

Deutsche Gesellschaft FÜR SÄUGETIERKUNDE



**86th Annual Meeting of the German Society of Mammalogy
Frankfurt a. M. (Germany), 4th-8th September 2012**

Abstracts of Oral Communications and Poster Presentations



Contents

Preface and invitation	3
Abstracts of all other oral communications and poster presentations	5
Author index	24

Editors:

R.H.S. Kraus, T.E. Reiners, C. Nowak

Scientific committee:

R.H.S. Kraus, C. Nowak, H. Ansorge, K. Hackländer, F. Hailer, A. Janke, V. Volpato, F.E. Zachos

Organising committee:

C. Nowak, R.H.S. Kraus, T.E. Reiners, C. Frosch, K. Steyer, V. Harms, A. Janke, F. Hailer, V. Kutschera, T. Bidon, C. Reisert, V. Volpato, T. Schikora

Photo: Wild male brown bear (*Ursus arctos*) captured on camera during (summer) night near the Finnish-Russian border. Most parts of the border zone in Finland are characterised by a high density of brown bears. Photo by Alexander Kopatz

The Guest Editors, the Editor and the Managing Editor of the journal Mammalian Biology are not responsible for the content published in this Special Issue of Mammalian Biology.

Elsevier GmbH, Hackerbrücke 6, D-80335 München, Germany

Preface and Invitation

You are heartily invited to participate in the 86th Annual Conference of the German Society of Mammalogy (Deutsche Gesellschaft für Säugetierkunde e.V.) hosted by the Senckenberg Research Institute and Natural History Museum and the Biodiversity and Climate Research Centre (BIK-F), Frankfurt am Main, Germany. The conference will take place within the historical buildings of the Senckenberg Natural History Museum in Frankfurt, which comprises one of Europe's largest natural history collections.

This congress addresses the topic: “The *Past, Present, and Future* of Mammalian Diversity”. We will experience the variety of mammalian life-forms and specifically address biodiversity patterns of this group across space and time. The conference covers a broad spectrum of research, spanning from the past origins of mammalian diversity, the present distribution of variation within species, the taxonomic, morphological, physiological, and behavioural diversity of living mammals to the future fate of this unique group and our strategies for its preservation in a world of rapid environmental change. However, presentations covering all topics of mammalogy are welcome, if they are of broad interest for researchers in mammalogy. The conference language will be English only.

Being mammals ourselves, humans have always had great compassion for this particular group of animals. Subsequent to the extinction of dinosaurs, it has been up to the mammalian lineage to fill many empty niches in (mostly) terrestrial ecosystems. Mammals are now a diverse class of animals, comprising well above 5000 species in more than 1000 genera.

One of the early and still unbroken interests of biologists is to understand how this diversity came about. Palaeontology has contributed greatly to our understanding of mammalian evolution. Great strides have been made in this field due to the technological revolution of the 20th century. For example, it is now possible to use high-tech imaging and image processing devices in the study of fossils. The indirect study of past biological diversity through inferring the tree of life – be it based on morphological or genetic characters – plays an ever increasing role in phylogeny. Advances in molecular biology have extended the study of fossil material into the field of genetics comprising the young discipline of palaeogenetics.

The study of mammals engages the public in nature conservation. Several mammal species play a significant role as so-called “flag-ship species”: they attract public attention and funding for nature conservation projects. Understanding processes that shape the present-day diversity and distribution of mammals, such as demographic dynamics at the population level or behavioural dynamics at the individual level, helps to form the basis for deciding how to preserve mammals as well as nature as a whole.

With knowledge about the past and present of mammalian diversity to hand, we can devise programmes to preserve this precious resource for the future. Nature conservation is traditionally difficult because of the conflicting interests of many stakeholders. Weighing the conservation of nature against human development is a difficult task and has profound implications for the future of us all human and non-human mammals alike.

The topics we study in mammalian biology are as diverse as is this class of animals. Technological advances in studying the past, present and future of mammals, paired with the emergence of globalised conservation agendas during the past decades, makes it a timely undertaking to organise a conference in which scientists from diverse disciplines come together – to study diversity at all temporal levels. We cordially invite you to participate in a census of mammalian diversity at this year's “86th Annual Conference of the German Society of Mammalogy”, this late summer in Frankfurt am Main, Germany.

More information is available at <http://www.senckenberg.de/dgs2012>

On behalf of the organising committee,

July 2012

Robert Kraus
Tobias Erik Reiners
Carsten Nowak



Abstracts

Which factors increase the risk for fatal collisions by bats at wind turbines?

F. ADORF, C. BRAUN, F. ADORF, Büro für Faunistik und Landschaftsökologie, Am Sauerplacken 2a, 55444 Schöneberg, Germany, email: frank.adorf@buero-t-grunwald.de

The occurrence of bat fatalities at wind farms is receiving much attention in conservation planning, especially because wind energy is becoming increasingly common in many regions, and because numerous bat species are highly endangered. Knowledge about the factors which lead to collisions by bats with wind turbines is thus important to reduce the impact of wind energy devices on bats. We here present results from three different types of surveys to quantify the occurrence of bat fatalities at wind parks: (1) ground-level searching for carcasses (which is very labour-intensive and may miss some collision instances due to the presence of scavengers), (2) surveys and landscape cover analyses to assess the biogeophysical characteristics of power plant sites and (3) automatic bioacoustics monitoring at rotor height (i.e., where the actual collisions occur, a height often neglected in bat activity surveys that are conducted from the ground). Sites of wind energy parks which have an especially high number of bat collisions show a range of typical characteristics, including proximity to rivers or lakes, woodlands, mountain chains, but other factors including the seasonal occurrence of migrating bats at some sites can also influence the risk for bat fatalities. Currently, some wind farms are being shut down temporarily at times of high collision risk, a procedure that will hopefully reduce the number of bat fatalities in the future.

Investigating nuclear and cytoplasmic mitochondrial sequences in the Eurasian lynx (*Lynx lynx*) and other Felidae

M. AUTENRIETH, J. FICKEL, D.W. FÖRSTER, Leibniz-Institut für Zoo- und Wildtierforschung, Alfred-Kowalke-Strasse 17, 10315, Berlin, Germany, email: marijke.a@hotmail.de

The largest European felid, the Eurasian lynx (*Lynx lynx*), has a broad Eurasian distribution. While the species is classified as “least concern” by the IUCN, the Eurasian lynx in Europe has gone through a severe bottleneck caused by habitat loss and hunting, and there are concerns regarding the sustainability of some European populations. A more complete understanding of the genetic differentiation among populations of continental Europe and Scandinavia is needed to make informed decisions about translocations to supplement endangered populations. In this study, we expand on previous work on the genetic diversity and phylogeography of the

Eurasian lynx using whole mitochondrial sequences (17,045 bp). To ensure that cytoplasmic mitochondrial sequences were obtained, a strategy involving large overlapping fragments (~6500 bp) generated by long-range PCR was adopted. Additionally, we also actively looked for NUMTs (Nuclear Mitochondrial Sequences). Because the latter are characterized by different evolutionary rates and constraints, they are usable as additional molecular markers, if detected. If not correctly identified, they are a source for errors in genetic analyses. Other felid species were included for comparison, and to serve as outgroups.

The curious case of *Gazella arabica*

E.V. BÄRMANN¹, D. ERPENBECK^{2,3}, S. BÖRNER^{2,4}, G.E. RÖSSNER^{2,3,4}, B. AZANZA⁵, C. HEBEL⁶, G. WÖRHEIDE^{2,3,4}, ¹Museum of Zoology, Department of Zoology, University of Cambridge, Downing Street, CB2 3EJ, UK, email: evb24@cam.ac.uk, ²Department für Geo- und Umweltwissenschaften, Ludwig-Maximilians-Universität München, Richard-Wagner-Strasse 10, 80333 München, Germany, ³GeoBio-Center^{LMU}, Richard-Wagner-Strasse 10, 80333 München, Germany, ⁴Bayerische Staatssammlung für Paläontologie und Geologie, Richard-Wagner-Strasse 10, 80333 München, Germany, ⁵Departamento de Ciencias de la Tierra (Paleontología) and IUCA, Universidad Zaragoza, Pedro Cerbuna, 12, 50009-Zaragoza, Spain, ⁶Al Wabra Wildlife Preservation, P.O. Box 44069, Doha, Qatar

Gazelles form a species-rich genus of horned ruminants (Bovidae) and are arguably amongst the most iconic and endangered animals. In the taxonomic literature of the past few years, 10–23 different species are recognized, depending on the author. One of the most enigmatic members of the genus is *Gazella arabica*, the earliest gazelle known from Arabia. The type material, one male, one female and one juvenile individual collected in 1825, has been the subject of many studies that tried to figure out what *G. arabica* actually is: a unique (possibly extinct) species? Or a synonym of *G. gazella* or *G. dorcas*? Especially the male, designated as the lectotype by Neumann (1906), has puzzled researchers for centuries, as no similar gazelle has ever been found. Using mitochondrial DNA of the type material, we wanted to clarify the taxonomic status of *G. arabica*. What seemed to be a simple task swiftly developed into a detective story. We found skin and skull of each supposed individual to belong to different animals, in the case of the female even to different species. Morphometric analyses of skull dimensions verified the results from the molecular phylogenetic analysis. Finally we can conclude that *G. arabica* (as defined by the male type

skin) represents a distinct gazelle lineage that is closely related to Mountain gazelles (*G. gazella*).

A robust multiplex PCR approach for gender identification in bears

T. BIDON¹, C. FROSCH², F. HAILER¹, A. JANKE¹, ¹ Biodiversity and Climate Research Centre (BiK-F), Senckenberg Gesellschaft für Naturforschung, Senckenberganlage 25, 60325 Frankfurt am Main, Germany, email: tobias.bidon@senckenberg.de, ² Conservation Genetics Group, Senckenberg Research Institute and Natural History Museum Frankfurt, Clamecystrasse 12, 63571 Gelnhausen, Germany

Knowledge of the gender of individuals in free-ranging wildlife population facilitates the understanding of many aspects of population ecology and can provide crucial data for management and conservation programs. However, determining sex in the field can be challenging. Advances in molecular techniques can overcome these constraints by amplifying sex-specific fragments from non-invasively collected samples. We developed a new and simple multiplex PCR approach to identify the sex of brown and polar bears. The risk of cross-amplification was minimized by the development of bear-specific primers. Two Y-chromosomal fragments and one X-chromosomal fragment of different sizes are amplified and can easily and economically be identified by standard agarose gel electrophoresis or by fragment length analysis. Our approach includes a double test for Y-specific amplification and an internal PCR positive control, making it particularly efficient and reliable. All fragments are under 200 bp in size and can thus be obtained from tissue and blood samples as well as potentially degraded DNA from non-invasive samples. The correct sex could be assigned to all tested brown and polar bears of previously known sex and the method yielded distinct banding patterns in individuals of unknown sex. The feasibility of using high as well as low quality DNA samples and the dual Y marker amplification render this method applicable in a wide variety of studies.

Cranial modularity and integration of Serbian roe deer (*Capreolus capreolus* L.)

M. BLAGOJEVIĆ, S. MILOŠEVIĆ-ZLATANOVIĆ, Faculty of Science, Department for Biology and Ecology, Radoja Domanovića 12, 34000 Kragujevac, Serbia, email: paulidealist@kg.ac.rs, svetlanamz@kg.ac.rs

By studying morphological integration and modularity as covariation pattern in the suite of 47 traditionally measured cranial characters of roe deer (*Capreolus capreolus* L.) originating from three Serbian populations, we were able to test spatial organization of cranial covariance in a single species. In opposition with commonly considered stability at a species level, both integration and modularity were found to vary between the populations and between sexes. Modules were defined based on common developmental/functional criteria and tested with theoretical, connectivity matrices, while morphological integration was assessed with the coefficient of determination. We found that, between populations with higher integration and lower modularity and with lower integration and higher modularity, there is an intermediate one, meaning that both of these features vary with population membership. As higher integration could be interpreted as an index of lower adaptability of a given structure we conclude that population history and complex environmental influences may have shaped the observed morphological variation pattern. Functional nature of the modules definition also aided us in explaining overall morphological variation, especially with respect to sexual differences. In males, tight integration of the vault

and facial modules may be linked to antlers and their role in male social interactions, while well defined temporal and facial modules of females may promote adaptability in a resource competitive environment. Finally we argue that urbanization and agriculture could promote roe deer adaptability as lowest integration and highest modularity were found in the population with the highest level of overall human activities.

The key to life (history)

T.G. BROMAGE^{1,2}, R.T. HOGG³, R.S. LACRUZ⁴, C. HOU⁵, ¹ New York University College of Dentistry, Department of Biomaterials & Biomimetics, New York, NY 10010, USA, email: tim.bromage@nyu.edu, tbromage@senckenberg.de, ² Senckenberg Research Institute and Natural History Museum, Paleoanthropology Section, D-60325 Frankfurt am Main, Germany, ³ Florida Gulf Coast University, Department of Physical Therapy and Human Performance, Fort Myers, FL 33965, USA, email: rhogg@fgcu.edu, ⁴ University of Southern California, Center for Craniofacial Molecular Biology, School of Dentistry, Los Angeles, CA 90033, USA, email: rodrigo@usc.edu, ⁵ Missouri University of Science and Technology, Department of Biological Sciences, Rolla, MO 65409, USA, email: HouCh@mst.edu

The life histories of mammals are described by a number of characteristics relating to the timing and duration of life stages. Body and organ masses are also included because body size is fundamental to an organism's physiology and metabolic ecology. Further, because metabolism is responsible for energy allocations that fuel all aspects of life history, metabolic rate is also included in the life history rubric. What particularly interests researchers on the life histories of higher taxa, such as that of the order primates, is the covariation that exists between traits, but despite this interest, the factor(s) regulating and defining the overall life history matrices of mammals remains completely unknown. Because life history traits reflect dependence on rate and time, a biological timing mechanism must be invoked to explain life history variation. Mammalian enamel contains time-resolved incremental lines in its microanatomy, including a long period secretion rhythm at some multiple of daily events, called the stria of Retzius; the number of days between striae is called the repeat interval (RI). RI is found to be highly and significantly correlated with all life history characteristics except estrous cycle length, and with metabolic rate. When statistically controlling for body mass, estrous cycle length is also highly and significantly correlated with RI. This long period rhythm, which we call the Havers–Halberg Oscillation, incidentally occurring as RI, coincides with body mass-dependent and body mass-independent mammalian hypothalamic-pituitary outputs, thus representing a centrally regulated and oscillating adjustable long-period developmental rhythm responsible for metabolism and organismal life history.

Genetic structure of the Eurasian Lynx (*Lynx lynx*) in Northern-Continental and Scandinavian Europe: Evidence from microsatellite and SNP data

J.K. BULL¹, K. SCHMIDT², D.W. FOERSTER¹, J. FICKEL¹, ¹ Institut für Zoo- und Wildtierforschung, Alfred-Kowalke-Strasse 17, 10315, Berlin, Germany, email: foerster@izw-berlin.de, ² Mammal Research Institute, Polish Academy of Sciences, 17-230 Białowieża, Poland

The Eurasian lynx (*Lynx lynx*) is the largest European felid. It historically existed throughout most of continental Europe and Scandinavia; a distribution that has been greatly reduced by habitat loss and direct persecution. In several European countries, attempts have been made to re-establish populations, but many

of these are still very small, and doubts regarding their sustainability have led to suggestions of population supplementation. However, the broad-scale population genetics of the species is still poorly known, raising concerns about the genetic outcome of proposed translocations. We investigated the genetic differentiation in Eurasian lynx across northern continental and Scandinavian Europe to help inform those making conservation/management decisions. We present the genetic structure detected when employing different markers: autosomal microsatellite loci, mitochondrial SNPs, Y-chromosome SNPs, and autosomal SNPs. Population definitions based on these markers partially contradict previous, occurrence-based definitions.

