, Germany
- 10:15 Hepatitis E virus in zoo housed primates
Carina Spahr, Stuttgart, Germany and Leipzig, Germany
- 10:30-11:00 Coffee break
- 11:00-12:00 Lecture of the Fritz-Frank-Awardee
Introduced by Rainer G. Ulrich, Greifswald – Insel Riems, Germany
- 12:00-12:30 Announcement of the winners of the Young scientist oral presentation and the poster prizes
- 12:30 - 13:00 Resumé and Farewell
- 14:00 Guided tour to the Tierpark Greifswald

One Health in the 21st Century

Karesh, William^{1,2}

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² *World Organization for Animal Health (OIE) Working Group on Wildlife*

In remarkable ways, the embracing of the One Health concept over the last decade has resulted in a dramatic shift in the discussions, practices, policies and partnerships that link the health of people, animals and our shared environments. In other ways, the efforts have been focused on improving on 20th Century approaches and meeting 20th Century goals rather than boldly leading us into the 21st Century. While the movement has had positive effects, the challenge remains to expand stakeholder engagement in One Health and think more broadly about where opportunities for impact may lie.

One Health is not only about infectious diseases; non-transmissible diseases, the health of plants and animals, the quality of our water and air, and the safety of the environment in which we live, share, and depend all fit within the rubric. But since infections shared among animals and people account for the majority of emerging human infectious diseases, and most of these are from wildlife, “low-hanging fruit” for collaborative benefits can be found at the human/animal/environment interface of infectious diseases and even pandemics. Ecology and the environment is key because we know that the leading drivers of disease emergence in humans result from activities such as land use change, food production systems, and trade and travel. This reality reveals the need to embrace a wider range of civil society and partners and indicates the valuable role that the private sector can play.

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Space, time and pathogens in the fastest radiation of mammals

Heckel, Gerald

University of Bern, Institute of Ecology and Evolution, Bern, Switzerland

Speciation research has gained momentum in recent years through the explicit consideration of adaptive processes in diversification. In some taxa, adaptation appears to be highly important for the onset of speciation but it is not clear whether this is a common phenomenon. Rodents have achieved the largest taxonomic diversity among mammals and feature extraordinary diversification rates yet they appear to fall short phenotypic divergence relative to other vertebrate groups. This presentation reflects on spatial, temporal, and other factors contributing to - and potentially limiting - the diversification of rodents. With a focus on the radiation of the *Microtus* genus, I report on recent investigations of the spatial patterns of divergence and the build-up of (incomplete) evolutionary boundaries in contact zones of multiple species and lineages of voles and their pathogens. Genetic and behavioral data show that the critical stages of divergence before completion of reproductive isolation among incipient species are often associated with sex-specific processes at pre- and/or post-zygotic levels. Recent genetic analyses demonstrate that the time required for reaching these critical stages might be shorter than often assumed. Sexual selection and other adaptive processes appear less prevalent in rodents than in other vertebrates, although important phenotypic and ecological traits and their consequences for the diversification of voles and their pathogens remain understudied. However, investigations that embrace analyses of more complex phenotypes and their interactions have proven fruitful for resolving the conundrum of apparent evolutionary stasis of some traits despite very rapid speciation in many taxa.

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Social interactions – causes and consequences

König, Barbara

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Social interactions are central to many organisms and influence behaviour and ultimately fitness. The social environment is considered to be the most complex and fluctuating component of an individual's environment because of its high degree of flexibility and intrinsic unpredictability. In social species individuals benefit from interacting with conspecifics, compete over identical resources and risk transfer of diseases and parasites. I will present data from a long-term study on wild house mice (*Mus musculus domesticus*) in a Swiss barn to discuss the significance of social interactions of a rodent in its natural environment, exposed to parasites and diseases. Individuals in this population use a variety of nesting places where they regularly interact with several reproducing and non-reproducing conspecifics belonging to the same social group. They further encounter emigration and immigration. Such a pattern underlines the significance of social partners and individualised social groups. Within groups, social relationships are structured by relatedness (females share a social environment with relatives), by cooperation (females cooperate by communal nursing) and by the existence and resolution of conflicts (pronounced reproductive skew in both sexes; females adjust their social behaviour to the circumstances and reduce their propensity to cooperate in a situation of high risk of exploitation). Interestingly, individuals further modify their social interactions when immune-challenged so that they feel sick, leading to localized changes of social connectivity that have a large impact on disease transmission within social groups.

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Anchored phylogenomics resolves the most successful late Miocene radiation of African rodents (tribe Arvicanthini)

Bryja Josef ^{1,2}; Nicolas Violaine ³; Šumbera Radim ⁴; Konečný Adam ²; Denys Christiane ³; Verheyen Erik ^{5,6}; Bryjová Anna ¹; Lemmon Alan R. ⁷; Lemmon Emily Moriarty ⁸; Mikula Ondřej ^{1,9}

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The tribe Arvicanthini is very successful group of African murid rodents with 17 currently recognized African genera and possibly two Asiatic ones. Some genera are species-rich and widely distributed (e.g. *Lemniscomys*, *Aethomys*, *Grammomys*), others are monotypic with very restricted ranges (e.g. *Lamottemys* from Mt. Oku in Cameroon, or *Desmomys* endemic to Ethiopian highlands). They colonized whole sub-Saharan Africa (with isolated populations even in northern Africa) and they live in very wide spectrum of habitats from lowland humid forests through savannas to semi-deserts. African diversification of these rodents began in late Miocene (TMRCA of Arvicanthini was estimated between 7-12 Mya) and the earliest records of modern genera are from the very end of Miocene. Despite intensive efforts and employment of mitochondrial and nuclear markers, the phylogenetic relationships among many lineages (= genera) remained obscured. Many nodes on the phylogenetic tree

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Isotopic signatures in small mammals, sharing limited territory of a seasonally flooded meadow

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We studied the small mammal (SM) community in a polder-restricted 7.06 ha area of spring flooded meadow in the Nemunas River Delta, Lithuania. In 2008-2016, using lines of snap traps and a trapping effort of over 7500 trap/days, 11 species of SM were trapped. This territory held exceptionally high densities of *Micromys minutus* and *Microtus oeconomus*, both being species that are generally not common in Lithuania. In earlier years, the dominant species were *M. minutus* or *M. oeconomus*, while in later years *Apodemus agrarius* was dominant. We found that species with similar ecological requirements occupied different microhabitats. In 2014, isotopic signatures were investigated and three distinct clusters of SM species were identified according $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$. The first cluster consisted of *Sorex araneus* and *S. minutus*, the second *A. agrarius* and *M. minutus* and the third *Myodes glareolus*, *Microtus agrestis* and *M. oeconomus*. In some species, isotopic signatures also differed depending on spatial distribution, i.e. between individuals trapped in neighbouring snap traps. Within the same SM species, there was a tendency for differences in isotopic signatures between males and females, as well as between age groups. We conclude that even in a quite uniform environment, isotopic differences in SM show diet differences, thereby permitting the coexistence of a diverse community in a limited area of changing habitat.

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Rodent outbreaks: patterns and prediction of population dynamics

Jacob, Jens¹; Imholt, Christian¹; Reil, Daniela^{1,2}

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Rodent population outbreaks are a typical feature of many small mammal species across the world. Multi-annual fluctuation of population size affects ecosystems beyond the small mammal community because of cascading effects through the food web as well as impacts on soil, seed bank, crops and the risk of transmission of rodent-borne disease.

Time series analyses can help to detect patterns in population dynamics and to identify relevant processes. Resulting predictive models can also be used to minimise unwanted effects of overabundant rodent populations in conservation, cropping and on human infection risk. In addition, long-term predictions can be utilised to assess effects of climate change on outbreak patterns.

We used long-term time series of rodent abundance and spatially and temporally corresponding weather parameters from several locations in Germany. Weather conditions were highly correlated to outbreaks in field and forest rodents. Most of the relevant weather parameters connected to field rodent abundance originated in the preceding winter and early spring. In contrast, there were delayed effects in forest rodents, which responded to weather parameters affecting seed mast of forest trees in the previous year.

Based on the A1B CO₂ emission scenarios we estimated the future occurrence of weather conditions that favour bank vole outbreaks. Results indicate that such conditions are likely to occur more frequently in the future than it is currently the case. This may also be true for other rodent species if dynamics are similarly related to weather conditions. This can potentially cause ecosystem-wide effects at several trophic levels.

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Is social dominance a part of animal personality? How dominance rank affects space use and fitness in social voles

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⁴ *Plant Ecology and Nature Conservation, Institute of Biochemistry and Biology, University of Potsdam, Potsdam, Germany*

Rank hierarchies are common in group living animals, but hierarchies should be flexible. Meanwhile, animal personality partly is an inherent, individual trait. Is there a connection between rank and personality? We used male common voles (*Microtus arvalis*), to test whether personality predicts social rank and whether dominance and personality affect space use, dynamic interaction, and fitness in experimental populations.

Wild captured voles were phenotyped for boldness and activity. Two bold/active and two shy/inactive males each were grouped, and ranked after six dyadic tests according to their within-group dominance. Ten such groups of males were released to large outdoor enclosures with 4 females each for 7 weeks. Space use of individuals was measured by automated radio-tracking, yielding >5,000 locations, 412 individual day-ranges from 20 males. Fitness was measured via paternity analysis of all offspring sired during the experiment.

Most bold males behaved dominant in dyadic encounters. Dominant males (DM) had larger day-ranges than subordinates when released to enclosures but smaller day-ranges later in the experiment. DMs spatially excluded each other, but overlapped by home ranges of subordinates. During estrus of females, DMs had extremely small day ranges, while subordinates had larger ones. Dominant males sired more offspring than subordinates.

Our experiment demonstrated that dominance was closely related to animal personality traits. Dominant/bold males had higher fitness than subordinate/shy males in the test conditions of low population densities in summer, however lower fitness of dominants during other conditions may help maintaining the existence of different behavioural types in populations.

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Group-level differences in a transport task emerge from individual differences in personality: a study in the mound-building mouse

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² *Department of Ecological and Biological Sciences, University of Tuscia, Italy*

Personality differences can have consequences on an animal's behavioural performance, which might even lead to emerging group-level phenomena. We studied such potential effects in sibling groups of juvenile mound building mice (*Mus spicilegus*). Juveniles of this small rodent cooperatively build large mounds made out of plant and soil materials during autumn, under which they dwell during winter. We asked whether personality was associated with individual transport performance and whether the group composition of personality types affected the group performance of cotton ball transport - the latter resembling the transport of plant materials during the mound building process. More proactive individuals - as assessed by the animals' stable behavioral responses in repeated open field, novel object and elevated plus maze tests - transported a consistently higher proportion of the available cotton balls from an adjacent box into their home cage than their group mates. Groups also differed consistently in their overall transport performance, and such difference was mainly driven by the personality of few ("keystone") individuals within groups. Thus, the mound building mouse provides a striking example of the impact of group personality composition on group performance in a cooperative working task.

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Thyroid hormones in a subterranean rodent - testing physiological implications for a life underground

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Living underground requires physiological adaptations to cope with the harsh subterranean conditions. While the exceptionally low resting metabolic rate (RMR) of subterranean rodents is broadly accepted as an important adaptation to restricted oxygen and food availability in underground burrow systems, the adaptive value of other features is not clear. For instance, the unique visual abilities of Ansell's mole-rats (*Fukomys anselli*) is puzzling. As in most mammals, Ansell's mole-rats possess a short-wavelength sensitive (S-)opsin and a long-wavelength sensitive (L-) opsin. However, while mammalian retinas are M-opsin dominant, the majority of cones in the mole-rat's retina express S-opsins. The thyroid hormones (TH) T3 and T4 are inevitable for M-opsin expression, but in Ansell's mole-rats T4 is extremely down-regulated, which might be causative for the low M-opsin expression. TH are also key regulators of the metabolic rate, hence we hypothesize that low T4 availability has evolved in order to downregulate RMR as an adaptation to the subterranean habitat, while opsin expression is passively influenced by TH-levels, since selective pressure on color vision is absent. To test this hypothesis, we treated Ansell's mole-rats with T4 and T3 as monotherapies to determine the effects on RMR and vision, respectively. RMR was measured by indirect calorimetry at different timepoints during treatment. Preliminary results indicate that TH-effects on RMR are marginal. To identify TH-related changes in visual properties, we will quantify the expression of several genes involved in the retinal phototransduction cascade by means of qRT-PCR. The results will be interpreted in light of Ansell's mole-rats' ecophysiology.

