

Contributions to the
**9th International Conference on Behaviour,
Physiology and Genetics of Wildlife**

18th – 21st September 2013, Berlin, Germany

Edited by

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Organised by

Leibniz Institute for Zoo and Wildlife Research (IZW)
Alfred-Kowalke-Straße 17
10315 Berlin
Germany

www.izw-berlin.de

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Executive Office
PO Box 20164
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ISSN 1865-4436

Published by

Leibniz Institute for Zoo and Wildlife Research (IZW)
Alfred-Kowalke-Str. 17, 10315 Berlin (Friedrichsfelde)
PO Box 700430, 10324 Berlin, Germany

Supported by

Deutsche Forschungsgemeinschaft (DFG) [German Research Foundation]
Kennedyallee 40, 53175 Bonn, Germany



Printed on Forest Stewardship Council certified paper

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Processing of abstracts:	Anke Schumann
Setting and layout:	Anke Schumann, Emil Knapschinsky, Jana Ehrhardt, Steven Seet
Cover photo:	African elephants, ©Jürgen Krause
Printing:	Spree Druck Berlin GmbH www.spreedruck.de
Order:	Leibniz Institute for Zoo and Wildlife Research (IZW); Forschungsverbund Berlin e.V. PO Box 700430, 10324 Berlin, Germany biblio@izw-berlin.de www.izw-berlin.de

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Foreword

This volume contains the contributions to the “9th International Conference on Behaviour, Physiology and Genetics of Wildlife”, a conference jointly organised by the Leibniz Institute for Zoo and Wildlife Research (IZW) Berlin and the European Association of Zoos and Aquaria (EAZA). This series of meetings brings together specialists from different disciplines and covers a variety of topics such as research on ecology, behaviour, stress and disturbance, reproduction biology, wildlife conservation and conservation genetics. The conference has developed a tradition of fostering an exchange of ideas and methods between scientists working with free-ranging and captive animals. A particular aim of the conference is to introduce participants to new methods and techniques developed within one discipline that may be very useful to answer questions in another.

The first section of this volume contains the abstracts of invited plenary speakers, followed by summaries of the seven workshops and the abstracts of introductory talks to workshops where appropriate. The main section contains the abstracts of submitted contributions. Contributions were invited for the following topics:

- Behavioural ecology
- Stress and disturbance
- Reproduction biology
- Conservation genetics
- Conservation biology
- Ecophysiology of wildlife
- Behavioural rhythms
- Urban wildlife ecology
- Using genetic tools for *ex situ* population management
- Making the best use of NGS (next-generation sequencing): difficult samples and/or loci

The abstracts in this volume are organised alphabetically by author name and were printed as submitted. To help you to find abstracts of interest we have included an index of first authors, a taxonomic index, and an index of keywords at the end of the volume.

We thank Anne Berger, Dagmar Boras, Martin Dehnhard, Marion L East, Joerns Fickel, Daniel Förster, Oliver P Höner, Katarina Jewgenow, Stephanie Kramer-Schadt, Kristin Leus, Gabriele Liebich, Karin Müller, Zjef Pereboom, Simone Sommer, and Christian C Voigt for all the assistance in the preparation of the conference and its scientific programme. We are very grateful to the workshop organisers as well as the many colleagues who have kindly reviewed all submitted contributions.

Berlin, September 2013

Sylvia Ortmann, Bettina Wachter, Anke Schumann, Steven Seet, and Heribert Hofer

PLENARIES

Is Mother Nature shortsighted?

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Popular accounts of evolution typically create an expectation that populations become ever better adapted over time, and some formal treatments of evolutionary processes suggest this too. However, such analyses do not highlight the fact that competition with conspecifics has negative population-level consequences too, particularly when individuals invest in success in zero-sum games. My own work is at the interface of theoretical biology and empirical data, and I will discuss several examples where an adaptive evolutionary process leads to something that appears silly from the population point of view, including a heightened risk of extinction in the Gouldian finch (*Erythrura gouldiae*), reduced productivity of species in which males do not participate in parental care, and deterministic extinction of local populations in systems that feature sexual parasitism.

Conserving adaptation and adapting conservation in a changing global environment

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The global environment is changing at a rate that is unmatched except for the one or few cataclysmic impacts of asteroids. This changes everything in how we do research on wildlife, how we conserve wildlife, and even what we mean by “wildlife”. Wildlife conservation can no longer be focused solely on the preservation of the products of evolution, but must protect also the processes of evolution. Biological research can no longer seek pure enlightenment of understanding the natural world, because the world which we seek to understand is being replaced by a different nature. At the same time, resource managers can no longer ignore basic scientists as mostly irrelevant, because predicting the responses of species and ecosystems to novel circumstances will have to come from theoretical and experimental investigations of complex mechanisms rather than from observations of past patterns. Conservation research can no longer be mostly field ecology, because the ecology of species depends critically also on responses that involve behaviour, genetics, and physiology.