Structure of the Corsican red deer population in the faunal protection reserve of Monte Genis

S. CONTU, Assessorato alle Politiche Ambientali, Energia e Tutela del Territorio, Provincia di Cagliari, Via Giudice Guglielmo, 46, I-09121 Cagliari, Italy, email: csilvia99@gmail.com

The Corsican red deer (*Cervus elaphus corsicanus*) was widely spread in the whole island up to two centuries ago. From then on the indiscriminate hunt and the deforestation aimed to produce coal constrained it to the wildest zones of the island and the population is today limited to three areas: Sulcis (South), the Sette Fratelli forest (South East) and Arbus (South West). Reintroduction, carried out mainly in the sites of Ente Foreste della Sardegna, increased the number of populations to 6000–6500 individuals. In this study we focus on a reintroduced population located inside the Oasi di Protezione Faunistica di Monte Genis a protected area in the province of Cagliari. Population structure was studied through sightings carried out along transects selected as to proportionally represent all the environmental types and the altitude belts of the area. In addition to the observations collected in transects, all the casual observations outside the standardized paths were recorded. The parameters considered were: sex ratio, the calves/females ratio, and the percentage of males in the different age classes. The sex ratio is 0.56, while the calves/female ratio is 0.28. The percentage of males in the different age classes shows a greater number of adult males than young males in all season. The population of Monte Genis shows a structure similar to populations in another area of Sardinia but slightly different from data of populations of red deer (*Cervus elaphus*) that might be the result of adaptation to the particular environmental condition of the island.

Hormones, parasites and male reproductive tactics in Alpine chamois: Clues for potential life history trade-offs?

L. CORLATTI^{1,2}, S. BETHAZ³, A. VON HARDENBERG⁴, B. BASSANO⁴, R. PALME⁵, S. LOVARI¹, ¹ Research Unit of Behavioural Ecology, Ethology and Wildlife Management, Department of Environmental Sciences 'G. Sarfatti', University of Siena, Via T. Pendola 62, 53100 Siena, Italy, email: luca.corlatti@gmail.com, ² Institute of Wildlife Biology and Game Management, University of Natural Resources and Life Sciences Vienna, Gregor-Mendel Str. 33, 1180 Vienna, Austria, ³ Department of Animal Productions, Epidemiology and Ecology, University of Turin, Via L. da Vinci 44, 10095 Grugliasco (TO), Italy, ⁴ Alpine Wildlife Research Center, Gran Paradiso National Park, Via della Rocca 47, 10123 Torino, Italy, ⁵ Department of Biomedical Sciences/Biochemistry, University of Veterinary Medicine Vienna, Veterinärplatz 1, A-1210 Vienna, Austria

One of the key issues in the study of alternative mating tactics (AMTs) is the mechanism that allows their maintenance within animal populations. AMTs may have different trade-offs between current reproduction and survival; however, the proximate

mechanisms of such trade-offs are still poorly understood. Among them, the trade-off between reproductive effort and parasitism mediated by hormonal secretion has received increasing attention. Here, we investigated the differences in potential mating costs associated with alternative mating tactics in male Alpine chamois, and the underlying physiological mechanism. During the rutting season 2011, we monitored 19 marked adult males within the Gran Paradiso National Park (Italy). Between the pre- and post-rut, we investigated the relationships between AMTs mating effort and their levels of hormones (faecal androgen – FAM and cortisol – FCM – metabolites) and parasite burdens (bronchopulmonary nematodes). Territorial males sharply increased mating effort, FAM, FCM and parasite levels during the rut, whereas non-territorial ones displayed a similar pattern only for FAM levels. During the rut, territorial males invested more in rutting activities, had higher levels of FCM and greater parasite burden than non-territorials. Before and after the rut, differences between male types were smaller. The increase in mating effort and parasite burdens were mediated by FAM secretion. The territorial strategy entails the maintenance of a mating ground long before the rut; the greater investment in rutting activities, which territorial males make, suggests potentially high mating benefits. However, mating benefits could be counter-balanced by greater risks of injuries, consumptions of fat reserves and higher hormone levels, which might favour the suppression of immunological defence and the subsequent augment of parasites, possibly increasing overwinter mortality.

Seven years of monitoring small mammals on privately conserved lands in Vermont—Implications for baseline studies and environmental impact assessments

J. DECHER¹, C.R. GRAY¹, C.W. KILPATRICK¹, N. PRADHAN¹, M. LAPIN², ¹ University of Vermont, Department of Biology, Burlington, VT 05405, USA, email: Jan.Decher@uvm.edu, ² Program in Environmental Studies, Middlebury College, Middlebury, VT 05753, USA, email: lapin@middlebury.edu

During seven summers, between the years 2000 and 2011, we monitored small mammal diversity in four habitats on 275.2 hectares of privately owned and “forever wild” conserved forest lands, as part of the Colby Hill Ecological Project. The study site is located on the lower western slope of the Green Mountains near Lincoln, Vermont, USA. Using standard Sherman live and pitfall traps 1245 small mammals were captured in 4334 trap nights. We verified 4 shrew species, 1 species of mole, 11 rodent species and 1 carnivore (weasel). Average trap success among the different habitats and years was 28.7%. Two closely related species, *Peromyscus maniculatus* and *P. leucopus* could only be confidently identified in the project area using molecular methods. The rare and patchily distributed southern bog lemming (*Synaptomys cooperi*) was captured for the first time in the 4th year (2005), the woodland vole (*Microtus pinetorum*) in the 5th year (2006), and the American water shrew (*Sorex palustris*) only in the 7th year of sampling (2011). This gradual accumulation of species underscores the need for long-term survey work in baseline surveys and environmental impact assessments, which typically employ a similar trapping effort, to account for rare and trap-shy species.

The Middle Eocene marine mammal sites of northern Germany – oldest seals of the world, and first sirens in the Pre-North Sea Basin – coevolution with predatory magatooth/white sharks

C. DIEDRICH, PaleoLogic Research Institute, Nansenstr. 8, D-33790 Halle/Westph., Germany, email: cdiedri@gmx.net

Early Middle Eocene (Lutetian) seal remains of *Praephoca bendulensis*, and oldest German sirenian records of *Protosiren cf. fraasi* have

been discovered near Fürstenu, (north-western Germany) in shark tooth-rich conglomerates of a coastal delta environment north-west of the European Rhenish Massif. Whereas the oldest seals indicate a cold upwelling water adaptation and main habitat in the Pre-North-Sea, instead for *Protosiren* it is the most northern of its genus whose global distribution was generally restricted to warm waters. Its presence can be explained by seasonal inflow of warm Tethys surface water. The old models of evolution of seals must be dated back into the Paleocene, whereas possibly in both upwelling influenced marine coastal regions of North America (north Atlantic) and Europe (Pre-Northsea Basin) those were already present within the Middle Eocene by well-developed species, recently known only from Europe. Also the siren evolution seems to be polyphyletic with an existence of two centers of sirenian evolution, that can be explained by the opening of the Atlantic and by upwelling that separated the warm water faunal province of North America from those of Africa and Eurasia. A modified evolutionary model was recently presented in which oldest Early Eocene manatee sirenians developed in the Caribbean of Central America. *Protosiren*, instead, appears to have developed polyphyletically along the African coastline of the Tethys, as the oldest dugong ancestor. Several up to eight cm large teeth of the megatooth shark ancestor *Carcharocles sokolovi* have been found in northern Germany, suggesting a spatial correlation with their prey, the sirenians (and probably also whales), correlating with their presence in warm waters only. In contrast, the smaller white shark ancestor *Carcharodon auriculatus*, from which some thousands of teeth have been found in the Middle Eocene gravels in northern Germany, was adapted to cold water, as were its main prey, the seals, which dates back the oldest seal hunt specialization over 50 Million years ago.

Genetic structure and range expansion of reintroduced roe deer populations in Great Britain

R. FAUTLEY, Imperial College London, Silwood Park Campus, Ascot, Berkshire SL5 7PY, United Kingdom, email: rf104@ic.ac.uk

Roe deer (*Capreolus capreolus*) were nearly extinct in Great Britain around 1700, with refuge populations surviving only in woodlands in Central and Northwestern Scotland. However, they are currently widespread throughout the country, having spread from the Scottish refugia and populations reintroduced to England from Continental Europe. Roe deer have a high capacity for demographic and spatial expansion, and they presently have the widest distribution of all British deer. We find that the rate of range expansion varies between the reintroduced populations. The scenario of rapid range expansion following reintroduction enables an examination of the population genetic diversity and structure of spatially expanding populations influenced by contemporary processes following a documented bottleneck. Additionally, geographically peripheral populations are expected to exhibit lower genetic diversity and higher differentiation than core populations because of their smaller size and greater spatial isolation. We test the hypothesis that genetic diversity within populations is lower at the range limits than at the geographic centre. Over 300 tissue samples were collected from 18 locations in Great Britain, spanning the core and periphery of the expanding populations. Using genotype data from AFLP markers, we assess the population genetic structure of the reintroduced populations, and compare levels of diversity at the core and periphery of their ranges. Gaining a better understanding of the landscape and genetic factors influencing the range expansion of roe deer may help with prediction of their movement into new areas.

Reintroduced red deer and threatened Apennine chamois: Can restoration of biodiversity elicit concern?

F. FERRETTI^{1,2}, I. MINDER^{1,2}, M. CORAZZA³, C. FERRARI³, N. TROIANI³, A. SADDI¹, S. LOVARI^{1,2}, ¹ Research Unit of Behavioural Ecology, Ethology and Wildlife Management – Dept. of Environmental Sciences – University of Siena, Via T. Pendola 62, 53100, Siena, Italy, email: lovari@unisi.it, ² BIOCONNET, Biodiversity and Conservation Network – Dept. of Environmental Sciences – University of Siena, Via P.A. Mattioli 4, 53100 Siena, Italy, ³ Department of Evolutionary Biology – University of Bologna, Via Irnerio 42, 40126, Bologna, Italy

In mountain ungulates, environmental conditions and access to high quality forage in the short warm season can influence the winter survival of offspring, in turn population dynamics. In a seasonal environment, in the warm months, interspecific overlap in resource use, i.e. potential for competition, may be a threat for rare taxa. In Abruzzo, Lazio and Molise National Park (ALMNP, central Apennines, Italy), a 30% decrease of numbers of Apennine chamois *Rupicapra pyrenaica ornata* (vulnerable, IUCN; ALMNP: from c. 650 to c. 450 individuals, in 2005–2010) has been recorded, whereas red deer *Cervus elaphus* (reintroduced in 1972–1987: 81 individuals) have greatly increased (2010: >2000 individuals, ALMNP archive), partly overlapping with summer ranges of chamois. Pellet group counts, micro-histological analyses of faeces, vegetation sampling and behavioural observations indicate: (1) a great space/diet overlap between deer and chamois; (2) an increase of unpalatable plant species and an apparent decreasing trend of the most grazed species by chamois, with a reduction of area available to grazing, with respect to 1982–1984; (3) irrespective from vegetation type, a reduced bite rate of adult female chamois in patches used also by deer, with respect to areas with no overlap. Our results suggest a negative effect of red deer on the quality of Apennine grasslands, in the warm season. We suggest that reintroductions of potentially competing species may be avoided in areas where small populations of rare taxa survive. The conservation of rare taxa should be locally prioritized, rather than the re-establishment of pristine assemblies.

Applying conservation genetics in Bulgaria and Romania to protect one of Europe's last brown bear (*Ursus arctos*) refugia

C. FROSCH^{1,2}, A. DUTSOV^{1,3}, C. DOMOKOS⁴, W. FREMUTH¹, M. WENZEL¹, C. NOWAK^{2,5}, ¹ Frankfurt Zoological Society, Bernhard-Grzimek-Allee 1, 60316 Frankfurt am Main, Germany, email: cfrosch@senckenberg.de, cnowak@senckenberg.de, ² Conservation Genetics Group, Senckenberg Research Institute and Natural History Museum Frankfurt, Clamecystrasse 12, 63571, Gelnhausen, Germany, ³ Balkani Wildlife Society, 67 Tsanko Tserkovski str, Entr.3, floor 2, apt.3, 1421 Sofia, Bulgaria, ⁴ "Milvus Group" Bird and Nature Protection Association, Crinului St. 22, 540343 Tirgu Mures, Romania, ⁵ Biodiversity and Climate Research Centre (BiK-F), Senckenberganlage 25, 60325 Frankfurt am Main, Germany

While most areas of Western and Central Europe are intensively used by means of agriculture, timber production, and human settlement, some eastern regions, such as the Balkans and parts of the Carpathians still comprise large, near-natural areas. Especially in vast, forested mountainous landscapes, large carnivores, such as brown bears still persist in considerable population sizes and provide a valuable genetic reservoir for the long-term persistence of this species in Europe. Bears as well as other wildlife in these regions, however, face increasing anthropogenic pressure due to the intensification of land-use. Here we present data from ongoing genetic bear monitoring activities in Bulgaria and the Carpathians

(including their foothills) in Romania. Genetic data were obtained through noninvasive collection of scat and hair or tissue from killed animals and subsequent molecular analysis (14 microsatellite loci, mitochondrial haplotype analysis, sex determination). The obtained genotypic data will help assessing the general level of genetic diversity, identifying functional ecological corridors used by bears and determine the numbers of populations and their sizes. Knowledge about the presence or absence of brown bears, the genetic diversity in and between populations and the actual number of individuals in every area, for instance, is a basis for refining management plans for hunting, steer tourist activity in, e.g., ski resorts, and for the coexistence of large carnivores and livestock. We here demonstrate the effectiveness of embedding genetic research methods in broad regional conservation projects.

Neogene and Quaternary Eulipotyphlan fossil assemblages in Spain: Synopsis of the last 23 Ma. of Erinaceomorpha and Soricomorpha evolution in Southwestern Europe

M. FURIÓ¹, L.W. VAN DEN HOEK OSTENDE², ¹Institut Català de Paleontologia Miquel Crusafont, Edifici ICP, Campus de la UAB (08193), Cerdanyola del Vallès, Barcelona, Spain, email: marc.furio@icp.cat, ²Netherlands Centre for Biodiversity-Naturalis, Darwinweg 2, 2333 CR Leiden, The Netherlands, email: lars.vandenhoeekostende@ncbnaturalis.nl

We present for the first time a calibrated biostratigraphic chart with the Neogene and Quaternary insectivore assemblages from Spain. Our database is based on almost 400 fossil associations, some directly studied by the authors, the rest taken from literature, covering the last 23 million years. This time span is herein reduced to the most significant events which resulted in the configuration of the recent communities living in Spain. Early Miocene records of insectivores are rare. The beginning of the Middle Miocene shows a stepwise entrance of new elements, including gymnures of the tribe Galericiini; and within Heterosoricidae, *Heterosorex* is replaced by *Dinosorex*. The Late Miocene is characterized by a renewal of the Galericinae and the extinction of Dimylidae, Heterosoricidae and Crocidossoricinae. Noteworthy are the entrance of Desmaninae and Amblycoptini, and a first increase of shrew diversity. The Pliocene records the last occurrences of galericines (*Parasorex*) and uropsilines (*Desmanella*), but it also represents the 'Golden Age' of shrews and the spread of Desmaninae. The beginning of glacial dynamics at the Early Pleistocene derived in a dramatic decrease of the diversity in Soricidae. Middle and Late Pleistocene do indeed record a low diversity at the genus level, similar to the modern one, represented by the living genera *Erinaceus*, *Galemys*, *Talpa*, *Sorex*, *Neomys* and *Crociodura*. *Suncus* and *Atelerix* were probably introduced in Spain by humans during the Holocene. In the Balearic Islands, this period sees the extinction of *Nesiotites*.

Evolutionary and ecological constraints in Neotropical monkey assemblages

S. GONZÁLEZ-CARO¹, P. STEVENSON², D. CADENA³, ¹Department of Biological Sciences, University of Los Andes, Colombia, email: sebastian.gonzalez.caro@gmail.com, ²Laboratory of Ecology of Tropical Forests and Primatology, University of Los Andes, Colombia, ³Laboratory of Evolutionary Biology of Vertebrates, University of Los Andes, Colombia

Since Darwin, ecological similarity among closely related species has been recognized as a common pattern of niche evolution. Additionally, ecologically similar species tend to compete by resources. We can expect that similar species do not coexist, and if evolution is conserved, coexisting species may be phylogenetically distantly related. We evaluate these consequences at different spatial scales

on new world monkey's assemblages. This clade is a well studied system and it has been established that their habitat and main resources (i.e., fruits) influence the composition of local ensembles. We used climatic niche models for 63 species of Neotropical monkeys and calculated ancestral states of these, to evaluate if climatic conditions such as potential evapotranspiration (proxy of forest productivity) affect spatial distribution. We also evaluated whether or not diet composition evolved in a conserved fashion, using a common metric (Blomberg's K). We found that both components of primate niche are similar among closely related species. Therefore, competition may be an important driver of local species assemblages. To test this idea, we compiled information from 59 primate assemblages in Neotropical forests. Additionally, we obtain a list of potential species, based on climatic niche models for each locality and ignoring species interactions. This list was compared to lists with observed species assemblages, using a limiting similarity model (Sorensen index). We found that climatic communities showed many more species than observed ones, but when we included a filter to avoid that similar species coexist in one community, the probability to find communities similar in species richness than observed ones was high (mean = 0.82, SD = 0.15). These results support the idea that Neotropical monkey assemblages are affected by competition.