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[illegible]

Origin and impacts of the causative agent of White Nose Disease on hibernating bats

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White-Nose Disease has killed millions of hibernating bats since it first emerged in North America in 2006. This infectious disease is caused by a pathogenic fungus, *Pseudogymnoascus destructans* that was suspected to be introduced to North America by human trade or travel. We applied eDNA analyses from bat hibernacula to demonstrate the widespread presence of the fungus across Europe and used genetic data from fungal populations from both continents to confirm the introduced origin in North America. This scenario explains the lack of associated mass mortality among European bats while the naive North American populations are collapsing. To investigate the consequences of the disease on bat populations, we assembled four decades of population counts from 1108 populations to compare the local abundances of bats in North America before and after the emergence of the disease to the situation in Europe, where the disease is endemic. We demonstrate a 10-fold decrease in the abundance of bats at hibernacula in North America, eliminating large differences in species abundance patterns that existed between Europe and North America prior to disease emergence. We document extensive local extinction in many species in North America. As the fungus range is still expanding in North America, we used a species distribution modelling technique - maximum entropy modelling - to predict its potential future distribution. Results indicated that the fungus is currently occupying only half of its potential distribution in North America, suggesting that the disease will soon threaten many more bat populations and species.

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When a virus uses another entrance - Immune mechanisms involved in innate anti-lyssavirus immune response in nasal cavity of European bats

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⁴ University of Veterinary Sciences, Brno, Czech Republic

Lyssaviruses are neurotropic viruses causing fatal encephalitis of central nerve system, rabies. In Europe, bats act as reservoir hosts for two specific types of lyssaviruses, European Bat Lyssavirus type 1 and 2 (EBLV-1 and -2). Although cases of rabies in bats caused by and transmission to humans of EBLV 1 or 2 are described, there are no reports about epidemics in bats. Moreover, lyssavirus specific antibody titers in European bat colonies were only rarely detected. This indicates that innate immune pathways might be responsible for the observed resistance without contribution of adaptive immune mechanisms in bats.

Therefore, we characterized the interferon (IFN) type I and III family of two European bat species *Eptesicus serotinus* and *Myotis myotis*. Both species do have a typical IFN structure with type I IFN β , δ , ϵ , κ , ω and τ and type III IFN λ . Until now there are no evidences for an active IFN α as only one pseudogene could be sequenced yet. Using established cell lines from nasal epithelium (MmNep), nervus olfactorius (MmNoI), brain (MmBr) of *M. myotis* we analyzed in-vitro the IFN responses along the aerosol infection route by investigation of IFN-specific signaling pathways, induction of IFNs/interferon stimulated genes (ISGs) and anti-viral effects in correlation to the expression of viral receptors in each cell line.

Interestingly, we found a gradually decreased susceptibility along the aerosol route combined with an increased IFN response indicating that the observed resistance of bats is based on a specific co-evolutionary relation between lyssaviruses and their reservoir hosts.

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[illegible]

Biology of murine cytomegalovirus infection in the European house mouse hybrid zone

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Murine cytomegalovirus (MCMV) is an enveloped dsDNA virus (family *Herpesviridae*) whose host species is the house mouse. MCMV occurs in relatively high prevalence and produces persistent asymptomatic or latent infections in its host. MCMV ecology and pathogenesis are well described, but in most cases studies are conducted on laboratory mouse strains. Two taxa of house mice, *Mus musculus musculus* (Mmm) and *Mus musculus domesticus* (Mmd) meet and hybridize along a 2500 km long front stretching from Scandinavia to the Black Sea. At this front the taxa form a narrow hybrid zone (the house mouse hybrid zone, HMMHZ). The two mouse taxa have been shown to harbour different MCMV strains that have likely co-diverged with their hosts. The goal of our study was to investigate the biology of MCMV infections in wild mice and how the viral load change across the host hybrid zone. MCMV load was measured by specific real-time PCR in different organs (lungs, kidneys, spleen and salivary glands) in 60 individuals (30 Mmm and 30 Mmd) sampled in 2014 across the Bavarian-Bohemian region of the HMMHZ. Viral load was higher in salivary glands compared to the 3 other organs in both mouse taxa in line with the pattern of infection found in laboratory mice. Mmd showed higher MCMV load compared to Mmm. This result likely reflects the co-adaptation of each MCMV strains for its mouse taxon.

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Multiple detection of zoonotic variegated squirrel bornavirus 1 in different squirrel species

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A recently discovered novel putative zoonotic bornavirus, variegated squirrel bornavirus 1 (VSBV-1), caused fatal encephalitides in three squirrel breeders and a zookeeper. Viral RNA was detected in brain samples from the patients as well as in organ samples of a variegated squirrel (*Sciurus variegatoides*) kept by one of the breeders.

Screening of more than 750 squirrels of 18 different species (oral swab samples and in parts fecal pool samples) using the published VSBV-1 specific RT-qPCR revealed a positivity rate of 3.5%, including squirrels of the subfamilies Sciurinae (1.5%) and Callosciurinae (8.5%). These squirrels belonged to private holdings as well as zoological gardens. VSBV-1 sequences of the 28 RNA positive squirrels were generated and phylogenetic analysis revealed a holding-related clustering of the sequences, independent from the squirrel species.

We were able to co-cultivate infected primary squirrel cells with a permanent cell line and to isolate infectious virus from these passaged cells. Electron microscopy exhibited the typical structure of a bornavirus. The virus isolate was used to infect neonatal rats intracranial. After a few weeks, two of four rats were VSBV-1 genome positive and virus re-isolation from rat brain material was successful.

In conclusion, the non-invasive sampling methods and the established workflow seems to be suitable for rapid screening of squirrels and revealed further infected animals of different squirrel species, representing a threat for humans handling squirrels. In addition, we were able to isolate the virus and passage it in rats, which is a precondition for further animal trials.

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Seasonal hantavirus dynamics in two rodent reservoir species

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Hantaviruses circulating in rodent populations are a major issue in public health. It is therefore imperative to understand the effects of host density and population specific demographic factors to estimate the relative contribution of functional groups to the virus transmission within the host population. This might however vary between different host/hantavirus systems.

Here we present results that highlight seasonal changes in density dependence and demographic drivers (age, sex, reproductive activity) of acute and persisting hantavirus infections in the two most common rodent host/hantavirus systems (Bank vole (*Myodes glareolus*)/ Puumala virus; Common vole (*Microtus arvalis*)/ Tula virus) in Germany. Trapping of rodents and sampling blood and tissue was conducted between 2010-2013 in four federal states with 3 woodland (*Myodes*) and 3 grassland (*Microtus*) replicates per state.

There was strong seasonality in the density dependence and the individual probability of acute infections or antibody presence for different functional groups for both species. For *M. glareolus*, demographics played a significant role during summer and autumn, while for *M. arvalis* this was restricted to autumn when populations on grassland reached their peak densities. In both systems older individuals and males were associated with higher hantavirus seroprevalence.

These results highlight underlying similarities and dissimilarities of species specific hantavirus transmission in different hantavirus/reservoir systems, and the need to consider functional groups in future efforts to understand hantavirus transmission and predict human infection risks.

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Bank vole evolutionary lineage association of Puumala virus in Germany

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Bank voles, *Myodes glareolus*, serve as natural reservoir for the hantavirus species Puumala virus (PUUV). This virus is responsible for the majority of human hantavirus infections in Germany mostly occurring in western and southern regions. During outbreak years more than 2,000 cases can be recorded, while in the northeastern part of the country human infections are only rarely detected. Therefore, this study aimed to identify possible reasons for the heterogeneous distribution of human PUUV cases in Germany.

For this purpose, 1,758 bank voles from Germany were investigated by serologic and molecular assays. A moderate to high PUUV prevalence was detected in bank voles from the endemic western and southern part of the country. In contrast, in northernmost and eastern parts of Germany no PUUV-positive bank voles were found. Further, *cytochrome b* gene sequence analysis indicated a geographic association of the PUUV occurrence in Germany and the Western evolutionary lineage of the bank vole. PUUV infections were detected also in voles of the Eastern and Carpathian lineages, but only when the Western lineage was present at the particular locations too.

In conclusion, our findings support the hypothesis that during or after the bank vole recolonization process after the last glacial period PUUV spread to Germany through the Western evolutionary lineage. Future analyses will have to investigate the susceptibility of the different bank vole lineages for infection by PUUV of different clades.

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First report of nutria (*Myocastor coypus*) in the Natural Reserve of the Lungo and Ripasottile Lakes (Rieti, Italy).

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The Nutria (*Myocastor coypus*) is a species originating from South America, allochthonous in Italy where it was introduced in the 1920s with productive purposes. Stanchion-tied stable livestock farming was intended for fur production. The subsequent fashion change, the economic crisis, and the advent of World War II made the breeding uneconomical. To avoid the costs of disposing of the livestock and the proper disposal of the remaining subjects, many animals were illegally released in the environment. The rapid acclimatization allowed these subjects to colonize numerous river courses in the central and northern area, and then the rest of the peninsula. This species causes considerable damage to vegetation and it is known as a cause for the local extinction of the present avifauna (*Botaurus stellaris*, *Circus aeruginosus*, etc.). Predating eggs and nidiacees, it can also negatively affect ground-nesting species (*Chlidonias hybrida*, *Tachybaptus ruficollis*, etc.). It's for these reasons that reports of attempts at new colonization are very important because they are the preparatory steps for eradication. Many years of monitoring projects in the Lungo and Ripasottile Natural Reserve have allowed us to detect, by sighting, the first nutrias in the protected area. The first sighting dates back to December 23, 2016, followed by another 2 in following dates. This report, formalizing the species presence in the reserve, may allow the agencies concerned to initiate the necessary procedures for the permanent removal. That before the nutria numerically stabilizes itself and begins to impact the biocoenosis, making the eradication difficult.

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Is sequence evolution of Puumala virus NSs protein related to bank vole population dynamics?

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The aim of this study was to identify the influence of bank vole population dynamics on Puumala virus (PUUV) prevalence and molecular sequence-evolution regarding the PUUV S-segment. PUUV is transmitted by the bank vole (*Myodes glareolus*) and is the main causative agent of human hantavirus infections in Germany. Rodent-borne hantaviruses have a tri-segmented genome. The S-segment contains two major overlapping open reading frames (ORF) coding for the nucleocapsid (N) protein and a non-structural (NSs) protein.

Blood and lung tissue samples of bank voles trapped during 2010-2014 in Baden-Wuerttemberg and North Rhine-Westphalia were analyzed by reverse transcription-polymerase chain reaction (RT-PCR) and serology. Parts of the S-segment, including the N/NSs overlapping coding region and the N coding region alone, were sequenced for all PUUV positive voles.

Of 851 voles, 28.4% were positive for PUUV-specific antibodies, whereas in 22.8% PUUV-specific RNA was detected. In the hantavirus outbreak years 2010 and 2012 PUUV prevalence at our trapping sites was higher compared to 2011, 2013 and 2014. From spring to autumn, decrease in the prevalence of PUUV infections of bank voles was observed. Amino acid and nucleotide sequence types of the NSs-ORF showed temporal and/or local distribution variation, whereas the N-ORF was highly conserved. In both federal states, one sequence type each persisted over the whole observation period. The NSs protein was highly divergent among trapping sites in the outbreak year 2012.

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Shrew-associated hantaviruses in Germany

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Recently, a large number of novel hantaviruses has been discovered in shrews, moles and bats. Seewis virus (SWSV) was initially detected in the Eurasian common shrew (*Sorex araneus*) and other *Sorex* species. After the initial detection of SWSV in Switzerland the virus was also found in Germany, Czech Republic, Slovakia, Hungary, Finland, and Far East-Russia. Asikkala virus (ASIV), a novel hantavirus was detected in pygmy shrews (*Sorex minutus*) in Finland, Germany and Czech Republic. A total of 213 shrews were trapped at different sites in Germany. In addition, 700 shrews originated from a monitoring study in four regions of Germany. Common and greater white-toothed shrews (*Crocidura russula*) were investigated for SWSV, whereas pygmy shrews were tested for ASIV.

For non-monitoring and monitoring areas SWSV-RNA was detected in 5 out of 213 shrews (2.3%), and 42 of 700 shrews (6.0 %), respectively. Viral RNA was mainly detected in *S. araneus*, but also in a few *S. minutus*, and for the first time in crowned shrews (*S. coronatus*). No SWSV-RNA was detected in greater white-toothed shrews. ASIV-RNA was detected in 2 out of 54 pygmy shrews (3.7%).

In conclusion, this study suggests a continuing abundance of SWSV and ASIV in shrew populations at several sites in Germany. Future studies will be dedicated to understand the potential influence of changes in shrew populations on the prevalence and molecular evolution of SWSV. The zoonotic potential of SWSV will be investigated by serological analyses in human risk groups.

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Ageing studies in African mole-rats of the genus *Fukomys* sp.

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African mole-rats (Rodentia, Bathyergidae) live in self-dug burrow systems where they feed mainly on tubers and roots and rarely emerge above-ground. Three genera (*Heliophobius*, *Georhychus*, and *Bathyergus*) contain only solitary species, whereas the other three genera (*Cryptomys*, *Fukomys*, and *Heterocephalus*) contain species that are highly social. Animals in these social genera typically live in large, multi-generational family groups in which reproduction is monopolized by a few individuals (usually the founder pair), whereas the other family members forego their own reproduction in the confines of their natal colonies, even after reaching full maturity.