Phylogeny of the common shrew (*Sorex araneus* L., Mammalia) in Eastern Europe

O. GRIGORYEVA, S. POTAPOV, V. ORLOV, A.N. Severtsov Institute of Ecology and Evolution, Laboratory of Microevolution and Domestication of Mammals, Leninskij Prospect 33, 119071 Moscow, Russia, email: grig.forever@mail.ru

The common shrew is a small mammal with unique karyotypic diversity. At least 70 chromosomal races have been described in *S. araneus sensu stricto* and five cryptic species in *S. araneus sensu lato*. We investigate here the variation of the *cyt b* gene in the *Sorex araneus* group in Eastern Europe. A total of 82 samples of *S. araneus* and 7 samples of the Caucasian shrew (*Sorex satunini*) was studied (accession numbers JN984059–JN984127, 953 b.p.). Additional data were taken from the GenBank. Phylogenetic analysis was performed using BIOEDIT, MEGA, NETWORK. Phylogeographic trees and networks show separation between haplotypes of *S. araneus s. l.*, but they show lack of separation of *S. araneus s. s.* Median networks display "star-like" phylogeny testifying the "bottleneck" evidence. A distinct haplogroup in *S. araneus s. s.* is formed by a population distributed near the Sea of Azov. Perhaps an autochthonous population of the southern refugium of Neroosa race was preserved in the last glacial period. We have found two haplogroups (A and B) in a population of *S. satunini*. The first one, type A, is the most genetically distant (*p*-distance with *S. araneus* is 5.7%), and is regarded as parental. The second one, type B, is genetically closer to *S. araneus* than *S. antinorii* and *S. granarius* (*p*-distance with *S. araneus* is 2.2%). We suppose that the type B haplotypes were obtained from some species close to *S. araneus* in Southern or Western Europe.

Nuclear genomic sequences reveal that polar bears are an old and distinct bear lineage

F. HAILER¹, V.E. KUTSCHERA¹, B.M. HALLSTRÖM¹, D. KLASSERT¹, S.R. FAIN², J.A. LEONARD³, U. ARNASON⁴, A. JANKE^{1,5}, ¹Biodiversity and Climate Research Centre (BiK-F), Senckenberg Gesellschaft für Naturforschung, Senckenberganlage 25, 60325 Frankfurt am Main, Germany, email: frashai@gmx.net, ajanke@senckenberg.de, ²National Fish and Wildlife Forensic Laboratory, 1490 East Main Street, Ashland, OR, USA, ³Conservation and Evolutionary Genetics Group, Estación Biológica de Doñana (EBD-

CSIC), Avda. Américo Vespucio, s/n, 41092 Seville, Spain, ⁴Lund University Hospital, Box 117, 221 00 Lund, Sweden, ⁵Goethe University Frankfurt, Institute for Ecology, Evolution and Diversity, 60438 Frankfurt am Main, Germany

Recent studies have shown that the polar bear matriline (mitochondrial DNA) evolved from a brown bear lineage since the late Pleistocene, potentially indicating rapid speciation and adaption to arctic conditions. Here we present a high-resolution data set from multiple independent loci across the nuclear genomes of a broad sample of polar, brown and black bears. Bayesian coalescent analyses place polar bears outside the brown bear clade, and date the divergence much earlier, in the middle Pleistocene, ca. 600 (338–934) thousand years ago. This provides more time for polar bear evolution, and confirms previous suggestions that polar bears carry introgressed brown bear mitochondrial DNA due to past hybridization. Our results highlight that multi-locus genomic analyses are crucial for an accurate understanding of evolutionary history.

A molecular eye on wolf recovery in Germany

V. HARMS¹, G. KLUTH², I. REINHARDT², H. ANSORGE³, C. NOWAK^{1,4}, ¹Conservation Genetics Group, Senckenberg Research Institute and Natural History Museum Frankfurt, Clamecystrasse 12, D-63571 Gelnhausen, Germany, email: vharms@senckenberg.de, cnowak@senckenberg.de, ²Wildbiologisches Büro LUPUS, Dorfstraße 16, D-02979 Spreewitz, Germany, ³Senckenberg Research Institute and Natural History Museum Görlitz, Department of Zoology, Section of Mammalogy, Am Museum 1, D-02826 Görlitz, Germany, email: hansorge@senckenberg.de, ⁴Biodiversity and Climate Research Centre (BiK-F), Senckenberganlage 25, D-60325 Frankfurt am Main, Germany

Wolves in Germany severely suffered from human persecution, leading to their complete extinction within the first half of the 19th century. Strict legal protection recently resulted in a successful reestablishment of wolf packs in the eastern part of the country. However, the recovery of a large carnivore in a densely populated country requires effective wildlife management strategies. Reliable estimates of population parameters are necessary for such effective management and conservation actions. The use of non-invasive genetic sampling has become an important tool to estimate population parameters for elusive and wide ranging species. Here, we present first results from the recently launched genetic wolf monitoring programme in Germany. Non-invasively collected samples of almost every German wolf pack were genotyped at 15 microsatellite loci and sexed using the ZFX/ZFY gene size polymorphism. Besides the delineation of pack structures (pedigrees) and population parameters, such as population size estimation and genetic variability, we provide evidence for recent long-distant migration of single wolves from both the German-Western Polish and the Italian/Alps population. The example of genetic wolf monitoring in Germany proves the effectiveness and power of non-invasive genetic approaches in wildlife monitoring.

Diversity and phylogeny of extant and fossil cervids (Ruminantia, Artiodactyla)

N.S. HECKEBERG^{1,2,3}, G.E. RÖSSNER^{1,2,4}, R.J. ASHER³, G. WÖRHEIDE^{1,2,4}, ¹Bavarian State Collections of Palaeontology and Geology, Richard-Wagner-Str. 10, D-80333 München, Germany, email: n.heckeberg@campus.lmu.de, g.roessner@lrz.uni-muenchen.de, woerheide@lmu.de, ²Department of Earth and Environmental Sciences, Ludwig-Maximilians-Universität München, Richard-Wagner-Str. 10, D-80333 München, Germany,

³Department of Zoology, University of Cambridge, Downing Street, Cambridge CB2 3EJ, UK, email: r.asher@zoo.cam.ac.uk, ⁴GeoBio-Center^{LMU}, Richard-Wagner-Str. 10, D-80333 München, Germany

Cervids form the second most diverse family of living ungulate mammals; a number of successive, adaptive radiations since their first appearance in the fossil record 19 million years ago (early Miocene) led to the diversity seen in the extinct and extant fauna. Despite their widespread distribution, ecological, economic and cultural popularity, knowledge on their morphological and molecular diversity is deficient effecting many questions related to the taxon, particularly its intrafamilial phylogenetic relationships. In this study, morphological data, consisting of 150 craniodental characters, and molecular data from fossil and living cervids are compiled for the first time to get more insight into phenotypic and genotypic diversity. Previous studies generally focused on subsets of data, i.e. including either fossils or living cervids or using either morphological data or molecular data. Molecular data, comprising some or all of the mitochondrial genome and nuclear gene regions (source: GenBank) for 40 living and one extinct species (cytochrome b only), were combined with morphological data in a supermatrix. Three different optimisation criteria, Maximum Parsimony (PAUP), Bayesian Inference (MrBayes) and Maximum Likelihood (RAxML) were used for phylogenetic analyses. The results show polyphyly for several taxa of the “New World deer” and indicate a very complex evolutionary history of South American deer. For most of their history, cervids were highly diverse only in Europe and Asia until they entered North America 5 million years ago. A relatively late migration into South America (3 Ma) followed by a rapid radiation, might explain these ambiguities.

A quantitative approach to characterize influences by ecological and taphonomical factors on composition and structure of fossil macromammal assemblages

C. HERTLER, D. HÖNEMANN, Heidelberg Academy of Sciences and Humanities “The role of culture in early expansions of humans”, Senckenberg Forschungsinstitut und Naturmuseum, Senckenberganlage 25, D-60325 Frankfurt am Main, Germany, email: christine.hertler@senckenberg.de, dinah.hoenemann@senckenberg.de

Fossil assemblages of large mammals provide an important body of information about former environments. Their composition and structure is used to reconstruct respective ecologies. 25 years ago, a set of bovid faunas from various hominid-bearing layers in East Africa was examined (Shipman and Harris 1987). This initial study set the basic principles for reconstructions in paleoecology. As a reference for ecological interpretations of fossil assemblages Shipman and Harris published a recent data set, which is based on bovid communities from 29 national parks in East Africa. This reference sample is widely used for the assessment of fossil faunas. The published reference sample has advantages but also some limitations. In this study we examine the reference sample, introduce improvements and test some of its features. The reference sample is based on abundances of bovid genera, which are taken as ecological indicators. However, the assumption that fossil precursors had similar ecological features as their nearest living relative is not necessarily justified. In order to compensate for evolutionary shifts we assigned a set of ecovariables to each of the taxa. These ecovariables are defined on the basis of measurable features and can be taken on fossil specimens directly. Besides, composition and structure of a fossil assemblage differ from the one of present communities simply because taphonomy may shift relative abundances. The ecological signal of an assemblage therefore merges

effects of taphonomy and paleoecology. We introduce an approach to distinguish between both factors on a quantitative basis.

Old bones and new tricks: Evolutionary genetics using ancient DNA

M. HOFREITER, Department of Biology, The University of York, Wentworth Way, Heslington, York YO10 5DD, UK, email: michael.hofreiter@york.ac.uk

The use of ancient DNA for studies of evolutionary genetics has made dramatic progress in recent years, mainly due to two key developments: first, the introduction and continued development of next generation sequencing methods, and second the development of DNA hybridization technologies and their application to ancient DNA. I will first discuss the achievements and prospects of full shotgun sequencing, with a focus on human evolution and then explore the potential of DNA hybridization technologies, which allow targeting genomic regions of interest on the megabase scale, thereby avoiding the sequencing of bacterial and fungal contaminating DNA, which represents the majority of DNA in most fossil samples. Examples for the use of this technology include mitogenomic studies investigating the population history of woolly mammoths as well as the domestication history of domesticated cattle. I will also explore the potential of SNP typing for population genetic studies using ancient nuclear DNA, using the domestication history of horses as an example for the power of such analyses. Finally, I will give an outlook what may be potentially fruitful areas for ancient DNA research in the future.

The use of different genetic markers to investigate the genetic distinctiveness of the Sardinian wild boar population

L. IACOLINA¹, M. SCANDURA¹, H.-J. MEGENS², D. BIOSA¹, R.P.M.A. CROOIJMANS², L. RUND³, M.A.M. GROENEN², L.B. SCHOOK³, G. BERTORELLE⁴, M. APOLLONIO¹, ¹ Department of Science for Nature and Environmental Resources, University of Sassari, via Muroni 25, I-07100 Sassari, Italy, email: liacolina@uniss.it, ² Wageningen University, Animal Breeding and Genomics Centre, De Elst 1, 6708WD Wageningen, The Netherlands, ³ University of Illinois, Laboratory of Comparative Genomics, 1201 West Gregory Drive, 374 & 382 ERML, Urbana, IL 61801, United States, ⁴ Department of Biology and Evolution, University of Ferrara, Corso Ercole I d'Este 32, I-44100 Ferrara, Italy

The Sardinian wild boar is believed to inhabit the island since the Early Neolithic and is currently recognized as a different subspecies (*Sus scrofa meridionalis*), but after the Second World War translocations of non-native wild boars have been reported. To identify the current status of the genetic diversity of the Sardinian wild boar population, we compared genetic diversity of the wild boar population throughout Europe with a sample of domestic pigs using three different classes of molecular markers: (1) 411-bp sequences of the D-loop region of the mitochondrial DNA, (2) 16 autosomal microsatellites, (3) genome wide scan of 60,000 SNPs (60KSNPs Illumina Beadchip). D-loop data showed that the Sardinian population shares a mtDNA lineage only present here and in peninsular Italy, with a high percentage of private haplotypes. Microsatellite data showed a clear genetic divergence of the population from all mainland populations ($F_{ST}=0.065$) and from domestic pigs ($F_{ST}=0.074$). A sharp genetic structure was also found within the island. SNP data confirmed the genetic distinctiveness of the Sardinian population from both other wild boars ($F_{ST}=0.081$) and domestic pig breeds ($F_{ST}=0.130$). Both microsatellites and SNPs highlighted a signature of moderate and localized genetic introgression from mainland wild boars (both Italian and

European) and from local domestic breeds. Our results demonstrate that the Sardinian wild boar population still shows significant divergence at both mitochondrial and nuclear loci, supporting its classification as a different subspecies and stimulating further investigations on possible genetic effects of local selective forces.

The brown bear genome: A rich source for evolutionary studies and wildlife management

A. JANKE^{1,2}, H.-G. EIKEN³, F. HAILER¹, B. HALLSTRÖM¹, ¹ Biodiversity and Climate Research Centre (BiK-F), Senckenberg Gesellschaft für Naturforschung, Senckenberganlage 25, 60325 Frankfurt, Germany, email: ajanke@senckenberg.de, ² Goethe University, Siesmayerstrasse 70, 60323 Frankfurt a. M., Germany, ³ Bioforsk, Norwegian Institute for Agricultural and Environmental Research, 9925 Svanvik, Norway

Brown bears (*Ursus arctos*) and polar bears (*U. maritimus*) are closely related sister-species that have evolved separately for some 600,000 years. In comparison to the strictly defined habitat and niche of the polar bear, the brown bear is a generalist with a wide distribution and ecological niche. These differences are expected to have left traceable signatures in the respective bear genomes for adaptation. We have sequenced the complete genome of the brown bear for comparative genomic studies with the polar bear and giant panda genomes. Today, genome sequencing has become feasible even for small research groups but this approach still has its own challenges. The assembly resulted in a good genome-coverage and the data are now being analyzed. The current screens for adaptive loci are yielding a wealth of genes that evolve differently in the two species. These loci are designated candidate loci that are specific for the evolution of the respective bears and are further studied in additional brown and polar bear individuals. The newly discovered loci allow verifying the findings in the brown and polar bear population and adding another level of tests for selection. The brown bear genome data has also allowed developing urgently needed new SNP and VNTR markers for population genetics and wildlife management.

Reconstruction of life history from hard tissue histology—Implications for paleobiology and conservation biology in large mammals

X. JORDANA¹, N. MARÍN-MORATALLA¹, B. MONCUNILL¹, M. KÖHLER^{1,2}, ¹ Department of Paleobiology, Institut Català de Paleontologia Miquel Crusafont (ICP), Universitat Autònoma de Barcelona, 08193 Bellaterra, Spain, email: xavier.jordana@icp.cat, meike.kohler@icp.cat, ² Catalan Institute for Research and Advanced Studies (ICREA), 08010 Barcelona, Spain

Life histories are strategies to enhance fitness by adjusting the developmental schedule to environmental conditions. Because life history traits are demographic traits, they provide insights into the ecological conditions that trigger shifts along the slow-fast life history continuum, which allows assessment of the degree of vulnerability of populations and species.

Hard tissue histology is a valuable tool in reconstructing life history traits in fossil and extant vertebrates. In reptiles and amphibians, bone tissue reliably records annual growth; dental tissue, however, is not useful because of the variation in the number of teeth and their irregular eruption and replacement patterns. In mammals, instead, dental microstructure in combination with the conservative eruption patterns is widely used to detect shifts along the fast/slow continuum through estimation of the rate of dental development. Nevertheless, mammalian bone histology is believed to provide little if any information because of the high

and constant growth rates of mammals. Here we show that seasonal growth cycles are recorded in the cross sections of long bone of all mammals, not only in small heterothermic hibernators but also in homoeothermic large mammals. We illustrate the usefulness of mammalian bone and dental histology for the study of life history traits (growth rate, age at maturity, longevity). Finally, we exemplify the importance of hard tissue histology as a tool in reconstructing long-term trends in response to changing environmental conditions from the past (fossil record), as well as its importance in assessing the vulnerability in the present (extant species) and in predicting demographic trends in the future.

Mammals of Berezinsky Biosphere Reserve: Modern species composition and status

A. KASHTALIAN, Berezinsky biosphere reserve, Domzheritsy, Lepel District, Vitebsk Region, 211188, Belarus, email: A.Kashtalian@tut.by

Berezinsky Biosphere Reserve that was established in 1925 (modern area is more than 85,000 ha) is one of few nature establishments in Belarus where study of theriofauna has a long history. It has begun as a scientific provision of activities on conservation of few aboriginal populations of European beaver (*Castor fiber*) and elk (*Alces alces*), later studies of mammals of the Reserve became complex ones. At present their main directions are faunistic and monitoring of conditions of individual species and communities of mammals. Along with standard zoological methods viz. censusing, tracking of animals by their vital activity traces, detection of key habitats, to gather basic data questionnairing of local people and Reserve's staff is used. Theriofauna of Berezinsky Biosphere Reserve, like Northern Belarus, has been formed in comparably recent historical period in a result of landscape-climatic changes after the Würm glaciation. Its base (up to 50%) is formed by species of nemoral fauna. Less falls to boreal and intrazonal species. Up to 10% make alien and synanthropic species that appeared on the Reserve's territory as a result of human activities. One species – European mink (*Mustela lutreola*) – has vanished from the Reserve during the time of its existence. The annotated list of mammals contains 56 species that make up 73% of the Belarusian theriofauna. Habitation of 54 is confirmed by data that were obtained during the last 20 years. 6 species are in the national Red Data Book, 5 species in the IUCN Red Data Book. Researches of last years (detector listening of Chiropterans, questionnairing, new data on mammal systematics) attest the possibility of finding 8 more mammal species on the Reserve's territory. The greatest interest presents the discovery of *Nyctalus lasiopterus* and *Myotis dasycneme*.

Skull observation of introduced raccoon dogs (*Nyctereutes procyonoides*) in Europe

S.I. KIM¹, Y.K. KIM⁵, D. KOYABU², S. SUZUKI⁴, J.W. OH⁵, K. KAUHALA³, T. OSHIDA¹, M.S. MIN⁵, J. KIMURA⁵, ¹Laboratory of Wildlife Biology, Obihiro University of Agriculture and Veterinary Medicine, Obihiro 080-8555, Japan, ²Paleontological Institute and Museum, University of Zurich, Zurich 8006, Switzerland, ³Finnish Game and Fisheries Research Institute, Turku 20520, Finland, ⁴The Kyoto University Museum, Kyoto University, Sakyo, Kyoto 606-8501, Japan, ⁵College of Veterinary Medicine, Seoul National University, Seoul 151-742, South Korea, email: kimura@snu.ac.kr

Raccoon dogs are today one of the most widely spread alien species in Europe. They were introduced to Europe from the Russian Far East for fur and leather industry approximately 70 years ago. To clarify the morphological variation between the original and introduced populations, skull traits were compared among Far Eastern

(Russian), Finnish and German populations. We examined cranio-metrical variation using 71 specimens from the Far East (Zoological Museum of Moscow State University, Moscow, Russia), 70 specimens from Finland (Finnish Game and Fisheries Research Institute) and 75 specimens from North Eastern Germany (Technical University of Dresden, Germany). 57 linear traits were measured by caliper and the data obtained were analyzed with ANOVA and PCA. Results of ANOVA indicated that 16 traits showed significantly larger mean values in Finnish populations ($P < 0.05$). PCA results explained that skull size mainly contributed to the separation of the Finnish from Russian and German populations. Compared to the Russian and German populations, Finnish raccoon dogs are significantly characterized by larger skull size in several traits including the zygomatic breadth by both ANOVA and PCA. Given these results, we suggest that severely cold climate in high latitude has caused rapid morphological selection in the Finnish raccoon dogs. On the other hand, the German population may have remained similar to the original Russian population due to the milder climate and the lack of severe selection pressure. Our findings provide an example of rapid microevolution which occurred within a short period.

Genetic monitoring and research of brown bears in Northern Europe

A. KOPATZ, S.B. HAGEN, J. SCHREGEL, H.-G. EIKEN, Bioforsk, Norwegian Institute for Agricultural and Environmental Research, Svanvik, Norway, email: Alexander.Kopatz@bioforsk.no

We present a summary of our brown bear (*Ursus arctos*) monitoring and latest results on the connectivity and structure of bears in Northern Europe. In Fennoscandia, the demographic history of bears indicates several extinction and re-colonization events. However, there is little known about the present gene flow among populations of the east and west. We used 12 validated microsatellite markers to analyze 3723 noninvasively collected hair and fecal samples as well as 68 tissue samples from legally harvested bears. The samples were collected in six years (2005–2010) from different core areas with high brown bear densities in Troms and Pasvik (Norway), Västerbotten (Sweden), Kainuu (Finland) as well as Karelia and Arkhangelsk (Russia) to investigate the genetic structure and connectivity among these regions. The genotypes sampled in these areas showed differentiation into several clusters with pairwise F_{ST} values of 0.05 up to 0.91. Heterozygosities of ~0.8 were among the highest reported in wild brown bear. Despite a demographic bottleneck, no genetic bottleneck could be detected in either of the sampled populations. Isolation-by-distance can only describe the found subdivision to some extent. With a special focus on the bear population at Pasvik and based on the intensive noninvasive sampling in that area, we calculated annual effective population sizes and found an overall high correlation between the yearly estimates of census and effective population size. While the brown bears in Eastern Finland and Western Russia showed considerable genetic exchange, results from populations further north and west suggest restricted gene flow.

Dispersal of juvenile edible dormice (*Glis glis*)

B. KOPPMANN-RUMPF^{1,2}, C. SCHERBAUM-HEBERER¹, K.-H. SCHMIDT¹, ¹Ecological Research Centre Schlüchtern, Georg-Flemmig-Str. 5, D-36381 Schlüchtern, Germany, email: koppmann-rumpf@t-online.de, ²Goethe University Frankfurt, Siesmayerstr.70, D-60323 Frankfurt am Main, Germany

The edible dormouse *Glis glis* is known to use nest boxes to sleep during the day as well as for raising offspring. Especially juvenile

and subadult dormice are often found sharing their nest sites during the activity period. The focus of the recent study lies on the dispersal and settlement of dormice marked in 2002 as juveniles, which were recaptured in at least one of the following years. In a sample area 65 km northeast of Frankfurt, Germany, all edible dormice captured were marked with passive transponders and daily nest box checks were carried out since 2002. Our results reveal that male and female juveniles become independent from their mother at different points in time and show different affinity to their relatives' home range in the following years.

Heterochrony and developmental modularity of osteogenesis in lipotyphlan mammals

D. KOYABU, M.R. SÁNCHEZ-VILLAGRA, Paleontological Institute and Museum, University of Zürich, Karl Schmid-Strasse 4, 8006 Zürich, Switzerland, email: daisuke.koyabu@pim.uzh.ch, msanchez@pim.uzh.ch

Here we provide the most comprehensive study to date on the ossification sequence in Lipotyphla, the group which includes shrews, moles, and hedgehogs. This unique group that encapsulates diverse ecological modes such as terrestrial, subterranean, and aquatic lifestyles, is used to examine the evolutionary lability of osteogenesis and to investigate the modularity of development. An acceleration of developmental timing of the vomeronasal complex and has occurred in the common ancestor of moles. However, ossification of the nasal has shifted late in the more terrestrial shrew mole. Among the lipotyphlans, sequence heterochrony shows no significant association with modules derived from developmental origins (i.e. neural crest cells vs. mesoderm derived parts) or with those derived from ossification modes (i.e. dermal vs. endochondral ossification). The drastic acceleration of vomeronasal development in moles is most likely coupled with the increased importance of the rostrum for digging and its use as a specialized tactile surface, both fossorial adaptations. The late development of the nasal in shrew moles, a condition also displayed by hedgehogs and shrews, is suggested to be the result of an ecological reversal to terrestrial lifestyle and reduced functional importance of the rostrum. As an overall pattern in lipotyphlans, our results reject the hypothesis that ossification sequence heterochrony is more likely to occur among different developmental modules. We suggest that shifts in the cranial ossification sequence are not evolutionary constrained by developmental origins or mode of ossification.

Novel SNP marker panels optimised for noninvasive samples and the study of elusive European carnivores

R.H.S. KRAUS¹, D.W. FÖRSTER², H. BAYERL³, R. KÜHN³, J. FICKEL², C. NOWAK^{1,4}, ¹ Conservation Genetics Group, Senckenberg Research Institute and Natural History Museum Frankfurt, Clamecystrasse 12, D-63571 Gelnhausen, Germany, email: robert.kraus@senckenberg.de, ² Leibniz-Institute for Zoo and Wildlife Research, Evolutionary Genetics, Alfred-Kowalke-Str. 17, D-10315 Berlin, Germany, ³ Molecular Zoology Unit, Department of Zoology, Technische Universität München, Hans-Carl-von-Carlowitz-Platz 2, 85354 Freising, Germany, ⁴ Biodiversity and Climate Research Centre (BiK-F), Senckenberganlage 25, D-60325 Frankfurt am Main, Germany

In Europe, systematic persecution has reduced most populations of large carnivores below a minimum viable population size. Western European brown bear (*Ursus arctos*), wolf (*Canis lupus*), and lynx (*Lynx lynx*) became fully extinct by the end of the 19th century. Smaller carnivores, such as wildcat (*Felis s. silvestris*) and the Eurasian otter (*Lutra lutra*), survived only in small relict populations. The current carnivore comeback in Europe has been

intensively studied. Data on distribution, population size, and dynamics is, however, difficult to obtain, due to the rarity and elusiveness of these species. Since the end of the 1990s, microsatellites have been used in wildlife genetics to genotype noninvasive samples such as hair or scat material. Recently, single nucleotide polymorphisms (SNPs) have gained attention as these have several advantages compared to microsatellites. However, development of SNP-based marker systems requires considerable genomic information. Thus, SNPs are almost exclusively used in genetically well characterised model species. Only recent advances in next generation sequencing now permit detection of SNPs in non-model species. In contrast to microsatellites, SNP-based genetic data can easily be standardised and do not depend on the laboratory or detection machine used. Thus, unlike most microsatellite data sets, SNP data can be readily implemented in genetic databases. A key limitation to the application of SNPs in wildlife genetics is the lack of genotyping technology optimised for noninvasive samples. We here present our current efforts to solve this issue which will provide the unique opportunity to merge data sets across laboratories and thereby produce genetic data sets for carnivores across Europe.

Eco-morphology of trawling *Myotis*

F. KRÜGER¹, S. GREIF², S. ZSEBÖK², S. TROXELL², R. SOMMER¹, B. SIEMERS², ¹ Department of Landscape Ecology, Institute for Natural Resource Conservation, Christian-Albrechts-University in Kiel, Olshausenstr. 75, 24118 Kiel, Germany, email: fkrueger@ecology.uni-kiel.de, ² Max Planck Institute for Ornithology, Sensory Ecology Group, Eberhard-Gwinner-Straße, 82319 Seewiesen, Germany

Morphology is crucial for foraging performance in bats. Especially in trawling bats the ability to fly low over water, take and lift prey from or beneath the water surface and to feed on prey of different size is likely to be limited by morphological adaptations. Therefore we describe different morphological parameters, which are helpful in discussing ecological niches and foraging ecology of trawling bats. Wing measurements as well as bite force measurements were taken from live bats in the field in northern Germany. Measurements of lifting performance were taken from live bats under lab conditions. All results were correlated with dietary results for the species in the same region. Despite significant morphological differences both species showed high dietary overlap and similar niche breath. But differences regarding the prey types, referring to the terrestrial or aquatic life-cycle of prey groups, seem to support spatial segregation and different hunting preferences also indicated by different morphological adaptations. High resource abundance is also likely to allow the coexistence of both species within the same hunting habitat.

Seasonal and geographical variation in a typical European trawling bat, *Myotis dasycneme* Boie, 1825

F. KRÜGER, R. SOMMER, Department of Landscape Ecology, Institute for Natural Resource Conservation, Christian-Albrechts-University in Kiel, Olshausenstr. 75, 24118 Kiel, Germany, email: fkrueger@ecology.uni-kiel.de

Many bat species depend on aquatic habitats as major food supply. Of the European Vespertilionidae at least five species can be found foraging along water bodies. The pond bat (*Myotis dasycneme* Boie, 1825) is probably the largest and most adapted European water foraging bat, strongly connected with aquatic ecosystems and predated mainly aquatic arthropod communities. To understand the trophic strategy of water hunting bats during reproduction,

animals' diets were studied across the distribution range of *M. dasycneme* considering time related shifts. Our study presents a detailed dietary analysis of pond bats, representing a typical trawling *Myotis* species, showing a rather consistent feeding behaviour across its areal. Prey items found in the diet of the studied bat represent as well trawling behaviour and aerial hawking. Pond bats seem to feed mainly on Chironomidae adults and sub-adults, especially during lactation, but shift predation towards other prey items, e.g. Lepidoptera, around the time of weaning. Thus feeding on small, but abundant prey seems to be favored against feeding on bigger, but less abundant prey during times of high nutrient demand, e.g. during gravity and lactation.

New phylogeography of the red fox (*Vulpes vulpes*) in Eurasia

V.E. KUTSCHERA, A. JANKE, F. HAILER, Biodiversity and Climate Research Centre (BiK-F), Senckenberg Gesellschaft für Naturforschung, Senckenberganlage 25, D-60325 Frankfurt am Main, Germany, email: verena.kutschera@senckenberg.de

The phylogeographic structure of the Holarctic red fox (*Vulpes vulpes*) is well-described for separate regions, including North America, Europe, and Japan, based on mtDNA control region data. Here we present a synthesis of previous studies and include new data from central Asian populations, which have not been studied to date. We will also present results of molecular dating of various evolutionary events in foxes. Eurasian red foxes form a single clade, while North American red foxes form three distinct clades. The Japanese population falls into two distinct clades. One Japanese clade consists of unique haplotypes that only occur on the northern island Hokkaido, suggesting several independent colonisation events of Japan. All newly sequenced Siberian red foxes belong to the previously described Eurasian clade, suggesting that Eurasian mainland populations have evolved separately from populations on Hokkaido and North America for a long time. Therefore, similar to data from grey wolves (*Canis lupus*), the red fox appears to be another generalist Holarctic carnivore which displays significant population genetic structuring. This is likely the result of climatic oscillations leading to past population fragmentation, but may also reflect habitat heterogeneity favouring region-specific adaptations.

Population genetics of Arabian Gazelles (*Gazella arabica*) living on the Farasan Archipelago in the Red Sea

H. LERP¹, M. PLATH¹, M. PFENNINGER², T. WRONSKI^{3,4}, ¹ Department of Ecology and Evolution, University Frankfurt/Main, Germany, email: lerp@bio.uni-frankfurt.de, ² Molecular Ecology Group, Biodiversity and Climate Research Centre, Frankfurt/Main, Germany, ³ King Khalid Wildlife Research Centre, Saudi Wildlife Commission, Riyadh, Saudi Arabia, ⁴ Zoological Society London, United Kingdom

Arabian gazelles (*Gazella arabica*) rank among the most critically endangered mammals on the Arabian Peninsula. The number of animals still living in Saudi Arabia was estimated as approximately 1700 only, with approximately 1000 animals occurring on the Farasan Islands. Two, not mutually exclusive hypotheses regarding the origin of Farasan gazelles have been forwarded: (1) colonization of the islands during the LGM and corresponding sea level minimum, and (2) an introduction by sea man, who may have moved animals to and from the islands. We established population genetic markers for mountain gazelles and genotyped 141 specimens from the Farasan Islands and the Arabian Peninsula. By applying 11 nuclear microsatellite markers we found a close genetic similarity of Farasan gazelles to populations occurring in the south of Saudi Arabia and in Yemen. Some of the island animals formed a separate cluster (which may be explained mainly

by genetic drift); still, overall genetic distinctiveness to mainland populations was weak. Furthermore, a considerable part of Farasan gazelles were clearly assigned to mainland populations. Thus, we propose that populations from Farasan islands did not evolve in isolation, and gene-flow—albeit nowadays reduced—is still ongoing, following a classical 'island-mainland model'. Therefore, mountain gazelles from Farasan Islands would neither be a distinct species nor subspecies, and may be a valuable source for future reintroductions on the Arabian mainland.