The extraordinarily long lifespan of naked mole-rats (*Heterocephalus glaber*) was first described some 15 years ago and is now known to exceed 30 years, making this species the longest-lived rodent species known to date. However, longevity of African mole-rats appears to be generally high, as proofed by the genus *Fukomys* in which at least two species (the Ansell's mole-rat, *F. anselli*, and the giant mole-rat *F. mechowii*) can live longer than 20 years, too. *Fukomys* species are of particular interest to biogerontologists because breeders of both sexes live on average approximately twice as long as their non-reproductive counterparts. This feature, unique among mammals, offers the opportunity to study highly divergent aging rates within one genotype, without the inevitable shortcomings of inter-species comparisons.

Here, I report results of an ongoing project to elucidate the proximate mechanisms of ageing in these animals on multiple levels, including gene expression, endocrinology, physiology and histopathology.

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Common voles and field voles as main reservoir for *Leptospira kirschneri* in Germany

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Leptospirosis is a widespread zoonosis occurring in humans, domestic and companion animals. In temperate areas *Leptospira* usually causes sporadic epidemics. In Germany, the incidence increased in 2007 and 2014 due to disease clusters among strawberry harvesters in North Rhine-Westphalia and Lower Saxony. The objective of this study was to evaluate the small mammal host specificity of *Leptospira*. Small mammals were trapped in spring, summer and autumn between 2010 and 2014 in forest and grassland habitats at four locations in Germany in Mecklenburg-Western Pomerania, North Rhine-Westphalia, Thuringia and Baden-Wuerttemberg.

Using an initial screening PCR, 524 of 3,950 (13.3%) small mammals were tested positive for *Leptospira* specific DNA. *Leptospira* DNA was detected in six rodent and three shrew species. Common voles (*Microtus arvalis*) and field voles (*Microtus agrestis*) were more frequently infected by *Leptospira kirschneri* than any other small mammal species. In contrast, bank voles, yellow-necked mice and common shrews were infected with multiple *Leptospira* species.

The study confirms a broad geographical distribution of *Leptospira* across small mammal reservoir species and suggests an important public health relevance especially of common voles and field voles as reservoirs of *L. kirschneri*. Further investigations should focus on population dynamics of common voles and field voles and their impact on the *Leptospira* prevalence and its putative influence on the human infection risk, especially for risk groups, such as field and forestry workers.

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The first molecular phylogeny of African striped grass mice (genus *Lemniscomys*) based on multilocus data

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Murine rodents form one of the most diverse, evolutionary successful as well as important group of extant mammals, due to the significant role as vectors and reservoirs of zoonoses or agricultural pests. The fast and relatively young diversification impedes our understanding of phylogenetic relationships and species delimitations of many murine taxa. The striped grass mice (genus *Lemniscomys*) are distributed throughout Africa in 11 currently recognized species. These are separated in three morphological groups characterized by different shape and numbers of stripes on the back: a) group *L. barbarus* (*L. barbarus*, *L. zebra* and *L. hoogstraali*) with several continuous pale longitudinal stripes; b) group *L. striatus* (*L. striatus*, *L. macculus*, *L. bellieri* and *L. mittendorfi*) with pale stripes diffused into short lines or dots; and c) group *L. griselda* (*L. griselda*, *L. rosalia*, *L. roseveari* and *L. linulus*) with a single mid-dorsal black stripe. We describe phylogenetic relationships between *Lemniscomys* species using mitochondrial (cytochrome b) and nuclear markers (RAG, L144, DHCR, IRPB, SMO and TRPV) by combining new and already published sequences. The results show four main lineages which do not always correspond to the phenotypic groups: a) *L. zebra* and *L. barbarus*; b) *L. griselda* and *L. rosalia*; c) *L. striatus*; and d) *L. mittendorfi*, *L. linulus*, *L. bellieri* and *L. macculus*. Our results present the most comprehensive molecular phylogeny of the genus *Lemniscomys* to date and suggest the need of further taxonomic investigation and reconsideration of current species.

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Rats from breeding colonies as pathogen reservoirs

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Rats are a reservoir for various pathogens with zoonotic potential, e.g. *Leptospira* spp. and *Acinetobacter baumannii*, as well as for pathogens with no or unknown zoonotic potential such as *Rattus norvegicus* polyomavirus 1 (RnorPyV1) or rat hepatitis virus. Rats infected with *Leptospira* do not show any clinical symptoms whereas in humans disease manifestations range from mild to severe or fatal. Infections of rats with the human pathogen *Acinetobacter baumannii* have only been described in animal models but not in wild rats. RnorPyV1 was initially detected in a German rat breeding colony and in German wild rats.

To determine the array of pathogens present in pet rats, wild rats and rats in breeding colonies, the network Rat-borne pathogens (RaBoPa) was established. In a pilot study 59 Norway rats (*Rattus norvegicus*) and 68 Black rats (*Rattus rattus*) from three breeding colonies were included. The rats were examined with pathogen-specific assays for 11 pathogens and with open-view methods, including isolation approaches.

The PCR-based investigations resulted in the detection of RnorPyV1-DNA in 36/72 (50%) tested animals (28/59 Norway and 8/68 black rats). There was no *Leptospira*-DNA positive rat of 127 investigated. *Acinetobacter baumannii* was isolated in tracheal samples of five rats (4 Norway rats, 1 black rat) from 125 analysed animals (3.2%). A few rat hepatitis virus-positive animals (3/127; 2.4%) were detected.

In conclusion, the results indicate a high infection rate of RnorPyV 1 in both rat species within different breeding colonies.

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Common vole (*Microtus arvalis*) as a host for pathogens: a review

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The common vole (*Microtus arvalis*) is a broadly distributed rodent species that can be found from central Spain to the western coast of Lake Baikal. It mainly inhabits open grassland habitat and crops, where it can cause damage, especially during outbreaks when population density can reach up to 3,000 individuals per hectare. The common vole is known as a reservoir of several pathogens including viruses, bacteria, parasites and fungi. Cowpox virus, Tick-borne encephalitis virus, *Leptospira kirschneri*, *Francisella tularensis* and *Coxiella burnetii* are pathogens with zoonotic potential that are transmitted to humans causing potentially severe diseases like cowpox, encephalitis, leptospirosis, tularemia and Q-fever. In addition, the common vole harbors Tula hantavirus, a pathogen without or with low zoonotic potential. Furthermore, hepatovirus and *Microtus arvalis* Cytomegalovirus 1 occur that are most likely non-zoonotic.

As several zoonotic pathogens are potentially present in the common vole it seems appropriate to identify and sensitize risk groups, especially when outbreaks are likely to occur. The presence of pathogens should also be considered in population and behavioral studies of common voles where outcomes might be affected by the effects of these infections.

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Phylogenetic studies on astrovirus sequences detected in German bats

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Among the different viruses that circulate in bat populations, the family of the *Astroviridae* exhibits particular characteristics due to its high variant diversity and its high prevalence of up to 50% in insectivorous bats. The small, positive oriented single strand RNA viruses were first detected in 1975 in humans, and several variants have since been detected in various avian and mammalian species. Clinical symptoms associated with an astrovirus infection may, depending on the variant and affected species, range from mild to severe diarrhoea, hepatitis, nephritis, respiratory syndromes and encephalitis.

However, the pathologic effect of astrovirus infections in bats it is still unclear as no clinical signs could be observed so far. Moreover, the mechanisms of astrovirus transmission and elimination in bats are still obscure. Here, we assess the astrovirus phylogenetic characteristics by amplifying 400 nt fragments from the RNA-dependent RNA-polymerase (RdRp)-gene via nested RT-PCR followed by Sanger sequencing. The faeces and urine samples from individually tagged bats of the species *Myotis nattereri*, *Myotis bechsteinii*, *Myotis daubentonii*, and *Plecotus auritus* have been analysed since 2011 at three sampling regions in Germany. This gives us the unique opportunity to perform studies of individual bats over long periods of time. Individuals that were tested at several points in time, give an insight into virus persistence rates in individual bats. Different astrovirus variants differ in prevalence and regularity of occurrence between 2011 and 2016.

Overall, this study will help us to improve our understanding of the astrovirus transmission dynamics and phylogenetics within the observed bat colonies.

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

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24 specimens of *Clethrionomys glareolus* and *A. flavicollis* each were given a mixture of seven seeds/fruits from trees typical for forests in Central Europe. Each individual was fed with this mixture on the first and second day again as well as on day 21 and day 22. The IVLEV's electivity index was calculated for every day and individual and grouped for the first and second day as well as for the 21st and 22nd day showing differences in learning behaviour. Data were evaluated by a Friedman test and a Wilcoxon test. A chemical analysis of all the seeds/fruits was made concerning cellulose, starch, glucose, lipids and nitrogen (proteins), then data were assessed by a PCA deducing a possible relationship between consumption data and nutritive value of every seed/fruit. There were only small differences between the two rodent species concerning preferences of all the tested seed/fruit except for acorns of *Quercus robur*. *A. flavicollis* had a more distinct preference than *C. glareolus*. Results point that seeds/fruits with a high or medium content of lipids and proteins (high caloric value) or glucose were preferred (*Fagus sylvatica*, *Picea abies*, *Pinus sylvestris* and *Tilia cordata*), those with high concentrations of starch or cellulose (*Carpinus betulus*, *Prunus avium*) were not an attractive source of food. Acorns were consumed in medium quantities by both rodent species only at day 21 and 22.

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Effects of fire on small mammal communities in the Busanga Flood Plain, Zambia

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We assessed effects of vegetation and fire on small mammals in open vegetation formations of the Busanga Flood Plain (Zambia) in areas of low and high fire recurrence. The impact of fire was related further to the time elapsed between the last fire and the time of trapping (fire age). Sampling sites covered three management zones: intensive utilization (tourist areas), wild (less used), and wilderness (no road access). Vegetation type, fire recurrence, fire age and management zone were independent variables. Communities were similar in grassland and on termitaria but differed from miombo. Species richness was highest on termitaria, followed by grassland and miombo. Species numbers declined with increasing fire frequency but were unaffected by fire age. In contrast, the average body mass of species occurring at any one site (only adult individuals considered) declined with the time elapsed between the time of capture and the last fire (the longer the time interval, the lower the average species body mass). This response could be a function of body mass or body size of the species present and implies higher vulnerability of the smaller species to fire and/or slower recolonization potential of smaller species after fire. The interactions between fire, vegetation characteristics and small mammals need to be reviewed, given their importance in the functionality of this ecosystem.

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Drivers of pathogen transmission in the system hanta-virus-bank vole-humans

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Rodents can carry a wide range of zoonotic pathogens that can cause mild to severe illness in humans. Some species show occasional population outbreaks, which can affect pathogen epidemiology and human infection risk. In Europe, the widely distributed bank vole (*Myodes glareolus*) is the reservoir species for the Puumala virus (PUUV), a hantavirus species causing a mild to moderate form of the haemorrhagic fever with renal syndrome in humans.

Population dynamics of bank voles were monitored by live trapping three times a year in 2010-2013 in three woodland plots in each of four regions in Germany. Bank vole population density was estimated and blood samples were analysed to detect PUUV specific antibodies. Furthermore, time series (2001-2012) of beech fructification (as a primary food resource for the PUUV host), bank vole abundance and human PUUV incidence from 7 Federal States of Germany were examined to uncover the link between these three parameters involved in human PUUV epidemics. Results show that multi-annual and seasonal rodent host population dynamics affect fluctuations of PUUV seroprevalence. Human PUUV infections strongly depend on the current bank vole abundance and on the preceding beech fructification on large spatial scale.

Our findings provide robust estimation of relevant patterns and ecological processes of the dynamics of PUUV epidemiology in Central Europe, which are useful to facilitate the development of predictive models to protect public health.

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Rat-associated hepevirus in European Norway and Black rat populations: a survey in 12 European countries

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The rat-associated hepevirus, rat hepatitis E virus (HEV), was initially discovered in Norway rats (*Rattus norvegicus*) from Hamburg, Germany, and subsequently detected in rats from other cities in Germany and in rats from Vietnam, the US, Indonesia, China, Denmark and France. Norway rats from the US and Japan were also found to be infected with human pathogenic HEV-genotype 3 (GT3).

A molecular survey was performed for Norway rats and Black rats (*Rattus rattus*) from Germany and eleven additional European countries using different hepevirus-specific reverse transcription-polymerase chain reaction assays.

In total 508 rats were collected and analysed with an overall ratHEV prevalence of 12.4% (63/508), with a range between 4% to 22.4%. Positive rats were detected in

eleven of 12 countries. RatHEV-RNA was detected in 13.8% (58/420) of Norway rats and 5.6% (5/88) of Black rats. Phylogenetic reconstructions indicated clustering of all European ratHEV sequences within designated ratHEV-genotype 1. The presence of multiple, well-separated sequence clades at the same sampling location might indicate the incursion of novel/different ratHEV strains into local Norway rat populations with a potential, parallel persistence of a local, ratHEV strain. This necessitates future studies on the population structure and potential immigration of individuals into existing rat populations and their association with ratHEV incursion. In addition, the finding of ratHEV infections in zoological gardens may allow future studies on the zoonotic potential of ratHEV based on the investigation of putative natural ratHEV transmission to non-human primates or animals like rabbits or goats.