The diversity and prevalence of tick-borne and other pathogens in wild rodents from Berlin, Germany

D. MAAZ¹, J. BLÜMKE¹, J. KRÜCKEN¹, D. RICHTER², F.-R. MATUSCHKA², S. HARTMANN³, J. DEMELER¹, G. VON SAMSON-HIMMELSTJERNA¹, ¹ Institute for Parasitology and Tropical Veterinary Medicine, Freie Universität Berlin, Königsplatz 67, 14163 Berlin, Germany, email: denny.maaz@fu-berlin.de, ² Institut für Pathologie, Abteilung Parasitologie, Charité Universitätsmedizin, Berlin, ³ Institute for Immunology and Molecular Biology, Freie Universität, Berlin

Wild rodents are considered to be reservoir hosts for a variety of pathogens and play a central role in the transmission cycle of tick-borne pathogens. Especially in urban agglomerations, peridomestic rodents may affect the risk of zoonotic infections for humans and their companion animals. Therefore, the present study aimed to determine the diversity and prevalence of tick-borne pathogens in rodents captured in Berlin as well as of their endoparasites which may influence the susceptibility to co-infections. From November 2010 to November 2011, wild mice were trapped alive every five or six weeks at four study sites in Berlin, euthanized and necropsied followed by a thorough parasitological examination. Overall, 257 rodents of six species were trapped. *Apodemus agrarius*, *Apodemus flavicollis* and *Myodes glareolus* were most abundant. Virtually every rodent (98%) was infested by ectoparasites, 55% by *Ixodes* ticks but also by mites, fleas and lice. After faecal flotation for detection of helminth eggs and examination of the gastro-intestinal tract, tapeworms and trematodes were found in every fifth (20%) and sixth mouse (16%), respectively. Nematodes were detected in 77% of the animals. Of the tick-borne pathogens, which were detected by PCR, only one mouse infected by *Babesia microti* was found (0.4%), whereas 14% of the mice were infected by Lyme disease spirochetes. In addition, *Anaplasma phagocytophilum* and the recently described "Candidatus *Neoehrlichia mikurensis*" were detected in 3% and 14% of the rodents, respectively. In summary, every fourth wild mouse (26%) in Berlin was infected by pathogens, which may be transmitted by ticks to humans or companion animals.

The last of the western European lions: A working hypothesis

M. MASSETI¹, P.P.A. MAZZA², ¹ Department of Evolutionary Biology 'Leo Pardi', University of Florence, via del Proconsolo 12, 50122 Florence, Italy, email: marco.masseti@unifi.it, ² Department of Earth Sciences, University of Florence, via La Pira 4, 50121 Florence, Italy, email: paul.mazza@unifi.it

Modern lions (*Panthera leo*) are believed to have reached Europe around 8000 years ago, after cave lions (*P. spelaea*) had disappeared around 14,500–14,000 years ago. Modern lions are also said to have dispersed up to the steppes of Ukraine and Hungary, without reaching the forests of Central Europe. In contrast, cave lions were widespread in western Europe. The paper intends to call attention to finds from Italy and Spain that bridge the alleged 6000 year-long absence of these formidable big cats. Fossil lion remains, both in the writers' possession and accessible in the literature, from reliably radiocarbon-dated levels have been plotted

against the $\delta^{18}\text{O}$ curve and mapped. To make all datings comparable uncalibrated radiocarbon ages have been converted into calendar years. By piecing together the available information, lions appear to have inhabited western Europe uninterruptedly from the early Middle Pleistocene up to the Early Holocene. Moreover, all latest Pleistocene/early Holocene lion-bearing localities do not range farther than the 44th parallel north and are located at relatively high altitudes. The writers formulate a working hypothesis, speculating that western European lions formed a lineage inaugurated by *P. spelaea*-like representatives and ended by modern-fashioned lions. Whether *P. spelaea* is or not conspecific with *P. leo* would therefore be pointless. The latest western European representatives would in fact be convergent with their African counterparts. The latter accessed eastern Europe between 8 and 6.5–6 ka but were prevented from penetrating further west by the obtrusive presence of their autochthonous European relatives. Lions outlived all major Middle and Late Pleistocene cold events. They also survived the cold snaps of the Allerød and Younger Dryas, but they rapidly demised thereafter. Their area of distribution drastically shrank, possibly because of the ever more intrusive presence of modern human populations.

Tamarin (*Saguinus*; Primates: Callitrichidae) biogeography and diversification determined by major geologic events

C. MATAUSCHEK¹, E.W. HEYMANN¹, C. ROOS², ¹Abteilung Verhaltensökologie & Soziobiologie, Deutsches Primatenzentrum, Kellnerweg 4, 37075 Göttingen, Germany, email: ehyman@gwdg.de, ²Gene Bank of Primates, Abteilung Primatengenetik, Deutsches Primatenzentrum, Kellnerweg 4, 37075 Göttingen, Germany

The uplift of the Andes, marine incursions, wetland formation, and the formation of the Amazon valley are major geological events that are hypothesized to have influenced the radiation and diversification of the Neotropical fauna. Our study examines the diversification of the Neotropical primate genus *Saguinus* (tamarins) in relation to these events. We sequenced 13 mitochondrial genomes of all callitrichine genera (except *Callibella*) and *Saguinus* species groups (sensu Hershkovitz 1977), and calculated the time of lineage divergences. Time estimates for geological events were extracted from the most recent literature. Our principal results are: (1) The initial diversification of callitrichines at around 13.3 mya coincides with the Andean uplift. (2) The basal position of *Saguinus* within the Callitrichinae is confirmed. (3) Within *Saguinus*, the *S. nigricollis* group split off from other tamarins in the late Miocene (ca. 9.5 mya), around the time when the Acre mega-wetland covered western and central Amazonia. (4) The other *Saguinus* species groups diverged between 7.5 and 5.3 mya, i.e., during the geological period when the Amazon River valley formed. (5) The more recent diversification of the genus is likely to be associated with the formation of riverine barriers. Our data support a West-Amazonian origin and an eastward dispersal of the genus *Saguinus* and the role of major geological events for the diversification of this genus.

Burrow configuration of Persian jird *Meriones persicus* in Iran

S. MOHAMMADI, Department of Environment, Faculty of Natural Resources, University of Zabol, Iran, email: mohammadi7517@yahoo.com

Meriones persicus is a widespread species in the Iranian plateau and is one of the most common jirds in desert rodents of Iran. We studied architecture of Persian jird's burrow systems in the central part of its geographic range in Iran for the first time in the

south of Shah-Reza in Isfahan Province, Iran. Three types of burrow were detected for this jird including temporary burrow, shelter burrow and breeding-nest burrow. The burrows of *M. persicus* were restricted to areas including cover and located mostly on flat and slightly sloping areas with clay-loam soil type. The design of burrows demonstrated *M. persicus* do not hibernate in the study area because we observed this species in winter and in cold temperature in the study area in active burrow systems. Also, the structure of nest chambers can be seen as an adaptation to adverse weather conditions in the central part of the Iranian Plateau, since they are likely to provide a stable microclimate that buffers conditions outside.

Wildcats and highways—Estimating barrier effects with citizen science

A. MUNDORF¹, T.E. REINERS¹, C. NOWAK^{1,2}, K. STEYER¹, ¹Conservation Genetics Group, Senckenberg Research Institute and Natural History Museum Frankfurt, Clamecystrasse 12, D-63571 Gelnhausen, Germany, email: ksteyer@senckenberg.de, ²Biodiversity and Climate Research Centre (BiK-F), Senckenberganlage 25, D-60325 Frankfurt am Main, Germany

Across Germany, several large-scale projects are presently carried out to study the abundance, population structure and hybridisation grades of European wildcats (*Felis s. silvestris*). Due to the recent development of a noninvasive lure stick method, the wildcat can now be monitored on much finer geographical scales, which facilitates the study of detailed gene-flow patterns in this species. Lure sticks are rough wooden sticks treated with valerian to attract wildcats and to obtain hair samples for subsequent genetic analysis. In the Main-Kinzig district of Germany suitable forest habitats are separated by the narrow Kinzig valley, which forms a dispersal barrier due to the presence of a major highway, a railway line, stretches of open land, and the Kinzig river. To investigate the effectiveness of this landscape barrier on wildcat dispersal and gene flow lure sticks were set up by >30 volunteers within 12 study areas along the highway. Sticks were inspected weekly for hair presence. More than 250 hair samples were collected in the mating period from January to May 2012. Hair samples were initially analysed with mtDNA markers to screen for correct species assignment. To test for potential barrier effects microsatellite analyses were carried out. We present to the results of this study and demonstrate the suitability of the lure stick method as a tool for initiating the participation of the public in research projects, named citizen science.

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

G. NADERI¹, B. RIAZI², N. AREF², M. KHALATBARI³, S. MOHAMMADI⁴, M. LAHOOT¹, ¹Environment Department, Islamic Azad University-Ardebil Branch, Ardebil, Iran, email: ghnadero@yahoo.com, ²Environmental Science Department, Islamic Azad University, Science and Research Branch, Tehran, Iran, ³Paiaime Noor university-Ardestan Branch, Ardestan, Iran, ⁴Department of Environment, Faculty of Natural Resources, University of Zabol, Iran

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

Mitochondrial cytochrome b gene reveals conspecificity of Hotson's Jerboa (*Allactaga hotsoni*) and Firouz Jerboa (*A. firouzi*)

G. NADERI¹, B. KRSTUFEK², E. BUZAN², S. MOHAMMADI³,
¹Environment Department, Islamic Azad University-Ardebil Branch, Ardebil, Iran, email: ghnadery@yahoo.com,
²Science and Research Centre, University of Primorska, Titov trg 4, SI-6000 Koper-Capodistria, Slovenia,
³Department of Environment, Faculty of Natural Resources, University of Zabol, Iran

Based on mitochondrial cytb sequencing, maximum parsimony, maximum likelihood and Bayesian analysis we demonstrated that Hotson's Jerboa and the Iranian Jerboa are identical, with very low molecular divergence. Mitochondrial cytb sequencing showed that *Allactaga firouzi* and *Allactaga hotsoni* are not reciprocally monophyletic.

Is noninvasive genetic wildlife monitoring really worth the cost? A critical evaluation of current monitoring approaches in Germany

C. NOWAK^{1,2}, K. STEYER¹, V. HARMS¹, C. FROSCH¹, T.E. REINERS¹, R.H.S. KRAUS¹,
¹Conservation Genetics Group, Senckenberg Research Institute and Natural History Museum Frankfurt, Clamecystraße 12, D-63571 Gelnhausen, Germany, email: cnowak@senckenberg.de,
²Biodiversity and Climate Research Centre (BiK-F), Senckenberganlage 25, D-60325 Frankfurt am Main, Germany

The emergence of highly sensitive approaches for obtaining genetic information from environmental trace materials, such as hairs, scats, and saliva has revolutionised the possibilities of population monitoring in free-ranging mammals. Without disturbing rare species in their natural habitats, DNA analyses from non-invasively collected materials allow for individual assignments, population size estimations, pedigree reconstruction, hybridization testing, or the identification of source populations. Especially for rare and elusive species under strict legal protection these techniques promise to provide solid data for an effective population monitoring. In Germany, both active reintroduction efforts and natural dispersal from distant source populations have led to the establishment of new species in previously unoccupied habitats. In this presentation we provide a first critical evaluation of recently started genetic monitoring projects for wolf, wildcat, and beaver populations in Germany. What are the costs of an effective genetic monitoring strategy? Are the results worth the efforts? Did genetic monitoring result in novel findings important for species conservation strategies? Our results document the indispensability of genetic tools for population monitoring of elusive, protected mammals such as wolves and wildcats. Past conservation strategies for wildcats, for instance, have severely suffered from a lack of accompanying molecular studies. Data on the fine-scale genetic structure of wildcats give important hints for currently applied population management. Molecular individualisation and population assignment reveals unexpected insights into long-distance dispersal of wolves in Germany. The example of a successfully reintroduced beaver population, however, also documents the limits of currently applied molecular strategies and hints to the need for an integration of new genomic tools in genetic population monitoring.

Palaeodiversity of cave bears and brown bears through times

M. PACHER, Institute of Palaeontology, University of Vienna, Althanstrasse 14, UZA II, A-1090 Wien, Austria, email: martina.pacher@univie.ac.at

Fossil and modern bears are well known to show a high variability in morphology and body size and a variety of species and subspecies have been established, therefore. Modern approaches like aDNA and isotope studies are employed to solve the problem of species diversity in bears. Nonetheless, comprehensive palaeontological studies on fossil material are still scarce. Body size is best reconstructed on weight bearing skeletal elements and strongly influenced by gender differences in bears. Size variability of cave bears (*Ursus spelaeus* group) and brown bears (*Ursus arctos*) from various regions and time periods is compared, mainly in uni- and bivariate studies. Intra- and inter-assemblage differences are analyzed in order to detect size ranges of males and females and significant differences between sites or regions. Results are compared with available genetic and isotope data to test for correlations, and provide basics for further discussions. The main factors of body size differences in bears seem to be food availability, competition between species and/or gender, and climate changes.

The future of mammal diversity

H.H.T. PRINS, Resource Ecology Group, Wageningen University, The Netherlands

"The world is green" - this was keenly observed by Hairston et al. in 1960, and it was explained through top-down control of vegetation biomass. He and others since him have reasoned that if there are no predators to keep the herbivores down, there would be no grass or foliage. Leaves of plants harness the sun's energy on which we, and the rest of the world (save some sulphur bacteria) depend. Basically we have two ways of accessing that energy, the first is through consuming herbivores or their milk and secondly directly through consuming the plants. Then we face competition with other herbivores, be it vertebrate or non-vertebrate; these competitors are kept in low numbers because of predators and pathogens. In other words, if there are no herbivorous mammals then we eat less, and if there are no predators (often mammalian too) we can consume less too. Can we thus live without all these other mammal species? In the past we could not, at present we cannot either. Perhaps we can in future, but the precautionary principle forewarns us not to take that for granted. Future presence of these food and control agents (mammal diversity) must thus be protected simply because of this precaution. But it is under severe threat. In this talk I will first explore the food web as explained above, then highlight some of the threats to large mammals that feature so importantly in it, including the effects of the rise of temperature of carbon dioxide and hampering of animal movements, and finally explore the concept of an herbivore toolbox. In the latter I will survey the question of how few species we need to get our basic set of requirements served by herbivores, in other words, to what extent is there a lower threshold of animal diversity below which we, and perhaps the rest of the world, are suffering from species loss.

Land use and behavioral patterns of brown bears in the South-Eastern Romanian Carpathian Mountains: A case study of relocated and rehabilitated individuals

I.M. POP¹, A. SALLAY², L. BERECZKY³, S. CHIRIAC⁴,
¹Environmental Protection Agency Covasna County, B-dul. Grigore Balan nr. 10, RO-520013 Sfantu Gheorghe, Romania, email: minelpop@yahoo.com,
²Institute of Wildlife Biology and Game Management, University of Natural Resources and Life Sciences, Gregor Mendel Str. 33, A-1180 Vienna, Austria, email: alexandra.sallay@goolemail.com,
³Association for Conserving Natural Values, 1st Decembrie nr. 22, RO-535200 Balan, Romania, email: natureconserving@yahoo.com,
⁴Environmental Protection

Agency Vrancea County, B-dul. Dinicu Golescu nr. 2, RO-620160 Focsani, Romania, email: silviu.chiriac@yahoo.com

Although brown bears are not drastically threatened by habitat loss and fragmentation at the present, the socio-economic development in Romania is proceeding rapidly and already came along with noticeable changes in landscape. Human-bear conflicts though exist for decades, requiring proper management and related research findings. We analyzed the habitat use on a landscape level of eight GPS-collared bears between 2008 and 2011. According to the type of human intervention we grouped our study animals into four classes: (1) non-relocated, non-rehabilitated; (2) relocated, non-rehabilitated; (3) non-relocated, rehabilitated; (4) relocated, rehabilitated. We tried to find out if bear types exhibit varied responses to landscape level habitat use by examining home range sizes and occurrence in the proximity of human settlements, defined as High Potential Conflict Areas (HPCA). We tested the effect of age and sex on presence versus absence and on the time spent in this buffer area. Home range sizes calculated with the minimum convex polygon varied substantially among bears and types but less for the 95% kernel estimators. Between 50.9% and 94.7% of all bear locations were in forest areas and shrubland. Agricultural fields were frequented moderately, urban areas were practically avoided. But bear presence remarkably increased within the HPCA, in bear type 1 up to 70%. There was no significant difference between relocated and rehabilitated bears (types 2 and 3), both being more present outside the buffer area. Bears of type 4 behaved wary and approached urban areas less frequently. Females tend to stay further away from human activities, whereas males did not have a special preference. Adults frequented more often and remained longer inside the buffer zone than subadults, which were four rehabilitated animals out of total five. Our findings could be useful for land use planning to consider habitat requirements of bears and with it mitigate human-bear conflicts.

Saving the genetic heritage of common hamsters *Cricetus cricetus* in Western Europe

T.E. REINERS¹, M.J.J. LA HAYE², K. NEUMANN³, C. NOWAK^{1,4}, ¹Conservation Genetics Group, Senckenberg Research Institute and Natural History Museum Frankfurt, Clamecystra(e 12, D-63571 Gelnhausen, Germany, email: tobias.reiners@senckenberg.de, cnowak@senckenberg.de, ²Bargerveen Society/Department of Animal Ecology and Eco-physiology, Institute for Wetland and Water Research, Radboud University Nijmegen, Toernooiveld 1, 6525 ED Nijmegen, The Netherlands, email: maurice.lahaye@wur.nl, ³Institute of Pathology/Molecular Diagnostics Section, Medical Centre Dessau-Rosslau, Auenweg 38, 06847 Dessau, Germany, email: karsten.neumann@klinikum-dessau.de, ⁴Biodiversity and Climate Research Centre (BiK-F), Senckenberganlage 25, D-60325 Frankfurt am Main, Germany

The common hamster *Cricetus cricetus* is among the most critically endangered mammal species in Western Europe. Since the 1970s they suffer from a dramatic and still ongoing decline at its western range. Even though western geographic lineages are considered to be a result of a relatively recent colonization, these lineages comprise distinctive genetic profiles.

In France, Belgium, Netherlands, and Germany current conservation programmes try to counteract the population decline by releasing animals out of breeding units into properly managed farm land sites. Although caged breeding and reintroduction actions are guided by genetic aspects to some extent, many questions concerning the genetic aspects of hamster reintroductions in some countries remain open. Here we present first results of the newly

established reference centre for common hamster genetics. This centre aims to clarify colonisation history, reveal the extent of historic levels of genetic diversity in the western distribution range, and to optimise and control breeding strategies with the aim to maintain high levels of genetic variation and minimize the risk of both inbreeding and outbreeding depression. These information are considered to be crucial for guiding conservation efforts for the preservation of the genetic heritage of the common hamster at its western range margin.

Past diversity of Tragulidae (Artiodactyla)—Lessons from fossils

G.E. RÖSSNER^{1,2,3}, ¹Bayerische Staatssammlung für Paläontologie und Geologie, Richard-Wagner-Strasse 10, D-80333 München, Germany, email: g.roessner@lrz.uni-muenchen.de, ²Department für Geo- und Umweltwissenschaften, Ludwig-Maximilians-Universität München, Richard-Wagner-Strasse 10, D-80333 München, Germany, ³GeoBio-Center^{LMU}, Richard-Wagner-Strasse 10, D-80333 München, Germany

Modern tragulids (*Hyemoschus*, *Tragulus*, *Moschiola*) are a group of small-sized ancestral ruminant artiodactyls including the smallest living hoofed mammal (*T. javanicus*). They live in disjunct distribution in tropical rainforests in Africa and Asia and exhibit a restricted diversity (currently ten species) when compared to other ruminant groups. The fossil record and molecular evidence indicate a Late Eocene tragulid origin, followed by an Oligocene gap, and a major diversification in the Miocene with a wide dispersal in the Old World.

First fossil tragulids were described as such even before extant representatives. Once recognized, several more species from Europe were established in the 19th Century, based on size differences. Since then the number of described taxa has multiplied, the documented geographical spread extended to a wide Afro-Eurasian distribution and Miocene Tragulidae have been known among palaeontologists to constitute typical faunal elements. However, palaeobiological research was never interested in tragulids until recently and paradoxically the fact that their remains are quite numerous in many fossil sites hampered their exploration.

Recent ecomorphological research has now uncovered an essentially higher adaptive diversity in extinct tragulids as represented by the living ones. Miocene tragulids are even quantitatively proven to have been serious competitors to pecoran ruminants. Hence, the fossil record of tragulids documents a much more complex course of their evolutionary history than previously thought with a peak in world wide diversity in between 16 and 13 Million years ago. Considering all the yet unstudied materials we can look forward to further exciting discoveries.

The decoded information from the Hc-4 molar in *Equus stenonis* requires renewing the Linnaeus paradigm

A. RUIZ BUSTOS, Instituto Andaluz de Ciencias de la Tierra, CSIC-UGR, Avenida de las Palmeras, 4, 18100 Armilla, Granada, Spain, email: aruizb@ugr.es

Owing to the uncertainties and anomalies that are historical constants in the Linnaean paradigm, it happens that the phylogenetic data obtained from the crown molars, although these morphologies are inherited, have a complementary scientific value with regard to the biochemical data. The Hc-4 molar (Betic Cordillera, Spain) is analyzed in order to obtain new data using two techniques. Its crown wear section is a biomineralized embryonic morphology (retrogerminative technique), and its enamel line draws hexagonal marks (superimposition technique). These data are the foundations of the mitosis area loop development hypothesis during morphogenesis. The tooth structure is a germination process of the

embryonic dermal masses (mitosis areas), and in relationship to (1) the moment they were born during loop process, (2) size, and (3) location when they constitute a specific cusps crown when they are petrified by an enamel mantle. In conclusion, Linnaean characteristics (morphology) are associated with two parameters: frequency percentage with which the cusps are inherited and their functional role. This parameter group is called “Biological Nature”. The reference series in each molar is a biological nature values group positioned in linear order. The reference series of each Linnaean holotype imply phylogenetic relationships using similarity percentages and the Linnaean uncertainties disappear from the phylogeny. If I express phenotype with the reference series and also the genotype (DNA) is displayed with a numerical sequence, then it happens that we have two numerical sequences and between them exist cause and effect relationship.

Large mammals at risk—Conservation challenges in four continents

C. SCHENCK, Zoologische Gesellschaft Frankfurt (Frankfurt Zoological Society), Bernhard-Grzimek-Allee 1, 60316 Frankfurt a. M., Germany, email: schenck@zgf.de

The threats for large mammals and charismatic inhabitants of last wilderness areas are manifold. By taking four mammal species from four different continents some of the most important challenges for conservation are shown in a spotlight manner. Additionally the measures taken by the Frankfurt Zoological Society to safeguard their survival are described.

Intra-specific variability of aardvarks (*Orycteropus afer*)—Last living representatives of the Tubulidentata (Mammalia, Afrotheria)

P. SCHEPSKY¹, A. HOCHKIRCH¹, M. VEITH¹, T. WILMS², T. LEHMANN³, ¹Department of Biogeography, Trier University, Universitätsring 15, 54286 Trier, Germany, email: sche6e02@uni-trier.de, hochkirch@uni-trier.de, veith@uni-trier.de, ²Frankfurt Zoo, Bernhard-Grzimek-Allee 1, 60316 Frankfurt am Main, Germany, email: Thomas.Wilms@stadt-frankfurt.de, ³Senckenberg Research Institute and Natural History Museum Frankfurt, Senckenberganlage 25, 60325 Frankfurt am Main, Germany, email: thomas.lehmann@senckenberg.de

Unique among mammals, the order Tubulidentata is represented by a single living species: *Orycteropus afer*, the aardvark. Aardvarks occur in sub-Saharan Africa and live in a broad range of habitats (semi-arid savannah to rainforests). To date, 18 sub-species of *O. afer* have been described, mostly based on skins and skulls brought back by explorers. However, the validity of most subspecies is doubtful and data on their ecology or genetic differentiation is missing. This represents also a problem for *ex situ* conservation programmes, as mixing of different genetic lineages could lead to outbreeding depression or gene pool swamping. Well defined management units are needed in order to avoid negative consequences of breeding in zoos. Therefore, from a conservation and systematic point of view, a study of the genetic and morphological variability of *O. afer* was required. We used multivariate morphometry and sequenced two mitochondrial genes (16s rRNA, COI) from fresh tissue (zoo individuals) as well as from skin and bones from the sub-species holotypes (museum samples). A phylogenetic analysis was performed to test the intraspecific genetic variability and the subspecies relationships. Preliminary results suggest that aardvarks living in savannah are significantly smaller than those living in forest and that their ears are longer. The existence of different genetic lineages of the aardvark would impact the assessment of their conservation status, the organization of zoo

breeding programmes and might trigger field work on the ecology of different management units.

Comparison of different mark-recapture intervals in an Edible Dormouse (*Glis glis*) population

C. SCHERBAUM-HEBERER, B. KOPPMANN-RUMPF, K.-H. SCHMIDT, Ecological Research Centre Schlüchtern, Georg-Flemmig-Str. 5, D-36381 Schlüchtern, Germany, email: cheberer@gmx.de

The data used for this study were obtained from a monitoring project focusing on the population biology of the Edible Dormouse *Glis glis* since 2002. The sample area is situated in a low mountain range 1 km south of the city of Schlüchtern (9°31'N, 50°20'O), 70 km northeast of Frankfurt, Germany. It consists of a total of 185 nestboxes arranged in a 25 m × 25 m grid. Dormice found in nestboxes were captured and marked using PIT-tags once a week. Between the weekly nestbox checks all nestboxes were scanned every day without opening them using a reader to register all tagged dormice inside. Based on the observation of high fluctuations of marked individuals we simulated fewer nestbox checks, i.e. weekly and monthly intervals which are commonly applied in population studies. The resulting population sizes were then compared to those obtained from daily observations. In addition a population estimate applying Jolly's method and the minimum number of animals known to be alive were calculated. The results showed that fewer nestbox checks and population estimates yield significantly lower numbers of animals compared to daily nestbox scans.

Past and present distribution of the North African-Asian lion subgroup: A review

A. SCHNITZLER, Laboratoire des Interactions Ecotoxicologie, Biodiversité, Ecosystèmes (LIEBE), CNRS UMR 7146, Université Paul Verlaine de Metz, UFR Sci Fa Sciences Fondamentales et Appliquées Campus Bridoux, Rue du Gal Delestraint, France, email: schnitz@univ-metz.fr

The North African-Asian subgroup (i.e. Barbary lion *Panthera leo leo* and the Asian lion *Panthera leo persica*) was nearly exterminated during the last centuries. The remaining free-ranging population of Asian lions consists of ca. 350 animals in India. The Barbary lion subsists as captive animals in zoos or circuses, all of which originate from the Moroccan Royal Collection. There have been multiple genetic hybridisations with sub-Saharan lions.

I examine here the distribution of these lions with the help of a larger database, extracted from zoological, archaeological and historical reports. Data were collected over a long period of time (from the Epipaleolithic to the modern times) in Eurasia, North Africa and the Arabic peninsula. Dispersal took place to latitudes as far south as 15°N (Yemen) to 18°N (Mali; Chad) and as far north as 45–48°N (Bulgaria); and to longitudes as far west as 5.57°W (Morocco) and as far east as 84°E (India). Expansion was probably constrained by natural ecological factors northwards (higher seasonality, harsher winters) and southwards (extension of aridity after 3000 BC). At latitudes between 40 and 43°N, lions seem to have become a permanent part of the fauna during 6–8 millennia. Lions were brought to extinction by humans through hunting, captures for exhibition in zoos, and by the associated natural fragmentation of wild populations. The dates at which extinction took place varied greatly according to the geographical sites: 3000 BC for temperate Europe; 1000 BC in the south of Greece; 12–13th century in the near East, Arabic peninsula, Trans-Caucasia or North of Afghanistan; 19–20th century for North Africa, the Middle East and India.

The diversity of rodent mandibles—Effects of size, diet, and taxon

A.C. SCHUNKE, D. TAUTZ, Max-Planck-Institute for Evolutionary Biology, Department for Evolutionary Genetics, August-Thienemann-Str. 2, D-24306 Plön, Germany, email: schunke@evolbio.mpg.de

Rodents are the most speciose order of mammals and display tremendous variation in ecology and morphology across the group. Some characteristics like size and diet type evolved independently in several taxonomic groups within the rodents and thus offer the opportunity to investigate parallelism in shape changes based on similar ecology. In order to contribute to a better understanding of this diversity we studied a large sample of rodent mandibles using 3D landmarks digitized on micro-CT scans. Besides using standard geometric morphometrics we also developed new methods for the separate analysis of different effects and correlations. The results showed that size plays a minor role, particularly for small differences. Differences in diet also display a remarkably low signal when compared across rodents, with the main effect being the affiliation to a certain taxon.

On the sexual dimorphism in elephants *Archidiskodon meridionalis meridionalis* from the Stavropol Territory (Russia, Northern Caucasus)

A.K. SCHVYREVA, The Stavropol Museum, Reserve of a Name of G.N. Prozriteleva and G.K. Prave, Nature Section, Dzerzhinskogo ul. 135, Stavropol 355 035, Russia, email: annashvyreva@mail.ru

In the Stavropol Territory almost complete skeletons of southern elephant *Archidiskodon meridionalis* were found twice. The first of them was found in 1960 in the sand quarry around the town Georgievsk. The second almost fully complete skeleton of *Archidiskodon meridionalis* (Nesti) was found in August 2007. It was found in the quarry which is located in the valley of river Egorlyk, on the left board of ravine Tverdova, between villages Rodionov and Rovninnyi. They are exhibited at a palaeontology hall of the Stavropol Museum. These animals have identical individual and geological age. Both are completed with fully preserved pelvic bones. The detailed study of the pelvic bones was made by using the methodology described by Adrian Lister (Lister, 1996). The data analysis showed that in a ravine of Tverdova near the village Rovninnyi the female pelvis of *Archidiskodon meridionalis* was found. The pelvis was examined by veterinarian Elena Kharlamova who confirmed the pelvis to be female. In addition, the veterinarian drew attention to the peculiarity joint of pubis bones. The front edge of the left pubic bone was pulled out ahead slightly compared with the right bone. Such a shift may be the result of female's births. Given the parameters of the pelvis, the skeleton of an elephant out of the town Georgievsk belongs to the male.

Effect of habitat loss on Austral African populations of Cape buffalo (*Syncerus caffer caffer*) based on microsatellite analysis

N. SMITZ¹, D. CORNELIS², A. CARON^{3,4}, M. DE GARINE-WICHATITSKY³, F. JORI⁵, K.L. KANAPECKAS⁶, P. CHARDONNET⁷, M. MELLETTI⁸, J. MICHAUX^{1,9}, ¹ Conservation Genetics, University of Liège, Boulevard du Rectorat 26, 4000 Liège, Belgium, email: nsmitz@student.ulg.ac.be, ² Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD), UPR AGIRS, Campus International de Baillarguet, F-34398 Montpellier, France, email: daniel.cornelis@cirad.fr, ³ Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD), Department Environment and Societies, University of Zimbabwe, P.O. Box 1378, Harare, Zimbabwe, email:

alexandre.caron@cirad.fr, ⁴ Mammal Research Institute, Department of Zoology and Entomology, University of Pretoria, Pretoria, South Africa, ⁵ Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD), Department of Zoology & Entomology, University of Pretoria, Pretoria, South Africa, email: ferran.jori@cirad.fr, ⁶ Department of Zool. and Entomol., Mammal Research Institute, University of Pretoria, Pretoria, South Africa, email: p.chardonnet@fondation-igf.fr, ⁷ International Foundation for the Conservation of Wildlife (IGF), Rue de Téhéran 15, 75008 Paris, France, email: mario.melletti@yahoo.it, ⁸ Department of Animal and Human Biology, University of Rome "La Sapienza", Vle. dell' Università 32, 00185 Rome, Italy, ⁹ Centre de Biologie et de Gestion des Populations (CBGP), UMR 1062, Campus International de Baillarguet, CS 30016, F-34988 Montferrier-le-Lez, France, email: michaux@supagro.inra.fr

Along with the elephant (*Loxodonta africana*) and the wildbeest (*Connochaetes* spp.), the Cape buffalo is the most dominant species in terms of biomass but also the most widespread herbivore in the savannas and open woodlands of East-Southern Africa. Habitat loss due to climatic changes, land use, and poaching are the main challenges currently threatening the species of Africa. The last natural parcels are reduced to an ill-assorted mosaic of refuges, generally corresponding to the rare protected areas. For wild species, which cannot coexist with humans, this situation reduces the original connectivity between their populations, which can lead to a significant erosion of their genetic diversity. The isolation of the populations of species with a large vital domain, such as the wild buffalo, clearly underlines the question of their survival. In this context, 264 samples distributed within 15 National parks of 6 countries of Austral Africa (Namibia, Botswana, Zimbabwe, Zambia, Mozambique, South Africa) were genotyped for 14 autosomal and 3 Y-chromosomal microsatellites. The main objective of this study was to determine the impact that such subdivision could have on the genetic diversity of the buffalo populations (i.e., genetic drift and correlation between the amount of genetic variation and population size/park size) and assess the "genetic health" of the surviving populations. This information is particularly essential within the context of translocation programs currently undertaken to restore genetic diversity in Austral Africa.