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Hantaviruses in the natural host and in “spillover”-infected animals

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Hantaviruses are pathogens that are carried and transmitted to humans by rodents. Puumala virus (PUUV) is one of the most important hantaviruses in Europe with the bank vole (*Myodes glareolus*) being its reservoir. PUUV infection of humans results in a mild to moderate form of hemorrhagic fever with renal syndrome. The target cells of hantaviruses are poorly characterized either in the natural reservoir or in “spillover”-infected animals.

Since 2005 rodents were trapped in the district Osnabrück (OS), Lower Saxony, an endemic region for PUUV. The animal carcasses were dissected according to standard protocols and tested for hantavirus-RNA by reverse transcription-PCR (RT-PCR), using lung tissue, and for serum antibodies by indirect IgG-ELISA. Furthermore, a *cytochrome b*-PCR and sequence-based classification of evolutionary lineages was done for all bank voles.

During spring and autumn of 2015 and 2016 a total of 197 rodents, including 101 bank voles, 73 yellow-necked mice (*Apodemus flavicollis*) and 23 wood mice (*Apodemus sylvaticus*) were trapped. The results show the continuous presence of PUUV in the bank vole populations with a higher prevalence in spring than in autumn. The PUUV seroprevalence ranged between 11 and 48% in bank voles, between 6 and 20% in yellow-necked mice and between 0 and 12% in wood mice. PUUV-RNA was detected exclusively in bank voles; the RNA prevalence ranged between 0 and 44%. Single “spillover”-infections in yellow-necked mice and wood mice were indicated by exclusive detection of PUUV-reactive antibodies. According to the *cytochrome b* sequences all bank voles belong to the Western evolutionary lineage.

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The susceptibility of wild rodents for Rift Valley fever virus and their potential role in the maintenance of the virus

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Rift Valley fever virus (RVFV) is a zoonotic arbovirus affecting humans and various other vertebrates, primarily domestic ruminants. The disease is characterized by a high mortality in young animals and spontaneous abortions. RVFV is transmitted by mosquitoes of several genera as main vectors of the virus. Infections of humans additionally occur after exposure to tissue of infected animals or by inhalation of contagious aerosols. Epidemics of Rift Valley Fever appear cyclical and are usually correlated to heavy rainfall or inundations that are followed by the abundance of vector-competent mosquitoes. During inter-epidemic periods the virus is maintained between vertically infected vectors and a yet unknown vertebrate reservoir. Wild rodents are suspected to play an important role in this epidemiologic cycle and it has been shown in numerous studies that several mouse and rat genera are susceptible to the disease. To elucidate more precisely the role of common African rodent species as reservoir hosts for RVFV, an experimental infection study on *Rattus rattus* will be performed with three different RVFV-strains, isolated from mosquitoes, humans and ruminants. Through a close meshed sampling scheme, potential virus shedding and the possibility of a horizontal transmission as well as the immunological and pathological reaction of the host organism will be evaluated. In a second experimental study other rodents like *Aethomys*, *Arvicanthis*, *Thryonomys* will be infected comparatively. The results will be analyzed subsequently to determine their possible role in the maintenance of RVFV. Additionally, an *in-vitro* approach, using different rodent cell lines should confirm and complement *in-vivo* results.

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Hantaviruses in the Czech Republic

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From a large number of zoonotic viruses present in Europe, we selected those that are well described in Europe, can cause diseases in humans with a scale of different symptoms and were also detected in the Czech Republic. We aimed at the detection of hantaviruses in the free-living rodents in the Czech Republic. For hantavirus detection, we used molecular screening method based on partial L or S segment. For serological screening, we used chest cavity lavage and in-house ELISA. From more than 500 trapped rodents in the Czech Republic, one field vole and more than 30 common voles were positive for Tula virus (TULV). To extend our research, we also tested rodents from Germany and France. Out of 104 common voles from Germany and 7 voles from France, in 15 and 4 of them, we found a TULV specific RT-PCR product, respectively. For TULV, it is well-described specific clustering according to its geographical distribution and reservoir animal. TULV is still considered as non-pathogenic to humans, but there is some evidence of infected patients. However, they all were immunocompromised. We confirmed the presence of this hantavirus not just in the Czech Republic but also in other European countries, and we suggested to continue these monitoring studies to evaluate its importance as a possible health threat to the human population.

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A first epidemiological model of mycoplasma (*Mycoplasma* sp.) infections in European Ground Squirrels (*Spermophilus citellus*) from eastern Austria

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To evaluate potential negative effects of infections with various pathogens on population dynamics of the endangered European Ground Squirrel (EGS), comprehensive epidemiological data are indispensable. We examined 152 EGS collected from 2013 to 2016 as roadkills in eastern Austria for infection with mycoplasmas by cultivation of lung isolates using SP4 broth and agar plates. Growth of mycoplasmas was semi-quantitatively evaluated by colony counting and isolates were identified by mitochondrial 16S rDNA gene sequences that all revealed close phylogenetic relationship to *Mycoplasma citelli* RG-2CT, a validly described bacterial species previously isolated from Richardson's ground squirrel (*Urocitellus richardsonii*) from the New World. Infection prevalence amounted to 55.9% in adults (n=111) and to 50.0% in juveniles (n=18, until begin of hibernation). Infection abundance was partitioned as follows: 9.9% very little (traceable after enrichment), 23.7% low, 13.8% moderate, 9.2% high. However, among all infected individuals only two adult males displayed moderate pathological and pathohistological alterations in the lungs, associated with the infections. Our ordered logistic regression models for one huge colony that comprised by far the largest regional sample revealed only a significant seasonal effect on abundance, indicating a more or less steady decrease from late March and April towards the begin of hibernation, but no clear effects of sex, age class, year, or body condition. Bigger sample sizes may help to better understand the potential role of the other factors currently considered in our models for the infection dynamics.

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10 years network “Rodent-borne pathogens”

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Rodents are important as pests in agriculture and forestry, as model organisms for biomedical studies and as reservoirs for zoonotic pathogens. The network “Rodent-borne pathogens” was established as a platform for an interdisciplinary collaboration of scientists working in mammalogy, ecology, genetics, immunology, toxicology, epidemiology, virology, microbiology, parasitology and human and veterinary medicine.

Major focus of the network is the interaction of infectious agents and their reservoirs. Previous work was mainly based on field studies to evaluate the geographical distribution and rodent host association of zoonotic pathogens, such as hantaviruses, orthopox viruses, *Leptospira* spp., *Rickettsia* spp. Ongoing studies of Puumala hantavirus consider the influence of bank vole reservoir population oscillation on the molecular evolution of the virus. Recent establishment of bank and common vole-derived cell lines allows studying factors involved in host specificity of selected pathogens.

Pilot studies within the network resulted in the discovery of novel viruses, some of them with potential to serve as models of human pathogens, such as bank vole hepacivirus, closely related to human hepatitis C virus, or rat hepatitis E virus (HEV). Additionally, the combined expertise from different fields allows studying the interactions between pathogens at various functional, ecological and evolutionary levels. Special emphasis is currently given on pathogens in Norway rats from breeding colonies, pest rats in zoos and from agricultural areas.

In conclusion, the network provides an important infrastructure for ongoing collaboration that is highly beneficial for interdisciplinary scientific work with high relevance in several fields of research.

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Early departure from the hibernaculum and its implications on mortality in bats

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It is well documented that hibernation is crucial for temperate bat species to survive periods with low food availability during the winter. However, how differences in individual hibernation behaviour influences mortality and whether individuals are plastic with respect to their hibernation behaviour are largely unknown. Because bats are of high conservation concern it is of prime importance to understand factors that might influence mortality during hibernation.

In this study we used an individual based data-set of the two bat species *Myotis nattereri* and *Myotis daubentonii* at a hibernaculum. Each PIT-tagged individual was automatically recorded while passing the entrances and, therefore, can be followed at the hibernaculum over its life time. We investigated the impact of their individual hibernation behaviour, precisely the timing of departure in late winter and early spring, on mortality, as well as differences within and between the two species from 2011 until 2015.

Our results suggest considerable differences among individuals within as well as between bat species with respect to emergence behaviour from the hibernaculum. Hence, our study highlights the necessity to further investigate the phenotypic plasticity of hibernation behaviour and to understand its effects on the demography of bats. We conclude that it is important for the conservation management of bat species to identify key factors for the survival of individuals during hibernation and to distinguish between species to select the best management tools for bat hibernacula.

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The duration of hibernation of indigenous bat species - results of multiannual field research

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There is little known about the duration of the hibernation period of indigenous bats. Our research attempts to close this gap. Our focus was, however not on the bats in the hibernation sites, but on bat activity at the roost entrances. Bat activity was recorded by light barrier systems and partly by digital cameras.

Typical for all species in the survey is that immigration into the hibernacula takes several weeks. In spring the emigration takes several weeks again. However, the moving in and out of the hibernacula follows a fixed pattern which is independent of the weather.

Daubenton's bats (*Myotis daubentonii*), Bechstein's bats (*M. bechsteinii*) and Geoffroy's bats (*M. emarginatus*) start immigrating into the hibernacula in the first half of September. While the immigration process of Geoffroy's bats is already completed at the end of September, the immigration of Daubenton's bats and Bechstein's bats lasts until late October. Greater mouse-eared bats (*M. myotis*) show a similar pattern, whereas the activity period of Natterer's bats (*M. nattereri*) lasts until December.

In spring Natterer's bats are the first to vacate the hibernacula. They start leaving their hibernacula in the first part of March, followed by the Daubenton's bats. The peak of vacating of the Greater mouse-eared bats is reached at the beginning of April, while the peak of vacating of Bechstein's bats is reached around mid-April. Geoffroy's bats use the hibernacula longest. The first individuals leave in the second part of April and the last leave at the end of May.

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Extreme flexibility in torpor patterns in a tropical bat (*Hipposideros commersoni*)

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The energy budget of an animal species is closely linked to its ecology and balancing energy expenditure with energy acquisition is key for survival. Changes in an animal's environment can be challenging and particularly bats are extremely affected since they are small endotherms with large uninsulated flight membranes. Bats make up nearly a quarter of all mammalian species worldwide and provide important ecosystem services vital to the preservation of natural ecosystems and human economies but little is known about Madagascar's bat fauna. Almost no information detailing their physiological requirements are available although especially this knowledge is crucial to understand their adaptive potential to habitat alterations. Heterothermy is a very powerful response to cope with changing conditions but only a handful of studies on it exist for free-ranging tropical bats in their natural environment, and none in Madagascar. Here, we will report first data on heterothermy found in the Malagasy bat *Hipposideros commersoni*.

We examined the energy management and thermal biology of *H. commersoni* directly in the field performing skin temperature and metabolic rate measurements. These were related to local environmental characteristics during a feasibility study in the dry season in 2016. *H. commersoni* showed extreme variability in torpor use and was exclusively found in one cave implying that this cave might be essential for the overwintering and reproduction success of this particular species. Interestingly, this cave was the hottest in the area (constantly above 30°C), raising intriguing questions about microclimate choice during a heterothermy-prone season.

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Stay cool or warm up? Individual variation in energy-saving strategies and the pace-of-life syndrome in eastern chipmunks (*Tamias striatus*)

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Understanding determinants and fitness consequences of individual energy management are key challenges in ecology because these individual-level processes are directly linked to population dynamics, community composition and trophic cascades in ecosystems. Heterothermy is a predominant physiological process to reduce energetic costs in many mammals. However, despite the ubiquity and importance of heterothermic variation in endotherms, we know very little about patterns of among-individual variation and its fitness consequences. Recently, it has been proposed that behavioural, physiological and life-history traits coevolved as response to long-term selection pressures forming the pace-of-life syndrome (POLS). Here, we aimed to test (i) whether among-individual variation in heterothermy have fitness consequences, and (ii) for among individual (co)variation between energy metabolism, behavioural phenotype and life-history in eastern chipmunks (*Tamias striatus*), food-hoarding hibernators. We quantified patterns of heterothermy, resting metabolic rate (RMR) and exploration of 55 free-ranging eastern chipmunks. Over five hibernation periods, we obtained a total of 7108 daily individual heterothermy indices. Based on an individual reaction norm approach, we found that the use of heterothermy was repeatable and varied among individuals of the same population under similar environmental conditions. This individual variation had consequences for winter survival and reproductive success and was related to RMR but not to differences in exploration. Our results support the hypothesis that fluctuating selection maintains heterothermic diversity and suggest that heterothermy-based energy-saving is part of a broader POLS. Overall, our study highlights that individualized ecophysiology can contribute to a more thorough understanding of the evolution of energy-saving strategies in endotherms.