Movement of the lower jaw during incisor interaction and mastication in the beaver—A biplanar X-ray analysis

C. STEFEN¹, P. IBE², M.S. FISCHER³, ¹ Senckenberg Naturhistorische Sammlungen Dresden, Museum für Tierkunde, Königsbrücker Landstraße 159, 01109 Dresden, Germany, email: clara.stefen@senckenberg.de, ² Landesverwaltungsamt Sachsen-Anhalt, Biosphärenreservat Mittelbe, Kapenmühle PF 13 82, 06813 Dessau-Roßlau, Germany, email: peter.lbe@lvwa.sachsen-anhalt.de, ³ Friedrich-Schiller-Universität Jena, Institut für Spezielle Zoologie und Evolutionsbiologie, mit Phyletischem Museum, Erbertstr. 1, 07743 Jena, Germany, email: Martin.Fischer@uni-jena.de

Biplanar X-ray films of the mandibular action during incisor action and mastication of a beaver will be shown. Incisors interact when particles are chipped off, e.g., a tree or of sweet corn. This interaction involves a variable movement of the mandible. When the jaw is opened the tip of the lower incisors can take different positions anterior to the upper incisors. Chipping includes movement of the mandible upwards and backwards so that the tips of the incisors are brought in to contact. The lower incisors slide along the wear facet of the upper to the ledge when the cheek teeth occlude. During incisor contact the glenoid fossa and condyle of the mandible are in close contact and no transverse movements are observed. During mastication the cheek teeth interact whereas the incisors

do not come into contact. A mastication cycle involves closing the jaws, and bringing the mandible forward and transverse or medio-lateral so warranting the contact of the teeth and alimentary bolus. In consecutive power strokes the jaw is moved alternately to the right and left side and is retrieved to a more centered position when the jaw opens. The position of the mandibular condyle to the glenoid change during mastication, the condyles are posterior to the glenoid. This position allows lateral movement of the mandible. With the lateral movements of the incisors one glenoid has to move posteriorly, the other anteriorly. So the alternating positions of the incisors during mastication require an alternation of condyle-glenoid position as well.

Data on mammalian diversity: Limitations and opportunities

P.A. STEPHENS, School of Biological and Biomedical Sciences, Durham University, DH1 3LE Durham, UK, email: philip.stephens@durham.ac.uk

Key to our understanding of mammalian diversity are studies that monitor the abundance of populations and quantify diversity across populations. The gold standard for investigating individual populations is the long-term, individual-based study; however, such studies are seldom directed at comparing between populations. Moreover, funding constraints suggest that fewer studies might now survive the critical early phases prior to achieving the status of long-term studies. Many mammal populations are also the focus of abundance monitoring but monitoring programmes are seldom conducted rigorously across a wide range of taxa and localities. Here, I use examples from ongoing work in my research group, in order to identify other sources of data that ecologists routinely use to make inferences about behaviour and population dynamics. I consider the potential of these alternative data sources, as well as their limitations. I argue that we cannot easily generalise from studies that focus on a single study population but that, because they are seldom collected for a specified biological purpose, data collected across multiple populations are usually strongly limited in what they can tell us. If anything defines the present, it is the need to answer big ecological questions at large spatial and temporal scales. That, coupled with the emergence of new technologies for remote monitoring, suggests that now is the time to initiate more coordinated and widespread programmes of mammalian study.

European wolf (*Canis lupus*) genetic structure indicates a primary north–south axis

A.V. STRONEN¹, S. CZARNOMSKA¹, M. NIEDZIAŁKOWSKA¹, W. JEDRZEJEWSKI¹, C. PERTOLDI², M. PILOT³, E. RANDI⁴, D. DEMONTIS⁵, I. KOJOLA⁶, M. SHKVYRYA⁷, E. TSINGARSKA⁸, A.A. KARAMANLIDIS⁹, J. KUSAK¹⁰, B. JEDRZEJEWSKA¹, ¹ Mammal Research Institute, Polish Academy of Sciences, ul. Waszkiewicza 1, 17-230 Białowieża, Poland, email: avstronen@ibs.bialowieza.pl, ² Ecology and Genetics, Department of Biological Sciences, University of Aarhus, Building 1540, Ny Munkegade, DK-8000 Aarhus, Denmark, ³ Museum and Institute of Zoology, Polish Academy of Sciences, ul. Wilcza 69, 00-679 Warszawa, Poland, ⁴ Laboratorio di genetica, ISPRA, via Cà Fornacetta 9, I-40064 Ozzano Emilia (BO), Italy, ⁵ Department of Human Genetics, University of Aarhus, Wilhelm Meyers Allé, DK-8000 Aarhus, Denmark, ⁶ Finnish Game and Fisheries Research Institute, Oulu 90570, Finland, ⁷ The Schmalhausen Institute of Zoology, National Academy of Sciences of Ukraine, Bohdan, Khmelnytsky str. 15, 01601 Kyiv, Ukraine, ⁸ BALKANI Wildlife Society, Str T Tserkovski 67/V-3, Sofia, Bulgaria, ⁹ ARCTUROS, Civil Society for the Protection and Management of Wildlife and the Natural Environment, GR-54624 Thessaloniki, Greece, ¹⁰ Department of Biology, Faculty of Veterinary Medicine, University of Zagreb, Croatia

Earlier research on mitochondrial D-loop and STR DNA has revealed genetic structuring in European wolves in the absence of geographic barriers, and across relatively short distances for this highly mobile species. Additional information on the location of, and divergence between, population clusters is required, particularly because wolves are presently recolonizing several areas of Europe. We evaluated genetic structure in 177 wolves from 11 countries using a Bead-Chip that screens over 67,000 single nucleotide polymorphism (SNP) loci. The results supported previous findings of an isolated Italian population with lower genetic diversity than that observed across other areas of the continent. Wolves from the remaining countries were primarily structured in a north–south axis, with Croatia, Bulgaria and Greece isolated from north–central wolves that included individuals from Finland, Latvia, Belarus, Poland and Russia. Wolves from the Carpathian Mountains in central Europe occupied an intermediate position. Furthermore, certain Ukrainian individuals were divergent from the primary north–south alignment. The overall profiles from north–central Europe suggested relatively high levels of admixture and the presence of a genetic cline. In contrast, wolves from Croatia appeared divergent from a cluster encompassing Greece and Bulgaria. Our results support differentiation between northern and southern areas of the continent, and the presence of at least three clusters within southern Europe. Expansion from different glacial refugia, adaptation to local environments and human-induced fragmentation may have contributed to the observed patterns. Our findings can help inform local and wide-scale conservation management of these apex predators and the ecosystems of which they are part.

Mammals and their parasites trapped by joint Mongolian–German Expeditions between 1995 and 2010 in steppe, semi-desert and desert regions of Mongolia

I.W. STUERMER¹, D. OTGONBAATAR², M. PFEFFER³, N. SODNOMDARJAA⁴, N. NARANTUYAA⁵, D. TSERENNOROV², A. POLOCZEK¹, K. MÄUSEZAHN¹, C. TITTMANN¹, B. BAJGALMAA², D. WOLL³, A. SARUULZARGAL⁴, C. KOHN⁶, D. MAAZ⁶, T. DAVADOORJ⁷, S. HEIDELBERGER⁸, B. STEPPUTIS⁹, R. WINDLER¹, D. SAJNBILEG¹⁰, R. SAMIYA¹⁰, W. HILBIG¹¹, ¹ Georg-August-University of Göttingen, Department of Morphology, Systematic and Biology of Evolution, Institute for Zoology, Berliner Strasse 28, D-37073 Göttingen, Germany, email: stuermer@med.uni-goettingen.de, ² National Center of Infectious Diseases with Natural Foci (NCIDNF), Songinokhairhan District, 211137 Ulaanbaatar, Mongolia, ³ Institute for Animal Hygiene and Veterinary Public Health, University of Leipzig, An den Tierkliniken 1, 04103 Leipzig, Germany, ⁴ State Central Veterinary Laboratory, Zaisan, Khan-Uul district, P.O. Box-53-03, 210153 Ulaanbaatar, Mongolia, ⁵ Mongolian Academy of Sciences (MAS), Department of Botany, A. Amar street 1, Sukhbaatar Sq. 3, Ulaanbaatar 210620A, Mongolia, ⁶ Abteilung Parasitologie, Institut für Pathologie, Charité, Medizinische Fakultät der Humboldt-Universität zu Berlin, Maltesserstraße 74-100, 12249 Berlin, Germany, ⁷ National University of Mongolia at Ulaanbaatar, Faculty of Medicine, Ulaanbaatar, Mongolia, ⁸ Bremen University of Applied Sciences, Neustadtswall 30, 28199 Bremen, Germany, ⁹ Institute of Baltic Sea Fisheries, Alter Hafen Süd 2, 18069 Rostock, Germany, ¹⁰ National University of Mongolia, Faculty of Biology, P.O. Box 377, Ulaanbaatar, Mongolia, ¹¹ Münchener Str. 8, 85238 Petershausen, Germany

Gerbils and squirrels are among the most abundant rodent species in arid areas of Mongolia. Rodents are playing a decisive role in the distribution of infectious diseases. Between 1995 and 2010, around 1100 wild mammals were collected during six Joint Mongolian–German Expeditions to the steppe, semi-desert and desert zones of Mongolia. Examination of 150 gerbils revealed

597 ectoparasites and 2992 endoparasites, documenting the severe burden of parasitism. Nearly half (44%) of all rodents were infected, and parasites causing human diseases (fleas, *Moniliformis moniliformis*) were described. Ectoparasite infestation was neither biased by sex nor by host species, but adult specimens showed higher infestation rates than juveniles. Investigations of liver from 133 rodents trapped by our expeditions revealed that 5% of samples were positive for *Y. pestis* (Riehm et al., 2011. Emerg Infect Dis 17, 1320–1322). Examination of squirrels ($n = 26$) collected 1995–2010 showing high infestation with ectoparasites in *Spermophilus dauricus* (75%) and *Spermophilus undulates* (32%). Fleas (Siphonoptera) were found in *Spermophilus alashanicus*, *Sp. dauricus* and *Sp. undulates*. Endoparasites found in squirrels included *Cestoda*, *Nematoda* and high amounts of *Acanthocephala*, revealing >100 thorny-headed worms in infected squirrels. Recent investigations by 6th Expedition collected 21 mammal species ($n = 158$) and their parasites between 24th June and 5th August 2010 at eastern and southern Mongolia (Dornod, Suhbaatar, Dornogovi, Omnogovi, Tov Aimak). Dissections and preliminary results indicate high infection (>50%) with fleas and other parasites, e.g., in *Rattus norvegicus*. Morphological analyses are supplemented by ongoing ecological and molecular analyses.

Searching for zoonotic pathogens in small mammals from Afghanistan

R.G. ULRICH¹, M. SCHLEGEL¹, K. BAUMANN¹, A. BREITHAUPT², A. BINDER³, U. SCHOTTE³, S. RUHL³, C. KROHMANN³, S. ESSBAUER⁴, D. FRANGOULIDIS⁴, P. KAYßER⁴, H. MEYER⁴, J. RIEHM⁴, M. FAULDE⁵, J. LEWITZKI⁶, S. SAUER⁶, J.P. TEIFKE², ¹Friedrich-Loeffler-Institut, Institute for Novel and Emerging Infectious Diseases, Greifswald – Insel Riems, Germany, ²Friedrich-Loeffler-Institut, Department of Experimental Animal Facilities and Biorisk Management, Greifswald – Insel Riems, Germany, ³Central Institute of the Bundeswehr Medical Service, Veterinary Medicine, Laboratory for Infectious Animal Diseases and Zoonoses, Kiel/Kronshagen, Germany, ⁴Bundeswehr Institute of Microbiology, Munich, Germany, ⁵Central Institute of the Bundeswehr Medical Service, Koblenz, Germany, ⁶Central Institute of the Bundeswehr Medical Service, Garching-Hochbrück, Germany

Wild rodents represent important reservoir hosts for a large number of zoonotic pathogens including viruses (e.g. hantaviruses, poxviruses, tick-borne encephalitis virus), bacteria (e.g. *Leptospira* and *Borrelia* spp.) and parasites (e.g. *Toxoplasma gondii*). The transmission of these pathogens to humans can happen through arthropod vectors, e.g. ticks, or by inhalation of aerosolized virus-contaminated rodent excreta. Alternatively, direct contact, bites or contaminated water or food can be the basis for transmission. A higher risk of infection with rodent-borne pathogens exists for humans with direct contact to rodents or their excretions, e.g. soldiers in operation areas.

This study aims to characterize the wild small mammal population in the camps of the German Federal Armed Forces (Bundeswehr) in Afghanistan and the prevalence of zoonotic pathogens in these animals. During 2009 and 2010 a total of 442 small mammals were collected at the camps of the German Federal Armed Forces (Bundeswehr) in Afghanistan (Mazar-i-Sharif, Fayzabad, Kunduz). According to morphological and *cytochrome b*-based molecular species determination (Schlegel et al., 2012) the trapped small mammals are represented by 391 house mice (*Mus musculus*), 41 gray dwarf hamsters (*Cricetulus migratorius*), 3 Siberian shrews (*Crocidura sibirica*), 3 lesser white-toothed shrews (*Crocidura suaveolens*) and one Etruscan shrew (*Suncus etruscus*). Pathomorphological inspection of the animals during necropsy revealed no obvious pathological findings. Preliminary bacteriological and

molecular investigations revealed the presence of endoparasites (*Piroplasma*), of methicillin-resistant *Staphylococcus* sp. and of extended-spectrum beta-lactamase-producing bacteria of different species. These pathogens were detected only in house mice. So far no indications for infections by zoonotic viruses were found. The ongoing investigations will prove the usability of rodents in army camps as sentinel animals to estimate the infection risk for military personnel, especially during out-of area missions. To improve the sensitivity of a foresighted health protection, future studies will establish novel open-view methods, i.e. next generation sequencing, for non-invasively collected small mammal samples.

Aardvark's ear (Mammalia, Tubulidentata): Not so primitive after all

M. VATTER, T. LEHMANN, Senckenberg Research Institute and Natural History Museum Frankfurt, Senckenberganlage 25, 60325 Frankfurt am Main, Germany, email: martin.vatter@senckenberg.de, thomas.lehmann@senckenberg.de

The order Tubulidentata, a member of the still debated mammalian clade Afrotheria, is represented nowadays by a single living species, the aardvark (*Orycteropus afer*). The anatomy and ecology of this highly specialised semi-fossorial species is still poorly known, but sight and hearing seem to be the most developed senses for this animal. Nevertheless, former studies have considered the ear of *O. afer* to be primitive for Eutherians. Unfortunately, there exist as yet no extensive analyses of the ear region of fossil aardvarks, so that most studies dealing with phylogeny and function consider the features displayed by extant aardvark as representative for the whole order. The aim of the present study is to compare the structure of the middle ear in the extant aardvark with that of fossil Tubulidentata. Our preliminary results show that fossil aardvarks of the genus *Amphiorcyteropus* for instance, differs from *O. afer* in having a more horizontal ectotympanic (lying on the petrosal), and a stronger post-glenoid process; but lacking a preotic crest and an ectotympanic/alispheoid contact. Moreover, the ear as a whole is somewhat of the same size in fossil and extant aardvarks, whereas the whole skull is significantly larger in *O. afer*. This would suggest that the ear region did evolve in Tubulidentata and that *O. afer* displays a derived configuration. Furthermore, this raises questions about auditory adaptations in fossil aardvarks. Hence, when considering ear features in supra-ordinal phylogenies (e.g. Afrotheria), one should take into account the state of characters shown by fossil aardvarks too.