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Seasonal adaptations and inter-specific differences of the energy budgets of two primates (*Lepilemur leucopus* & *L. ruficaudatus*)

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Animals experience seasonal changes in terms of environmental and ecological conditions in most of their habitats. Fluctuations in ambient temperature have a strong influence, particularly on small endothermic mammals, and are therefore an important source of functional constraints. However, different mammalian species react differently to these temperature changes. It is important to understand the physiological responses of organisms to different seasons and to analyze the mechanisms that account for intra- and interspecific physiological traits and the ecological consequences of these variations. Through the use of open-flow respirometry and measurements of skin temperature in the field, we sought to identify adaptive changes in the energy budgeting of the small Malagasy folivorous lemur, *Lepilemur leucopus*. Furthermore, we compared the interspecific adaptations of two *Lepilemur* species (*L. leucopus* & *L. ruficaudatus*) to the harsh dry season in South- and South-west-Madagascar. Our study did not detect any signs of heterothermic episodes in either species, despite the fact that such episodes have been observed in other lemurs of similar size and life style. The metabolic rate of *L. leucopus* was consistently higher in the cooler dry than in the wet season. Surprisingly, the thermoneutral zone in the wet season was lower (25-30°C) than in the dry season (29-32°C). *L. leucopus* and *L. ruficaudatus* demonstrate one of the lowest weight-specific metabolic rates measured for mammals so far. These findings highlight the importance of studying physiological parameters, in different seasons, and considering the differences between various species - even if they are closely related.

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Possible causes and consequences of different hibernation patterns in Malagasy lemurs? Mitovy fatsy sahala

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All dwarf lemurs (*Cheirogaleus* spp.) hibernate, decreasing energy and water demands drastically to survive the harsh Malagasy winter. However, the different species are very flexible in the modus operandi and timing of hibernation, and even within species differences are considerable, depending on habitat and climatic parameters. We compare different dwarf lemur species and discuss possible causes of consequences of different hibernation patterns. Whereas dry forest species hibernate in tree hollows of various insulation properties, rainforest species retreat underground for hibernation. These different strategies have extensive consequences on hibernation parameters and patterns. In underground hibernacula and in well-insulated hollows in large trees energy expenditure and body temperature (T_b) during the hibernation bouts are almost constant and spontaneous arousals occur regularly. In contrast, in thinner trees, insulation capacities are decreased, and energy expenditure and T_b are fluctuating with the ambient temperature (T_a). When these passive fluctuations are pronounced, arousals become dispensable. As expected, the colder the habitat is during winter, the greater the energy savings by hibernation are. There is evidence suggesting that more stable environments in the hibernacula are preferred and thus possibly represent the ancestral condition, indicating that the hibernation machinery was originally adapted to and runs best at mostly constant T_a. However, it is also conceivable that hibernation in tree hollows could have been the original modus operandi, implying that hypometabolism in some species is truly independent of T_a, and fluctuating T_a might even be advantageous, allowing for extended, continuous bouts of hypometabolism by avoiding interruptions by active arousals.

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Ecology of the overwintering bear (*Ursus arctos marsicanus*) semi-hibernation in the middle of the Valle del Salto in 2016-2017. Some remarks on the employed environments (Rieti Province, Italy).

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In the winter of 2016-2017, the first case of semi-hibernation of a Marsican Brown Bear in the middle of the Valle del Salto (province of Rieti, central Italy) was found, a stepping stone in the movements of the species to and from the Monti Sibillini. The overwintering took place in an unprotected territory and outside the Bear's core area. The study, conducted by volunteer researchers and unknown to the institutional channels of fauna monitoring, benefited from the support of local informants, citizens who, for work or individual passion, are frequently visit the investigated territory. The monitoring was based on collecting presence signs by: transects, scout/stealth camera use in reporting sites, and the selection of reports with a high degree of reliability. The Waypoints of the presence sites found between the 6th of January and March the 4th allowed the definition of the MCP used by the subject investigated during the semi-hibernation. The analysis of this territory with ArcGIS ESRI 10.2 has returned the following minimum ecological/environmental variability used in the semi-hibernation: total utilized area 77.82 km², composed in percentage as follows of the present topsoil categories: broad-leaved trees 44.22%, grassland and natural pastures 21.26%, bushy-wooded transition areas 11.48%, mainly agricultural area with vegetal areas 7.08%, arable lands without irrigation area 4.37%, mixed woodland 4.27%, coniferous forests 2.01%, naked rock 1.59%, burned areas 1.34%, sparsely vegetated areas 1.17%, grassland 0.98%, orchards and suffrutexes 0.23%.

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A case of bear (*Ursus arctos marsicanus*) overwintering in a stepping stone. Winter of 2016-2017, middle of the Valle del Salto, Rieti Province, Italy

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The most recent studies on the distribution and use of the territory by the *Ursus arctos marsicanus* agree to locate it in the core area of the southeastern part of the Abruzzo, Lazio and Molise National Park. The main phases of the life cycle are spent there. From this area, there are some ecological corridors pointing north-west, connecting with the Monti Sibillini National Park. In such ecological corridors, there are some stepping stones frequently used by the bear and associated with transit to and from the core area. The information given here comes from the middle of the Valle del Salto (Province of Rieti), considered a stepping stone due to the recurrent presence of the bear. There, for the first time in recent times, in the winter of 2016-2017 there was a semi-hibernation overwintering case; case studied by volunteers and unknown to the institutions in charge. In the summer of 2016, some casual sources (shepherds, peasants, woodcutters, hunters, mushroom pickers, hikers) reported their first sighting reports. Tracking by transects and scout cameras placement on the reporting sites was immediately planned. As a result, a collection of presence signs with detailed space/time references, such as images of snow and mud imprints. A scout camera video of the bear while destroying some hooves, in the semi-hibernation period, is the most significant document. This requires the beginning of specific on-site studies, so far conducted in other areas, less frequented by the species but politically more influential (see some protected areas).

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Bat hibernacula are more than just a place to spent the winter: activity patterns in different seasons show the almost year-round importance of hibernacula for bats

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In the temperate zone, bats depend on hibernacula that protect them from adverse weather in order to survive the winter. In addition, it is known that several species aggregate in late summer and autumn at hibernacula for mating. Consequently, protection of hibernacula against human disturbances such as visitations by cavers and tourists is typically limited to the time between September and April. However, at present, the species specific phenology at hibernacula is largely unknown and therefore current bat conservation plans for hibernacula may be insufficient. In our study we analysed individual activity-data from a hibernaculum in northern Germany of six consecutive years. Bats of two sympatric species with different diets and foraging capabilities, *Myotis nattereri* and *Myotis daubentonii*, were automatically monitored using PIT-tags. Our data show that with the exception of July, bats are present at the hibernaculum throughout the whole year. Our results suggest that *Myotis daubentonii* follows the same annual activity patterns every year, whereas *Myotis nattereri* shows activity differences between the years. We observed differences in the seasonal activity between the two species and between the sexes of the same species. Our findings can be used to implement more appropriate protection plans for hibernacula taking into consideration the phenological, species and sex specific aspects. Based on our results, we strongly recommend to strictly protect bat hibernacula during the whole year.

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Results of a multiannual monitoring with focus on bat activity and population size in a former air-raid shelter in the city of Kiel, Germany

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The former air-raid shelter is located in the city of Kiel, Schleswig-Holstein. The roost is inhabited almost exclusively by Daubenton's bats (*Myotis daubentonii*). The bats can only enter the roost via a 30 cm long pipe (radius 10 cm). These are perfect conditions for registering the individual bats, while crawling into or out of the roost. Thus a light barrier system was installed to monitor the bats and has been in use for 20 years.

Annually, between 250-300 individuals have been recorded hibernating in the shelter. Visually only about 50% of the hibernators are found, although the site is not very structured.

About 6,000 passages through the light barriers per year are recorded. Five activity phases, partly overlapping, can be distinguished. 1) From early August until mid-October many bats visit the shelter. Initially the activity is high. Later, from the beginning of September until mid-October activity decreases continuously and an increasing number of bats starts hibernating. (2) From mid-October to the end of February activity is low while the bats are hibernating. (3) From March until mid-April activity increases rapidly because the bats leave the hibernaculum (4). From May to mid-June activity reaches a fairly high level again when male visitors roost in the shelter. (5) From mid-June until the beginning of August the level of activity is low. Only few individuals visit the air-raid shelter.

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How to spent the winter: Species and sex specific hibernation phenology of two sympatric European bat species

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Detailed phenological insights in the timing of hibernation in bats of the temperate zone are needed to better understand the peculiarities of their unusual life cycle. Moreover, they are important for dealing with the increasing threats to bats such as human interference with habitats, insects decline, climate change and infectious diseases. However, individualized information of the phenology of bats are currently largely lacking. Long-term phenology studies of hibernating individually marked bats are rare due to limitations of traditional field methods. More modern automatized methods, such as light barrier census or acoustic surveys, also cannot provide individualized information necessary to understand the fitness consequences of different hibernation strategies. Here, we provide individualized hibernation data based on PIT-tagged individuals of two sympatric species, *Myotis daubentonii* and *Myotis nattereri*, for six consecutive years from a large hibernaculum in northern Germany. Our study species have different foraging as well as reproduction strategies, which should influence their hibernation strategies. We analysed the start and end of hibernation of each individual. Our results suggest that hibernation timing of individual *M. daubentonii* is similar every year whereas that of individual *M. nattereri* can vary between years. In general, hibernation length of *M. daubentonii* was longer than that of *M. nattereri*. Furthermore, the results indicate individual differences in hibernation timing even within species. As a consequence, we conclude that differences in hibernation strategies within and between bat species might lead to varying risks due to the abovementioned threats and, therefore, need to be considered in conservation management.

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Stress assessment in wild ruminants: can we quantify an influence of stress on forest damages by foraging deer?

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As it has previously been shown by experiments in enclosures, a general stress level of wild ungulates is detectable by cortisol metabolite analysis from the faeces. However, it is still unclear, if this method allows the analysis of wild animals in their habitats with respect to their general stress status and, in addition, if it is possible to detect a correlation to feeding behaviour, and especially to forest damages by browsing and barking.

Using red deer (*Cervus elaphus* L.) as an example, we have to evaluate, if cortisol metabolite analysis, working under experimental conditions in enclosures, is suitable for analysing wild living animals. In addition, well defined regeneration areas and stands of the most important forest tree species are to be examined for impact of browsing and barking.

Additionally a comprehensive analysis of the different habitats in the investigated areas is used to identify important factors that may influence the stress level of wildlife as a possible cause of feeding damage and thus provide recommendations to reduce this kind of damage.

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Common leopards and humans: a difficult coexistence?

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We studied food habits, space use, habitat loss and socioeconomic implications of coexistence with humans, of common leopards in a densely inhabited area of Pakistan (Ayubia National Park and Murree). In our study area, wild ungulates were near-absent and livestock dominated the diet of leopards (absolute frequency of occurrence: 80%; N scats=525). Goats were the staple (61%), followed by domestic dogs (12%) and *Bos* spp (6%). Wild prey included canids, rhesus monkeys and smaller mammals/birds.

GIS analyses revealed that, between 1992 and 2011, the forested area decreased by 6.6% (65.5 ha/year), whereas areas covered with human settlements and agricultural land increased by 81.5% and 15.4%, respectively. One male common leopard was fitted with a GPS radio-tag and tracked for 16 months. His home range (95% Fixed Kernel: 72.6 km²) encompassed a densely inhabited area (c. 124000 people). 18.5% of interviewed households (N=1016) had suffered livestock depredation by leopards, with an overall loss of 123 USD/km²/year, in an area of 328 km². At least 19 attacks to humans were documented in 2005-2014, with 10 casualties, whereas 40 leopards were killed by man in retaliation, in 1998-2014.

Common leopards are endangered in Pakistan. Habitat fragmentation and forest shrinking lead to habitat loss. At the same time, human attacks and livestock losses make the leopard a difficult neighbour. Reintroduction of wild ungulates, improvement of livestock management and forest protection/restoration are needed to mitigate human-carnivore conflict and enhance the long-term survival of leopards in our study area.

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The phylogeny of the hominoids: results from molecular and morphometric data

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The phylogenetic relationships between nearly all of the extant species of the Hominoidea (if we avoid exaggerated splitting in the case of gibbons) can be deduced by use of strongly conserved characters of the mitochondrial encoded proteins. Only in the case of the hoolock gibbon *Hylobates (Hoolock) hoolock* HARLAN 1834 the sequence of the mitochondrial DNA is still too incomplete to decide from the molecular data where the edge leading to the hoolock branched off within the phylogenetic tree of the lesser apes. But if we combine the molecular data with data describing the skulls of the hominoid primates we get indications where the hoolocks branched off. Moreover we can deduce the phylogenetic position of well-preserved fossils (*Homo floresiensis*, *Homo erectus*, *Homo habilis*, *Australopithecus africanus*, *Australopithecus crassidens*, *Australopithecus afarensis*, *Sahelanthropus tchadensis*) within the tree of the Hominoidea and reconstruct skulls belonging to the inner vertices of the phylogenetic trees although we lack fossils of such extinct species.

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Dark grey gazelles *Gazella* in Arabia: Threatened species or domesticated pet?

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True gazelles (genus *Gazella*) are a prime example of a mammalian group with considerable taxonomic confusion. This includes the descriptions of several dark grey taxa of questionable validity. Here, we examined captive dark grey putative Neumann's gazelle *Gazella erlangeri*. Our concerted efforts to retrieve mitochondrial sequence information from old museum specimens of two dark grey gazelles, putative *G. erlangeri* and putative Muscat gazelle *G. muscatensis*, were unsuccessful. We did, however, find the mtDNA haplotypes of extant putative *G. erlangeri* to be nested within the haplotype variation of the Arabian gazelle *G. arabica*. The observed population genetic divergence between *G. arabica* and putative *G. erlangeri* (based on 11 nuclear microsatellites) was driven by genetic impoverishment of putative *G. erlangeri*. These results, along with morphological signatures of domestication (e.g., reduced brain case size), suggest genetic bottle necks and domestication effects as a consequence of prolonged captive breeding. Three hypotheses are discussed: (a) *G. erlangeri* and *G. muscatensis* are valid species but are now extinct; (b) one or both taxa represent phenotypic variation within *G. arabica* and, therefore, are synonyms of *G. arabica*; and (c) captive stocks, exhibiting the effects of domestication and inbreeding, are the sources for the descriptions of *G. erlangeri* and *G. muscatensis*. As concerns the conservation of gazelles, based on current knowledge, we strongly advise against using putative *G. erlangeri* for any introduction initiative but recommend the continued captive management of putative *G. erlangeri*.

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External morphology and chondrocranial development in therian mammals

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Embryonic staging of model organisms gives just a coarse picture of the varieties in external morphology of developing mammals. As opposed to traditional staging, we documented embryogenesis using a standardized staging system, which serves to compare timing in organogenesis analytically. Internally, placentals and marsupials reveal major differences, exemplified in the shape of the developing cranium. The brain region represents a large portion of the head in placental embryos, whereas the snout region with anterior oriented nares is relatively smaller. In contrast, in the pouch young of marsupials, the snout region is pronounced, whereas the brain occupies a proportionally smaller space of the head. The nares are oriented laterally and change shape during development. We hypothesized that functional requirements at the time of birth shape the embryonic cranium of marsupials, and lead to apomorphic features in the development of the anterior part of the chondrocranium, namely the mouth region and nasal passage. To test this hypothesis and to address other issues in comparative anatomy, we documented the development of the non-model species *Atelerix albiventris*, *Acomys dimidiatus*, and *Echinops telfairi* (Placentalia) and *Petaurus breviceps*, *Macropus eugenii*, and *Caluromys philander* (Marsupialia). We studied, using histological sections, the anterior part of the chondrocranium. Three-dimensional reconstructions of the chondrocranium display derived disparity in chondrocrania proportions but conservatism in shape of the cupula nasi in marsupials. The diversity in external development is partly mirrored in chondrocranial developmental disparity. As such, both can, to a certain extent, serve as morphological proxy for one another through development.

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The lacrimal bone diversity in Cervidae - what size and shape tells us about cervid evolution

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Most mammals possess a lacrimal bone, which builds the rostral rim of the orbita. In deer (Cervidae, Artiodactyla), the bone acquires considerable size compared with other mammals. It is characterized by a depression hosting the lacrimal gland, whose secretion is used for territory marking. The lacrimal bone and its depression are very variable in both size and shape within cervids being useful for systematics. However, the underlying causes for this variability remain so far unexplained.

Given the central position of the lacrimal bone in the facial skull (it articulates with the nasal, frontal, sphenoid, jugal, and maxilla), it is likely that the bone reflects adaptations to different ecological niches and different behaviour. This hypothesis coincides with the evolution of cervids, where early small forest dwellers from tropical /subtropical habitats grew in size and adapted to temperate and subarctic regions.

In our presentation, we give an overview of size and shape in some living cervid species and the correlation with behaviour and habitat. We use the results to infer on behaviour and ecology in fossil cervids.

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To fight or not to fight? Behavioural interference between ungulate species

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Disentangling mechanisms of interspecific interactions can shed light on evolution of animal populations. Interspecific competition occurs through exploitation of scarce, shared resources, or through interference, i.e. direct behavioural interactions. Interference is widespread in carnivorous mammals, with larger species often killing smaller ones and affecting their behaviour, ecology and numbers. A synthesis is lacking for ungulates, although they have potentially killing weapons (e.g. horns/antlers) and may be expected to use them in interspecific aggressive interactions.

We reviewed information on interference between ungulates, to evaluate (i) whether some species are dominant over others, (ii) relationships between dominance and body mass, (iii) effects on population dynamics. Displacements of smaller ungulates by African mega-herbivores (elephants/rhinos) at waterholes were documented. Additionally, interference events have occurred for 12 species, in 24 pairwise interactions. Fifty-four percent of them involved at least one allochthonous species, with fallow deer being the most dominant one. Native European roe deer was the most frequently displaced ungulate. Body mass explained dominance in interactions involving native species, but not in those involving allochthonous ones. Globally, interference has been suggested to affect population trends of the displaced species in 5 cases, 3 of which involving allochthonous ungulates, although only one was supported by substantial data (>200 events).

In ungulates, similarly to birds, the formation of multi-species groups may have been favoured by anti-predator behaviour. If so, interference potential would be enhanced by absence of recent coevolution (e.g. through introductions of allochthonous taxa) and/or presence of limited resources.

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Reproductive strategy in female Alpine mountain hares (*Lepus timidus varronis*): adaptation to different elevation?

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In *Lepus*, litter size is inversely related to the duration of the reproductive season resulting in a consistent yearly production of around ten leverets per female. In high latitudes, animals have few litters with large litter sizes, whereas in low latitudes, several litters with small litter sizes are common per year. Knowledge on reproductive performance of Alpine mountain hares (*Lepus timidus varronis*) is scarce. In this study, we analysed 89 hares from Grisons, Switzerland, by examining placental scars and eye lens weight. The general aim of the survey was to examine the reproductive performance of female Alpine mountain hares. In particular, we focused on the question whether this subspecies adjusts the reproductive strategy in relation to elevation such as other *Lepus* species do in relation to latitude. All adults of our sample reproduced, whereas none of the subadults had leverets. 39% of the females littered twice and 61% three times a year with a median litter size of 3.00. We identified a significant effect of elevation on litter size, whereas the elevation did not influence the number of litters. We found no significant difference of yearly reproductive output across elevation range. Hence, some reproductive parameters seem to indicate that the Alpine mountain hare changes the reproductive strategy in relation to elevation similar to the mountain hares living further north do in relation to latitude.

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Seeing clear: New insights on magnetoreception in mammals

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Many species across the animal kingdom including mammals are able to sense the Earth's magnetic field. Although this has been proven in several behavioural studies, the position of the responsible receptors and the underlying mechanism of magnetoreception remain unclear. Since biological tissue is permeable for magnetic fields the receptors could be localised anywhere in the body but a position in the head region is most likely. The two most commonly accepted hypotheses on sensing magnetic information are the radical-pair hypothesis relying on biochemical reactions in photoreceptors and the so called magnetite-hypothesis, which is based on biogenic magnetite in the receptor cells. Only finding and analysing the primary receptor cells can finally solve the riddle on how magnetic stimuli are detected.

In order to gather information about the magnetoreceptors we used a top-down neurobiological approach. Using the modern iDISCO+ technique for tissue clearing we can determine neuronal activity due to magnetic stimulation across whole brains in laboratory mice and mole-rats. The active neurons are detected by immunohistochemical labelling of the immediate early gene c-fos. Afterwards the software ClearMap automatically maps the distribution of active neurons onto a digital brain atlas and identifies the differentially activated brain regions of different treatment groups. This allows us to get new insights on the processing of magnetic information in the brain which can provide important information about the location of downstream receptors.

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[illegible]

Species-specific responses to human-induced habitat modifications - A population genetic survey of neo-tropical bats

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Human-induced landscape modifications are often associated with habitat loss and fragmentation. Especially in the tropics where biodiversity is high, these habitat alterations pose serious threats to wildlife populations as they are known to impact species richness and abundance. Moreover, they may cause reductions in gene flow that might ultimately affect the potential of animals to adapt to environmental change through loss of genetic diversity. Consequently, populations with low genetic diversity are expected to suffer more severely from diseases and parasites. We investigated six different phyllostomid bat species (*Artibeus jamaicensis*, *Carollia perspicillata*, *Uroderma bilobatum*, *Dermanura watsoni*, *Dermanura phaeotis* and *Trachops cirrhosus*) native to the area around the Panamá Canal which has been highly modified by humans. While some of these species exhibit a high degree of mobility, others have been shown to be less mobile which limits their capability to reach isolated forest fragments. We obtained at least 150 genetic samples per investigated species - in some species data amounts to more than 400 individuals. Using a set of 10 to 16 nuclear microsatellite markers per species we determined levels of genetic differentiation and dispersal patterns for these species. While bat species with a high degree of mobility seem to be resilient to the habitat fragmentation within our study area, gene flow is restricted for less mobile species as indicated by population genetic structure. Our results emphasize the importance of examining the effects of habitat fragmentation at the species level, as differences in responses to habitat alterations appear to be species-specific.

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Negligible senescence in mammals? The case of *Myotis bechsteinii*

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Across the tree of life, some species such as the olm *Proteus anguinus* and the rougheye rockfish *Sebastes aleutianus* are attributed with negligible senescence, meaning that in those species mortality is low and both mortality and fertility are independent of age. Bats are well-known for being extremely long-lived given their small body size, but it is as yet unclear whether bats show senescence. As a consequence of the very low annual reproduction rate in bats with usually only one offspring each season, strategies to maximize the reproductive output are limited. This scenario would favor selection for a long reproductive lifespan. Here, we present results from a 19-year field study monitoring four different colonies of adult female Bechstein's bat *Myotis bechsteinii*. We used two different approaches to characterize senescence: a) age dependent mortality (=actuarial senescence), and b) age dependent fertility. We could not detect actuarial senescence within the first 11 years, which is twice as high as the median age in our population. Due the low sample size of old bats (>11 years, n=5) it is impossible to surmise what happens after age 11. Fertility, defined as the probability to give birth within a season, also does not decrease with age. Our findings support the absence of a significant effect of age on survival and reproduction in adult female Bechstein's bats, making them the first potential candidate for a mammal with a very late or even negligible senescence so far.

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This image shows a single page of white paper with horizontal ruling lines. The lines are evenly spaced and extend across the width of the page, typical of notebook or legal stationery. There are no margins, text, or other markings on the page.

Hepatitis E virus in zoo housed primates

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Hepatitis E virus (HEV) has been detected in humans and various wild-living, farmed and pet mammals in various parts of the world. Zoo-housed primates are in close contact with their keepers and potentially susceptible for human pathogens. The knowledge on natural HEV infection in non-human primates and the corresponding risk for zoonotic transmission is scarce. To determine whether primates in captivity are affected by HEV infection, we investigated sera of clinically healthy primates of 14 species from nine German zoos. Using two commercial ELISAs, ten of 259 (3.9%) animals were detected to contain HEV-reactive antibodies in at least one assay. Seroreactive animals belong to three ape and one Old World monkey species: bonobo (*Pan paniscus*), gorilla (*Gorilla gorilla gorilla*), lar gibbon (*Hylobates lar*) and drill (*Mandrillus leucophaeus*). The absence of anti-HEV-IgM antibodies and viral RNA for all of the animals indicates the absence of acute HEV infections. Our results suggest, that non-human primates in zoos can get naturally infected with HEV without showing clinical signs of hepatitis. To identify potential sources and transmission routes of these infections and their impact on human health, future HEV monitoring in captive primates and potential reservoir species, such as pigs, deer, rabbits and rats, is highly recommended for zoos.

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Numerical containment of the wild boar (*Sus scrofa*): comparison of the efficacy of some methods. A case study in the province of Rieti, Italy.

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In Italy, the wild boar has become an overabundant species that severely affects agricultural systems and zoocoenosis, especially on the ground-nesting avifauna. A recent estimate indicates at least 1,000,000 subjects currently present. Although the annual hunting activity is 50-60% of the total, the Yearly Profit Increase makes the species steadily growing. In order to encourage the hunting, ordinary and extraordinary legislation has been updated, procedures for the implementation of extraordinary hunting plans have been facilitated, damage compensation has been allocated to the hunting authorities. Moreover, the latter are compelled to activate several systems: different forms of hunting, selective hunting, the girata "turning" method, seizures. The only entities that have adapted to the new legislation are some protected areas. This study, conducted in the Regional Nature Reserve of the Lungo and Ripasottile Lakes, aims at a comparative assessment of the effectiveness of the sampling systems adopted, with the sole exception of hunting, because it is not allowed in protected areas. Below the number of wild boars captured per session in the period 2011-2016; Seizures: 4.9 subjects per session; Shootings: 0.7 subjects per session; Girata "turning" method: 1.0 subjects per session. The results indicate that seizure is the most effective hunting system. The limit of its application in unprotected areas is that is being opposed by hunters, which, by favouring the recreational aspect instead of the management one, prevent the application of the system that more than anything else is able to counter the numerical growth of the suid.