Structures of carnivore guilds and hominid carnivory

R. VOLMER¹, H. O'REGAN², S. REYNOLDS³, C. HERTLER¹, ¹Heidelberg Academy of Sciences and Humanities "The Role of Culture in Early Expansions of Humans", Senckenberg Forschungsinstitut und Naturmuseum, Senckenberganlage 25, 60325 Frankfurt am Main, Germany, email: volmer@bio.uni-frankfurt.de, ²Liverpool John Moores University, School of Natural Sciences and Psychology, James Parsons Building, Byrom St., Liverpool L3 3AF, UK, email: H.J.ORegan@ljmu.ac.uk, ³Institute for Human Evolution, University of the Witwatersrand, and Liverpool John Moores University, School of Natural Sciences and Psychology, James Parsons Building, Byrom St., Liverpool L3 3AF, UK, email: S.Reynolds@ljmu.ac.uk

We examine the nature of hominin–carnivore interactions, and how hominin involvement would have affected previously existing carnivore guilds in two parts: (1) understanding guild structure prior to hominin involvement in southern Africa, Europe and southeastern Asia and (2) attempting to model how the appearance of a new competitor would have affected these existing guild

structures. We use modern ecological and palaeontological data to create the model structure of carnivore guilds in the Pleistocene. These guilds are defined by the number of members, their body sizes, their prey mass spectra and their relative number in the sample. When new members enter the guild, the existing structures change. Typical predicted changes involve adaptational shifts in body size, decrease of population sizes, decrease of predator abundances in certain size classes and/or shifts in carnivore species richness. These responses may be mediated by the degree of sociality in the different carnivore species, and the degree of behavioural flexibility. In the second part of this study, we use the carnivore guild model to model the potential effects of a new guild member attempting to access the guilds in the three geographic locations. This will enable us to postulate when and how hominins could have entered the guild, and how other carnivores would have responded.

Neumann's enigmatic gazelle (*Gazella erlangeri*)—Endangered species or domesticated gazelle?

T. WRONSKI^{1,2}, E.V. BÄRMANN³, T.M. BUTYNSKI^{1,2}, M. PLATH⁴, H. LERP⁴, ¹King Khalid Wildlife Research Centre, Saudi Wildlife Commission, Riyadh, Saudi Arabia, ²Zoological Society London, United Kingdom, ³Department of Zoology, University of Cambridge, United Kingdom, ⁴Department of Ecology and Evolution, University Frankfurt am Main, Germany, email: lerp@bio.uni-frankfurt.de

One of the most challenging questions with regard to Arabian gazelles is the status of *G. erlangeri* Neumann, 1906. Gazelles currently kept in captivity at King Khalid Wildlife Research Centre in Saudi Arabia and Al Wabra Wildlife Preservation in Qatar show the described combination of diagnostic features, and thus, were considered to represent *G. erlangeri*, even though the exact provenance of these gazelles remains obscure. In our study we provide a phylogenetic framework based on the analysis of mtDNA sequences (360 bp cytochrome *b* and 213 bp Control Region) as well as results from population genetic analyses using microsatellite markers. Furthermore, we used morphometrical data to investigate possible characteristics of these forms. Morphometric results as well as population genetic analyses clearly showed diagnostic differences between putative *G. erlangeri* held in captivity and other mountain gazelles (*G. gazella* and *G. arabica*). Nevertheless, phylogenetic analyses did not find a monophyly of putative *G. erlangeri* and placed them within the mountain gazelles. Therefore, we argue that animals held in captivity are the product of selective breeding leading to smaller, darker and tamer forms of mountain gazelles with no equivalent found in the wild. These findings correspond with the historic mention of pet gazelles from Yemen and southern Saudi Arabia.

The variation of extinct Northern African Urus as reflected in rock art

T.W. WYRWOLL, Rock Art Research Center, P.O. Box 111 101, D-60046 Frankfurt am Main, Germany, email: tw@felsbilder.de

The wild cattle of Northern Africa is a southern representative of the Eurasian urus, commonly labeled *Bos primigenius*. Probably it is specifically distinct from the urus of Europe and hence should be named *Bos mauritanicus*. Most of the African populations became extinct already in prehistoric times, and their last remnants thrived until the early historical period of the region. Bone finds are scarce in number, and as in most larger-Bovid remains, their taxological expressiveness is rather limited. Therefore, in order to understand the diversity of North African urus in their vast area of distribution, one has to look for additional evidence. A valuable such source is provided by archeological pictures, above all rock engravings

and wall-paintings. Many of them do perfectly depict morphological details of the animals, including their horn form, peculiar traits of the skull, and not in the least the form and extension of the *sattelfleck* (saddle-splodge). There is a clear variation between the urus of each geographical subregion of Northern Africa, so that this author considers these peculiar populations as individual races each. It is argued that the newly emerging field of archeotherioiconology can provide valuable insights into microevolutionary processes especially in larger mammals and also contribute to our understanding of the overall change of the environment. In addition, the rock images investigated also give hints for a local domestication of African urus and/or their crossbreeding with introduced domestic cattle. In conclusion, the genetic impact of African urus on extant Mediterranean cattle breeds is briefly discussed.

Spotted hyena (*Crocuta crocuta*) coexisting at high density with people in Wukro district northern Ethiopia

G. YIRGA¹, W. ERSINO^{1,2}, H.H. DE IONGH^{3,4}, H. LEIRS^{4,5}, K. GEBREHIWOT⁶, J. DECKERS⁷, H. BAUER⁷, ¹Department of Biology, Mekelle University, P.O. Box 3072, Mekelle, Ethiopia, email: gidey1998ec@yahoo.com, ²Department of Biology, Debre-Tabor University, P.O. Box 272, Debre-Tabor, Ethiopia, ³Institute of Environmental Sciences, Leiden University, P.O. Box 9518, 2300 RA Leiden, The Netherlands, ⁴Evolutionary Ecology Group, University of Antwerp, Groenenborgerlaan 171, 2020 Antwerpen, Belgium, ⁵Aarhus University, Department of Agro-ecology, Slagelse, Denmark, ⁶Department of Land Resource Management and Environmental Protection, Mekelle University, P.O. Box 231, Mekelle, Ethiopia, ⁷Department of Earth and Environmental Sciences, Catholic University of Leuven, Celestijnenlaan 200E, B-3001 Heverlee, Belgium

We surveyed population density and abundance of spotted hyena (*Crocuta crocuta*) in the highly degraded and prey depleted Wukro district, northern Ethiopia, with a human population density of 98 persons per square kilometer. A total of 117 spotted hyenas responded to callups. Estimates give a hyena density of between 54 and 108 hyenas per 100 km² or a total population estimate of 254–508 hyenas in the district. We quantified the economic impact of spotted hyena predation on livestock using semi structured interviews with randomly selected households. Respondents indicated a total loss of 203 domestic animals to hyena depredation over the past five years. Average annual depredation per household was about 0.13 livestock worth US\$ 6.1. The diet of spotted hyenas was assessed in three sub-districts by scat analysis and showed 99% prey items of domestic origin, only three of 211 scat contained hair of Ethiopian hare (*Lepus fagani*) and porcupine (*Hystrix cristata*). We conclude that spotted hyenas in our area occur at high density and depend almost exclusively on anthropogenic food sources.

Ma(i)nhattan goes wild!

M. ZIEGE, H. LERP, M. PLATH, Department of Ecology & Evolution, J.W. Goethe University Frankfurt, Max-von-Laue-Str. 9, 60438 Frankfurt am Main, Germany, email: madlen.ziege@googlemail.com

Animals that colonize human settlements need to cope with a set of novel, potentially stressful factors, like the permanent presence of humans or various forms of environmental pollution. Those stressors could have profound effects on various aspects of individuals' life history but to date only few studies addressed the behavioural, physiological, or population genetic characteristics of wildlife in metropolises. Knowledge about potential adaptations will be vital for future management plans for urban wildlife populations. One example of a species that successfully colonized several German

cities, but is on decline in rural areas, is the European rabbit (*Oryctolagus cuniculus*). In a recently started multi-biological project, the influence of anthropogenic factors on intraspecific communication, activity patterns and habitat use, as well as on parasite loads and population genetic patterns are being investigated. We ask, e.g., whether altered environmental conditions in urban areas lead to differences in communication within and among groups, and whether reduced predation leads to altered activity patterns (with urban rabbits being active also during the daytime). The use of radio tracking and population genetic analyses based on microsatellites provide further tools for a holistic understanding of how rabbits use the highly fragmented urban habitats and whether migration between rural and urban population is still on-going, or interrupted.

Downtown bunnies and their gut feelings

M. ZIEGE, A. SCHIESSL, M.-L. SCHRÖDL, M. PLATH, Department of Ecology & Evolution, J.W. Goethe University Frankfurt, Max-von-Laue-Str. 9, 60438 Frankfurt am Main, Germany, email: madlen.ziege@gmail.com

Mammalian wildlife in urban regions tends to show higher population densities compared to populations inhabiting rural or natural habitats. This can be attributed, in part, to reduced predation, as

well as new food sources (or reduced competition with ecologically similar species) leading to increased food availability. Increased population densities clearly increase the likelihood of disease transmission, so urban populations would be predicted to suffer from elevated levels of parasitism. A typical city-dwelling mammal in Germany is the European rabbit (*Oryctolagus cuniculus*). As rural populations are currently declining at an alarming pace this renders studies on parasite infection and transmission all the more timely and pressing. We hypothesized that gastrointestinal parasite loads increase with increasing levels of urbanity and over a period of several months we collected fecal pellets from rural sites, suburban parks and the inner city center of Frankfurt am Main. Egg numbers per gram feces (EPG) were quantified for different species of nematodes and cestodes; furthermore, we determined the abundance of 8 different coccidian species. An individual parasitization index (I_{PI}) was calculated for each sample and Principal Component Analysis applied to test for differences in parasite communities based on abundance data. Our study detected significant differences in overall parasite loads between all three levels of urbanity; also, parasite communities differed across sites. We discuss that beside increased host population densities, also factors like higher mean temperatures and frequent grass cutting need to be considered when interpreting patterns of gastrointestinal tract parasite transmission in urban regions.

Author index

- Adorf, F., 5
Ansorge, H., 10
Apollonia, M., 11
Aref, N., 15
Arnason, U., 9
Asher, R.J., 10
Autenrieth, M., 5
Azanza, B., 5
- Bajgalmaa, B., 20
Bärmann, E.V., 5, 22
Bassano, B., 7
Bauer, H., 22
Baumann, K., 21
Bayerl, H., 13
Bereczky, L., 16
Bertorelle, G., 11
Bethaz, S., 7
Bidon, T., 6
Binder, A., 21
Biosa, D., 11
Blagojević, M., 6
Blümke, J., 14
Börner, S., 5
Braun, C., 5
Breithaupt, A., 21
Bromage, T.G., 6
Bull, J. K., 6
Butynski, T.M., 22
Buzan, E., 16
- Cadena, D., 9
Caron, A., 19
Chardonnet, P., 19
Chiriak, S., 16
Contu, S., 7
Corazza, M., 8
Corlatti, L., 7
Cornelis, D., 19
Crooijmans, R.P.M.A., 11
Czarnomska, S., 20
- Davadoorj, T., 20
De Garine-Wichatitsky, M., 19
Decher, J., 7
Deckers, J., 22
Demeler, J., 14
Demontis, D., 20
Diedrich, C., 7
Domokos, C., 8
Dutsov, A., 8
- Eiken, H.-G., 11, 12
Erpenbeck, D., 5
Ersino, W., 22
Essbauer, S., 21
- Fain, S.R., 9
Faulde, M., 21
- Fautley, R., 8
Ferrari, C., 8
Ferretti, F., 8
Fickel, J., 5, 13
Fickels, J., 6
Fischer, M.S., 19
Foerster, D. W., 6
Förster, D.W., 5, 13
Frangoulidis, D., 21
Fremuth, W., 8
Frosch, C., 6, 8, 16
Furió, M., 9
- Gebrehiwot, K., 22
González-Caro, S., 9
Gray, C. R., 7
Greif, S., 13
Grigoryeva, O., 9
Groenen, M.A.M., 11
- Hagen, S.B., 12
Hailer, F., 6, 9, 11, 14
Hallström, B., 11
Hallström, B.M., 9
Harms, V., 10, 16
Hartmann, S., 14
Haye, M.J.J., LA 17
Hebel, C., 5
Heckeberg, N.S., 10
Heidelberger, S., 20
Hertler, C., 10, 21
Heymann, E. W., 15
Hilbig, W., 20
Hochkirch, A., 18
Hofreiter, M., 11
Hogg, R.T., 6
Hönemann, D., 10
Hou, C., 6
- Iacolina, L., 11
Ibe, P., 19
Iongh, H.H., DE 22
- Janke, A., 6, 9, 11, 14
Jędrzejewska, B., 20
Jędrzejewski, W., 20
Jordana, X., 11
Jori, F., 19
- Kanapeckas, K.L., 19
Karamanlidis, A.A., 20
Kashtalian, A., 12
Kauhala, K., 12
Kayßer, P., 21
Khalatbari, M., 15
Kilpatrick, C. W., 7
Kim, S.I., 12
Kim, Y.K., 12
Kimura, J., 12

- Klassert, D., 9
 Kluth, G., 10
 Köhler, M., 11
 Kohn, C., 20
 Kojola, I., 20
 Kopatz, A., 12
 Koppmann-Rumpf, B., 12, 18
 Koyabu, D., 12, 13
 Kraus, R.H.S., 13, 16
 Krohmann, C., 21
 Krücken, J., 14
 Krüger, F., 13
 Krystufek, B., 16
 Kühn, R., 13
 Kusak, J., 20
 Kutschera, V.E., 9, 14

 Lacruz, R.S., 6
 Lahoot, M., 15
 Lapin, M., 7
 Lehmann, T., 18, 21
 Leirs, H., 22
 Leonard, J. A., 9
 Lerp, H., 14, 22
 Lewitzki, J., 21
 Lovari, S., 7, 8

 Maaz, D., 14, 20
 Marín-Moratalla, N., 11
 Masseti, M., 14
 Matauschek, C., 15
 Matuschka, F.-R., 14
 Mäusezahl, K., 20
 Mazza, P.P.A., 14
 Megens, H.-J., 11
 Melletti, M., 19
 Meyer, H., 21
 Michaux, J., 19
 Milošević-Zlatanović, S., 6
 Min, M.S., 12
 Minder, I., 8
 Mohammadi, S., 15, 16
 Moncunill, B., 11
 Mundorf, A., 15

 Naderi, G., 15, 16
 Narantuyaa, N., 20
 Neumann, K., 17
 Niedzialkowska, M., 20
 Nowak, C., 15, 16
 Nowak, C., 8, 10, 13, 17

 O'regan, H., 21
 Oh, J.W., 12
 Orlov, V., 9
 Oshida, T., 12
 Otgonbaatar, D., 20

 PACHER, M., 16
 Palme, R., 7
 Pertoldi, C., 20
 Pfeffer, M., 20
 Pfenniger, M., 14
 Pilot, M., 20
 Plath, M., 14, 22, 23
 Poloczek, A., 20

 Pop, I.M., 16
 Potapov, S., 9
 Pradhan, N., 7
 Prins, H.H.T., 16

 Randi, E., 20
 Reiners, T. E., 15, 16, 17
 Reinhardt, I., 10
 Reynolds, S., 21
 Riaz, B., 15
 Richter, D., 14
 Riehm, J., 21
 Roos, C., 15
 Rössner, G.E., 5, 10, 17
 Ruhl, S., 21
 Ruiz Bustos, A., 17
 Rund, L., 11

 Saddi, A., 8
 Sajnbileg, D., 20
 Sallay, A., 16
 Samiya, R., 20
 Sánchez-Villagra, M.R., 13
 Saruulzargal, A., 20
 Sauer, S., 21
 Scandura, M., 11
 Schenck, C., 18
 Schepsky, P., 18
 Scherbaum-Heberer, C., 12, 18
 Schiessl, A., 23
 Schlegel, M., 21
 Schmidt, K., 6
 Schmidt, K.-H., 12, 18
 Schnitzler, A., 18
 Schook, L.B., 11
 Schotte, U., 21
 Schregel, J., 12
 Schrödl, M.-L., 23
 Schunke, A.C., 19
 Schvyreva, A.K., 19
 Shkvrya, M., 20
 Siemers, B., 13
 Smitz, N., 19
 Sodnomdarjaa, N., 20
 Sommer, R., 13
 Stefen, C., 19
 Stephens, P.A., 20
 Stepputis, B., 20
 Stevenson, P., 9
 Steyer, K., 15, 16
 Stronen, A.V., 20
 Stuermer, I.W., 20
 Suzuki, S., 12

 Tautz, D., 19
 Teifke, J.P., 21
 Tittmann, C., 20
 Troiani, N., 8
 Troxell, S., 13
 Tserennorov, D., 20
 Tsingarska, E., 20

 Ulrich, R.G., 21
 Van Den Hoek Ostende, L.W., 9
 Vatter, M., 21
 Veith, M., 18

Volmer, R., 21
Von Hardenberg, A., 7
Vonsamson-Himmelstjerna, G., 14

Wenzel, M., 8
Wilms, T., 18
Windler, R., 20
Woll, D., 20

Wörheide, G., 5, 10
Wronski, T., 14, 22
Wyrwoll, T.W., 22

Yirga, G., 22

Ziege, M., 22, 23
Zsebök, S., 13