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James Peter Hill and the Australian mammal fauna

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James Peter Hill, a Scottish born zoologist based in Sydney at the turn of the last century was intrigued by the Australian fauna that he encountered in many collecting trips. He developed a special interest in the reproduction of native monotremes and marsupials and obtained a large number of specimens in the wild and from other sources. These make up a major part of his collection that now is housed in the Museum für Naturkunde in Berlin as part of the Embryological Collection. Besides rare developmental stages of monotremes and marsupials, many other mammal and vertebrate groups are found in this collection consisting of wet specimens and histological sections alike. Hill's interest in the reproduction of Australian mammals led to a chair at the University College London, where he devoted most of his professional life to reproductive biology. Based on archival and published material, this presentation looks into Hill's years in Australia and his expedition into the Blue Mountains hunting for monotremes and other animals.

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Historic records and recent development of Golden jackal (*Canis aureus*) distribution in the Austrian - Hungarian border region

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The golden jackal (*Canis aureus*) is expanding its range from the source countries in the Balkans. A first wave of expansion took place in the 1950s and a second one in the 1980s. In Hungary jackals were already confirmed to be part of the Pannonian Basin fauna in the 19th century and after a near extinction in the 1940s, reproduction was again affirmed in the 1990s. Austria's first substantial golden jackal proof originated in 1987 in Styria. Afterwards some vagrants were reported and first reproduction was confirmed near lake Neusiedl in 2007. Since then, additional observations of single individuals scattered throughout Austria indicated golden jackal presence.

In 2016 the first actively sought out record confirmed one territorial golden jackal group by means of bioacoustic monitoring. On the basis of reported evidence and information from hunters, we performed additional surveys in several dozens of pre-selected and presumed suitable areas close to the Austrian-Hungarian border. As a result of these surveys new territorial golden jackal groups could be verified in presumed areas.

Previously shot specimen in adjacent regions on Hungarian side and observations from local hunters both suggest that recorded groups have already occupied their territories in past years and did not settle there recently. Only a few territorial jackal groups were confirmed in surveyed areas; future studies will complement presented preliminary results. Further surveys are needed to determine whether confirmed jackal groups will keep their territories in the coming years. Selected regions will be monitored in detail to detect future dispersal.

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Patterns of tail reduction/loss among different locomotory types in Rodentia

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In addition to the limbs the axial skeleton of vertebrates plays an important role in locomotion. Numerous studies addressed the anatomy and the Hox gene expressions of the pre-sacral vertebral series of mammals. The most flexible part of the axial skeleton, the tail, has been given less consideration (except for primate tails). Often the caudal vertebral series is dismissed because the number and length of vertebrae is too variable, and their anatomy is regarded as too uniform. Thus the variation/pattern of homologous structures has been understudied. Yet, tails with significant functions (e.g. prehensility) generate high constraints on the morphology of caudal vertebrae. Conversely, constraints on tail morphology are diminished when function is low. Here we present the first results of a quantitative and morphological ongoing study on the patterns of tail reduction/loss in Rodentia as part of the project "Forward Genomics" interconnecting phenotype and genotype. Rodents display multitudinous locomotory adaptations (arboreal, gliding, semi-aquatic, fossorial, saltatorial, cursorial). We compared the caudal vertebrae anatomy of different locomotor types in selected rodent species. Linear measurements were taken on each caudal vertebra. First results reveal main anatomical variations and changes between long-tailed rodents (e.g. *Coendou prehensilis*, *Pedetes capensis*) and short-tailed rodents (e.g. *Cavia aperea*, *Dolichotis patagonum*). A correlation between a shorter tail and shift/loss of characters seems to be present, indicating loss of function. The ontogeny of the tail might reveal the pattern of character shift and which tail sections are reduced or weren't even present in earlier ontogenetic stages.

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News from the Bonn Bat Banding Centre

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In 2005 the Bonn bat banding centre (Fledermaus-Beringungszentrale Bonn) summarized all banding records for the report "Bat migrations in Europe" (Hutterer et al. 2005). Concurrently, the bat banding centre in Dresden (Feldermausmarkierungszentrale Dresden) collated 40 years of banding records from its banding activity (Steffens et al. 2004). Since 2005 no new banding records were published by the Bonn banding centre and banding records were mostly kept in binders or stored in Excel-spreadsheets. In 2013 we decided to adopt the same database software (MultiBaseCS) to be fully compatible with the Dresden centre. Since then we made a concerted effort to enter all available banding records in the database and assess how many bat bandings and band recoveries were reported back to Bonn to obtain a more complete picture of bat movements for the different species in the regions covered by the Bonn bat banding center. We report here some statistics of reported bands, including still missing data, and graphically show some additions to the known migratory routes of selected bats since 2005. Between 2005 and 2016 a total of 47,500 bands were released to banders. However, to date only 23% of the released bat bands were reported to the Bonn banding centre (covering 24 bat species). Nevertheless, this resulted in 5,091 recoveries in that time period. Between 2005 and 2017 the maximum recorded one-way flight distance was a Nathusius bat (*Pipistrellus nathusii*) with 1,013 km. The previous record, from 1988, was also held by a Nathusius' bat with 1,905 km.

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Diversity and molecular phylogeny of *Crocidura hirta-flavescens* species complex (Eulipotyphla: Soricidae)

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White-toothed shrews (genus *Crocidura*) are with 195 species the most diverse mammalian genus. They comprise almost half of all insectivorans. Due to their high diversity, morphological similarity, mostly small size and hiding life-style, *Crocidura* shrews are one of the least known and taxonomically complicated Old World mammals. This can be illustrated by the fact that more than 11% of *Crocidura* species have been described in the 21st century, and not only thanks to molecular methods.

In our contribution we present molecular phylogeny of the East and South African *C. hirta-flavescens* species complex - an Afrotropical *Crocidura* clade, sister to widely distributed sub-Saharan giant shrews of *C. olivieri* species complex. Based on molecular analysis (maximum likelihood and Bayesian approaches) of mitochondrial and nuclear DNA genotypes of specimens from Ethiopia to South Africa, we identified several well-supported lineages. *Crocidura flavescens* s. str. is distributed along South African coast, but its sister lineage was found in south-western Zambia, and another closely related lineage in arid central Tanzania. *Crocidura hirta* has wide distribution in open habitats of Tanzania, Mozambique and Zambia and consists of three genetically and geographically well separated groups. Specimens from Ethiopia and Mozambique formed significantly distinct lineages, sister to *C. hirta*, and their species status should be further explored. Despite the fact that taxonomy of this complex will require further work, analysis of its genetic diversity can be very informative about past evolutionary processes in tropics.

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"Mammalian Forward Genomics": an ontogenetic approach

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Throughout placental mammals, a great diversity in morphological adaptations has evolved. In a joint project between several German research institutions, the genomic origin of morphological traits is studied in order to elucidate mammalian evolution. The morphological traits linked to these adaptations are the basis for the genomic analysis. An interdisciplinary team of morphologists, bioinformaticians, evolutionary genomicists and experimentalists works together to address this problem. The project is based on "Forward Genomics" which makes use of the independent loss of traits to identify the respective genes. To achieve this goal a profound documentation of phenotypic traits in the different sub-projects is essential. This sub-project deals with morphological aspects during ontogeny. Phenotypic data of selected mammal species covering all current orders is collected from macerated museum specimens and histological slides. Selected skeletal and visceral traits of the head from pre- and postnatal stages are in the focus of this sub-project including transient characters. After an initial extensive literature search, fetal material of the Embryological Collection and crania housed at the Museum für Naturkunde in Berlin are considered. To explain the genetic source of phenotypic diversity, the data is fed into a database incorporating ontologies for subsequent bioinformatics analysis.

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The remarkable auricle of shrews (Soricidae): Form follows function

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The family Soricidae actually includes 28 genera and about 400 species of shrews. They occur almost world-wide except for Australia and the Polar regions. At first sight all species look very similar, but a closer look reveals various anatomical adaptations to different lifestyles. The shape, size, and inclination of the outer ear (auricle) varies considerably among species, from large and complex (*Suncus meg-alura*) to completely reduced (*Nectogale elegans*). The shrew auricle is also unique because it possesses a pocket-like structure formed by the plica principalis, helix, and scapha. In this study we tested whether different feeding and foraging strategies are reflected in the anatomy of the external ear of shrews. Based on drawings of the heads of well-preserved specimens of 41 species of shrews we measured the inclination value of the auricle in relation to the nostril-eye-line. Results show that there is a clear difference in visibility and inclination of the auricle between the different subfamilies of shrews, reflecting different lifestyles. Large ears are found in terrestrial and scansorial species, small and reduced ears in burrowing and water-adapted species. The inclination value of the auricle follows the same trend, however within the phylogenetic limits of the subfamilies.

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Introgression of sika deer into native populations of red deer in Bavaria and their consequences

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It is well-known that red deer and sika deer hybridize in sympatric occurrences, producing fertile offspring. Thus, they may even be regarded to belong to one and the same biological species. For some cases, such as in large parts of Ireland, this phenomenon can lead to a stable hybrid population. In Bavaria, sika deer is increasingly to be observed for some years, migrating from a large population in the Karlovy Vary region/West Bohemia to Eastern Bavaria.

The aim of the present study was to provide initial information to what extent migration into Bavaria takes place and if there are already indications for hybridisation events between red deer and sika deer. Simple sequence repeat (SSR) markers were used to distinguish between the two species, in addition to the collection of morphological characteristics. Therefore, 30 SSR markers were tested with 56 samples phenotypically classified as red deer and 29 samples phenotypically classified as sika deer. Fourteen markers showed good amplification results in both species after the optimization of PCR conditions, but only eight SSR markers provided a clear assignment to red deer or sika deer with probabilities of 98.3% to 98.7%. Twenty-five other samples from the study area in Bavaria are currently under investigation and further sampling is planned for hunting season 2017/2018. Based on the results, the consequences of possible migration are evaluated for the native red deer and practical recommendations for the future are worked out.

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Form alignment in European hare *Lepus europaeus*: the effect of the geomagnetic field

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Mammals show a directional response to the geomagnetic field. This magnetic alignment represents a spontaneous, fixed directional response in which mammals align their bodies along or perpendicular to the magnetic field lines. We tested the potential effect of the geomagnetic field on the position of forms used by European hares (*Lepus europaeus*) in an arable landscape in Lower Austria. For 400 forms we determined their direction to the nearest 5° and classified them into the categories N, NE, E, SE, S, SW, W, NW. The statistical analysis revealed no significantly preferred direction but a rather uniform alignment (Rayleigh-Test: $p = 0.4798$, Chi-square: $p = 0.05877$). There is no evidence for dependence of form direction on vegetation height, ground cover or main wind direction in our study site. Effects of agricultural land orientation on form alignment could be explored in cropland with cereal grain only. We suggest hares adjust form alignment on small-scale structures like machine tracks or plow furrow and on prevalent environmental conditions. To sum up, magnetic alignment in European hare seems to be negligible under natural conditions and largely suppressed by numerous other orientation determining factors.

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Seasonal infectivity of edible dormice infected by Lyme disease spirochetes

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Edible dormice *Glis glis* serve as reservoir hosts for the tick-borne Lyme disease (LD) spirochete *Borrelia afzelii*. These long-lived rodents may contribute more infected ticks to the natural transmission cycle than do non-hibernating rodents. After hibernation, however, DNA of LD spirochetes is not detected in the skin of edible dormice until July. To determine when edible dormice encounter ticks and become infected and infectious, we captured them throughout their season of activity in various field sites in Czech Republic, northern and southern Germany, inspected them for ticks and examined these ticks for spirochetal DNA by PCR. Hosts acquire spirochetal infection from infected nymphs feeding on them. Nymphal infestation rates on dormice increased twenty times from June through September. Because LD spirochetes are not inherited, the detection of spirochetal DNA in larval ticks removed from an edible dormouse reflects its infectivity. No edible dormouse infected its larval ticks before July. The number of dormice infecting ticks increased strikingly during August and September. Increasing infectivity of dormice throughout the season reflected the increasing likelihood of nymphal infestation. Taken together, edible dormice appear to lose their spirochetal infectivity during hibernation and to become re-infected once nymphal ticks start feeding on them.

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Dietary preferences of the European hare (*Lepus europaeus*): a herbivore selecting its diet for a high fat content

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European hares (*Lepus europaeus*) rely on fat reserves, particularly during the reproductive season. Therefore, hares should select dietary plants rich in fat and energy. However, hares also require essential polyunsaturated fatty acids (PUFA) such as linoleic acid (LA) and alpha-linolenic acid (ALA). Although hares are able to absorb PUFA selectively in their gastrointestinal tract, it is unknown whether this mechanism is sufficient to guarantee PUFA supply. Thus, diet selection may involve a trade-off between a preference for energy versus a preference for crucial nutrients, namely PUFA. We examined the diet selection of European hares by analysing both the botanical and chemical composition of stomach contents and comparing these values with the food plants available in four seasons for three years in an arable area in Austria. We found that European hares selected their diet for high energy content (crude fat and crude protein), and avoided crude fibre. There was no evidence of a preference for plants rich in LA and ALA. We conclude that fat is the limiting resource for this herbivorous mammal, whereas levels of LA and ALA in forage are sufficiently high to meet daily requirements. As hares preferred weeds/grasses and various crop types while avoiding cereals, our results are in line with the suggestions to promote heterogeneous habitats with high crop diversity and set-asides to stop the decline of European hares across Europe.

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Feeding ecology of Eurasian lynx (*Lynx lynx*) in the Harz Mountains, Germany

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The dietary spectrum and prey selection of Eurasian lynx (*Lynx lynx*) were studied in the Harz Mountains and the surrounding area, located in Central Germany. Between 2008 and 2016, 119 scats from lynx were collected and investigated for prey remains. In addition, 170 lower jaws from lynx killed ungulates were prepared for a precise age determination. Wild ungulates constituted more than 90 % of lynx's diet, while roe deer (*Capreolus capreolus*) was selected significantly. Inside the Harz Mountains, an area with low roe deer densities, red deer (*Cervus elaphus*) constituted the most important alternative prey. Lynx did not select roe deer forage, but significantly preferred juvenile red deer. Male lynx were more able to prey on adult red deer than female. Further differences in the dietary spectrum of female and male lynx's were less pronounced. Non-ungulate prey had no importance for lynx's diet, even though hares (*Lepus europaeus*) may be underestimated at least a little. The same applies to small mammals. Remains of voles (Arvicolinae) occurred quite frequently in lynx's scats, but were negligible concerning consumed biomass. The present study confirms findings from previous surveys and expands the knowledge about lynx's feeding ecology in Central Europe.

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Sequencing and analysis of a mitochondrial genome of the European mink (*Mustela lutreola*)

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De novo sequencing (NGS) of complete, previously non-characterized mitochondrial genome of the critically endangered European mink (*Mustela lutreola*) was provided and its physical map was developed. Analyses involved DNA samples from 5 individuals. Based on collected mitogenome data, bioinformatic and phylogenetic analysis were performed to identify conservative and variable regions and to assess interspecific genetic variability. Obtained reference mtDNA sequence is of 16 523 bp and shows similarity at the level of 95-99% with known mitochondrial genomes of other mustelid species. Sequencing allowed direct genotyping (Genotyping-by-Sequencing) and highly informative multilocus analysis. Obtained results allow to formulate specific recommendations for active and passive protection of the species, providing ready-to use tools for the European mink conservation, based on professional knowledge from the conservation genetics. This, in turn, increase possibility to design protection plans for the European mink, through providing measureable and highly informative tool (complete mitogenome sequence) to define operational taxonomic units, evolutionary units, reveal phylogenetic dependencies, plan protection breeding and also to plan, realize and assess efficiency of reintroduction activities.

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Phylogeography and past demographic processes of brown hares (*Lepus europaeus*) in Europe and the Middle East

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The brown hare (*Lepus europaeus*) is one of the temperate mammal species whose present distribution of genetic lineages has been strongly shaped by the climatic oscillations during the Late Quaternary. Based on mtDNA control region sequences of 243 brown hares from 37 sampling localities across the Balkans, together with all publically available sequences from Europe and the Middle East, we aimed at delineating the most likely glacial refugium wherefrom the postglacial northward expansion into central Europe has originated. Three major haplo-groups ("Anatolia/Middle East", "the Balkans", and "central Europe") were revealed with apparent south-north gradual decrease in molecular diversity indices. The southeastern central Balkans was presently identified as the putative origin of most populations in the southern and northern Balkans, while populations from central Europe have originated from the northern Balkans. This scenario was further supported by coalescence theory-based estimates of population expansion, which clearly indicated the oldest expansion period (20,000BP) for the southeastern Balkans, whereas brown hares from the southern Balkans (e.g., sampling localities in central and southern Greece) started to expand slightly later (17,000BP), and brown hares from the northern Balkans, central, north-central, and western Europe expanded even much later (8,000BP).

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MHC class II DQA genotypes in golden jackals (*Canis aureus*) expanding towards central Europe

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In Europe, golden jackals have continuously been expanding their distributional range from the southern and southeastern Balkans towards central Europe since the 1960ies. Given the high diversity of pathogens reported in those expanding populations, we expected significant geographic immunogenetic variation due to adaptation to regional pathogenic landscapes. Here, we studied DQA exon 2 polymorphism in 157 individuals from Bulgaria (n=33), Serbia (n=90), and Hungary (n=34) by direct sequencing. We determined individual genotypes by phasing, including all available canid sequences from GenBank. Among all four alleles detected presently (DQA1*00402, DQA1*03001, DQA1*00101, DQA1*01401, with frequencies amounting to 0.704; 0.290; 0.003, and 0.003, respectively), DQA1*00402 and DQA1*03001 occurred with similar frequencies across our study area, respectively, whereas DQA1*00101 and DQA1*01401 were found in single individuals from Serbia only. Although there was neither a significant deviation from Hardy-Weinberg equilibrium in the overall data set ($FIS(W\&C)=-0.026$, $p=0.53$) nor when tested separately for each of the three regional samples, a codon-based selection test (using OmegaMap software) returned significant signals of positive selection at two codon positions, when accounting for potential recombination effects. These findings accord to an earlier study on jackals from Croatia, and do not support our initial hypothesis of regional MHC variation due to adaptation to supposedly heterogenous pathogen environments. The high level of gene flow across populations, as observed earlier by neutral molecular markers, may blur weak patterns of regional adaptation that could

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Ambient temperature affects occurrence of mitochondrial ATP synthase 6 OXPHOS protein variants in hares (*Lepus spp.*) from Ethiopia

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The adaptive significance of the thirteen mitochondrial (mt) genes encoding for components of the oxidative phosphorylation (OXPHOS) pathway that contributes most to the cellular energy production is hardly investigated. Recent studies suggested positive selection on mt OXPHOS genes in hares (genus *Lepus*, Lagomorpha) due to varying climatic conditions. Here, we examined whether the occurrence of protein variants encoded by the mt ATP synthase 6 (MT-ATP6) locus was affected by ambient temperature in hares from different environments in Ethiopia. Individual protein variants were obtained by translation of nucleotide sequences of 64 *Lepus habessinicus*, 13 *L. fagani*, and 27 *L. starcki*. Multinomial linear modelling revealed a significant effect of ambient temperature (as expressed by principal component scores of six temperature parameters for sample locations) on the occurrence of the three most prevalent protein variants found, independent of geographical sample distribution, which, too, had an effect on the occurrence of those protein variants. Potential effects of species and altitude of sample location on the occurrence of protein variants could not be tested, due to their high collinearity with geographical coordinates and ambient temperature, respectively. Our model results were complemented by significant signals of positive selection as returned from codon-based Maximum Likelihood and Bayesian tests. Our present results confirmed earlier findings of ambient temperature affecting the occurrence of MT-ATP6 protein variants in hares from Tunisia. Ongoing studies on hares from different environmental/climatic provenances should elucidate the role of positive selection in shaping diversity of the whole mtOXPHOS gene complex in different evolutionary lineages.

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Modelling sperm production in wild living hares (*Lepus europaeus*) from Bulgaria

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In Bulgaria, population densities of hares (*Lepus europaeus*) have been stagnant country-wide at a very low level over the last ten to fifteen years (maximally approximately eight hares/100 ha in spring). Potential local inbreeding at low density may over many years have led to a significant reduction of breeding performance. Here we examined whether individual heterozygosity based on eleven microsatellite loci and mitochondrial (mt) haplotype lineages affected sperm production in 101 males collected in 2011-2013 across Bulgaria. Specifically, we tested for reduced sperm production, as classified from histological epididymis sections, in males with low heterozygosity or that harbored "Anatolian-type mtDNA" that is phylogenetically more distantly related to the common "European-type mtDNA". Our logistic linear models included the classification "massive or high amount of sperm present" vs. "sperm present at moderate or low level" as dependent factor and individual heterozygosity, mtDNA-phylogroup assignment, age class ("subadult" vs. "adult", as inferred from dry eye lens weights), mean testicle mass, body condition (i.e., retroperitoneal fat mass related to body mass), infection intensity of *Taenia pisiformis* cysts and of small liver flukes (*Dicrocoelium lanceolatum*), as well as geographical location (longitude, latitude), sampling month and year as fixed independent factors/variables. However, only testicle mass, age class, and collection month returned significant effects on the two categories of sperm quantity. Those results were confirmed when using mean testicle mass as dependent variable. Obviously, sperm production was not reduced by the considered genetic factors and factors potentially reducing body condition.

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Population Viability of Bezoar Ibex (*Capra aegagrus*) in Northeastern Turkey

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Population viability analyses may be used for expectation of viability of critical population after habitat loss, fragmentation and degradation. The aim of the study is to determine the effects of dams to Bezoar Ibex (*Capra aegagrus*) population viability in Çoruh Valley and Verçenik Mountains Wildlife Reserve Area in Northeastern Turkey. GPS collar, camera traps, field observations and inventory techniques were used for determination of the effects of dams on Bezoar Ibex. It was shown that the cliffs of the Coruh Valley were critical habitat for the feeding and mating of Bezoar Ibex. The home range size was estimated as 3000 ha for male and 1000 ha for female and yearlings of Bezoar Ibex. The optimum carrying capacity of Bezoar Ibex is 3000 individuals for Coruh Valley and 2000 individuals for Verçenik Mountains Wildlife Reserve Area. The population viability analyses showed that as long as the current habitat use, Bezoar Ibex populations can be possibly viable (80-90%). Arkun Dams caused the destruction 730 ha priority habitat used by Bezoar Ibex in Verçenik Mountain Area. It was estimated that Yusufeli Dams can lead to 3670 ha habitats to impoundment. Population viability analyzes showed that the amount and survival rate of breeding female was crucial for population viability. Also, yearling survival rate may be thought another crucial component for population viability. The viability analyses should be used to determine the effects of poaching and illegal hunting to Bezoar ibex.

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The Turbinal Skeleton in the Dolichocephalic Russian Wolfhound (*Canis lupus familiaris*)

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The domestic dog shows the highest intraspecific morphological diversity in its overall skull shape. In contrast to the external bones the intracranial structures are less well known. High-resolution computed tomography (μ CT) gives noninvasive access to structures like the turbinal skeleton inside the nasal cavity. The dog's nasal chamber has been studied only in a few breeds, mainly short-snouted (brachycephalic) ones due to medical treatments. The turbinates of long-snouted (dolichocephalic) breeds have been less well studied as they have no respiration difficulties. Here we present the first study on the morphology and ontogeny of the turbinal skeleton of selected Russian wolfhounds (borzois: 5 adults, 1 juvenile) based on μ CT scans and virtual 3D models. The borzoi's turbinates have an unexpected large surface area, high complexity, and also a higher number of lamellae (14 to 20) in comparison to medium-snouted breeds (e.g., German shepherd), and the European wolf (*C. lupus lupus*). Our results clearly contradict the former hypothesis that sighthounds have less and reduced lamellae because of restricted space in the slender snout. In a recent study greyhounds failed at an odor-discrimination task. Either it was for ethological or physiological reasons is yet unknown. However, the turbinal morphology of the borzoi clearly shows no evidence for a reduced olfactory sense. This research provides a basis for future histological, neurological, and ethological studies that are needed to understand the effects of the intranasal bony structures on the sense of smell in dogs as well as mammals in general.

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Austrian Barcode of Life (ABOL): DNA-Barcoding of Austrian mammals - difficulties and challenges

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DNA-barcoding is a method for efficiently identifying samples to species level based on short standard DNA sequences. However, reliable species assignment requires the availability of a comprehensive DNA barcode reference library. The ABOL (Austrian Barcode of Life, www.abol.ac.at) initiative aims to do this for Austria's fauna, flora and fungi. With more than 100 species in Austria, mammals pose a significant part of its vertebrate fauna, and several taxa are important flagship species for conservation. Yet, generating a comprehensive DNA barcode reference library for Austrian mammals is not straight-forward as collecting fresh (voucher) material is often very difficult to (nearly) impossible because of the special animal welfare and conservation regulations that apply to vertebrates in general, and mammals in particular. Moreover, even great efforts might not guarantee sufficiently complete sampling of fresh material in a short period of time. Thus, historical museum collections represent invaluable sources for the DNA-barcoding of many taxa. However, DNA extracted from historical samples is usually degraded, such that only short fragments can be amplified, rendering the recovery of the barcoding region as a single fragment impossible. Consequently, amplification and sequencing of the entire barcoding region needs to be done in several short overlapping fragments, multiplying the effort and costs per sample necessary to generate a DNA barcode. A recently developed PCR primer set that reliably amplifies the barcoding region in most Central European mammals in six overlapping fragments greatly extends the utility of historical mammal specimens from museum collections for large-scale barcoding studies.

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