Wildlife researchers cannot ignore the dramatic changes occurring to the environ-

ment. Previously contiguous populations are now scattered in small isolates. Therefore social systems and dispersal behaviours will often be maladaptive to the landscape in which they are found. The genetics of populations may reflect neither the past nor current population structure, but instead a transitional phase. The world is getting warmer, rainfall patterns are changing, and oceans are becoming more acidic. Therefore, many physiological responses to environmental cues will be mis-directed. The composition of new ecological communities may force us to replace studies of niche, stability, succession, and co-evolution with an ecological science of unstable interactions in artificial assemblages.

Wildlife conservation needs answers – fast – to many questions that stretch the prior limits of wildlife research. How quickly can species adapt? What promotes or hinders adaptation? What happens when species that did not co-evolve are tossed together? What is the role of gene flow between species in allowing rapid evolution? Gene flow and dispersal for most species are being disrupted by habitat fragmentation, but human transport of diseases, vectors, and invasive species is accelerating: What are the implications for metapopulation dynamics? How flexible are animal social systems? When can acclimation to new conditions overcome typical physiological responses? Making use of research on behaviour, physiology, and genetics to conserve wildlife will require integrated studies that reveal how impacts cascade through the interconnected components of complex systems.

The application of assisted reproductive technology to wildlife conservation

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A variety of assisted reproductive technologies (ART), mostly developed in livestock and humans, have been successfully applied to a diverse array of wildlife species (fauna and flora). However, the efficiencies have either been consistently low or highly variable, and that is due to a number of factors including: 1) the lack of knowledge regarding natural reproductive processes which hampers the development of methodologies to mimic appropriate conditions artificially; 2) the lack of compatible hormone/gonadotropin preparations to reliably induce folliculogenesis and ovulation to collect oocytes and/or embryos; 3) the species-specific differences in protocols for producing embryos *in vitro* and cryopreserving embryos and sperm; 4) the limitation in instrumentation designed for unique reproductive anatomies to perform artificial insemination and embryos transfer; and 5) the limited numbers of animals, resources and funding available to develop effective ART in wildlife. Nevertheless, ART has been clearly recognised to have a potentially vital role in wildlife conservation programmes by maintaining genetic diversity, particu-

larly when gametes and embryos can be cryopreserved for long-term storage, even when gametes are harvested *post-mortem*. It is also apparent, based mostly on livestock models, that ART can benefit future populations by eliminating certain infectious pathogens by using specific processing methods for embryos and semen. Several endangered amphibian species have been rescued from the global extinction crisis using ART, as well as a variety of endangered plants which were propagated *ex situ* and then returned back to their countries of origin. Relative to livestock and humans, however, ART is still considered to be novel and ineffective in most wildlife conservation programmes. Therefore, research should continue on developing basic methodologies for sperm and oocyte collections, *in vitro* embryo production and, for long-term benefit, sperm and embryo cryopreservation. More advanced reproductive technologies such as somatic cell nuclear transfer or induced pluripotent stem cells have been explored, but their application at this time is too premature to be considered as viable options for conserving endangered species. Rather, research efforts should continue on improving the success and reliability of basic procedures such as artificial insemination and embryo transfer if ART can ever truly be regarded as essential to prevent species extinctions.

The role of comparative phylogeography in the conservation of southern African taxa

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Southern Africa is home to at least three terrestrial biodiversity hotspots. By making use of phylogeographic patterns for multiple co-distributed taxa, it is possible to document regional genetic diversity. These data also provide an evolutionary context for the current patterns of diversity and are particularly valuable to explain the processes that generated biodiversity in the region. In concert these inferences present much needed baseline data for a more holistic approach to conservation. For example, barriers to dispersal have been identified in several mammalian, reptilian and some parasitic invertebrates and the location of the genetic breaks coincides with the current positions of the Orange River system and the Drakensberg Escarpment. The latter barrier system is of particular importance in conservation planning for the critically endangered riverine rabbit, *Bunolagus monticularis*. Through the use of molecular dating it is also possible to link the cause of the genetic patterns to distinct environmental features. It is well documented that the establishment of the Benguela current at the beginning of the Miocene resulted in the formation of a stable winter rainfall zone in the Cape Floristic region and this event also led to the establishment of the current day regional biomes. Comparative phylogeographic investigations also allow for the documentation of geographic regions characterised by high levels of genetic diversity. It is believed that these

regions represent evolutionary refugia that are maintained by climatic stability. Since it can be hypothesised that refugia can act as buffer to prevent extinctions, these regions are clearly of particular importance for the future persistence of species. By understanding the various processes involved in generating the biodiversity of Southern Africa, we are in a much better position to take appropriate conservation decisions. Since all of the phylogeographic inferences made are based on sound evolutionary theory, it is hoped that the outcome of these studies will ultimately contribute towards the conservation of the evolutionary potential of the majority of species in the region.

The power of poo: temporally-based physiological ecology

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While stress physiologists often try to separate stress into chronic or acute categories, this makes little sense when characterising stress in free ranging wildlife. Rarely does one stress occur in isolation in nature. Where there is one, there are many, and the stressors vary in intensity and occurrence over time. The challenge is to determine the relative impacts of these stressors and to tie them to their demographic consequences. Faeces provide an ideal vehicle to address these challenges because of its accessibility in the wild and the large number of physiological, genetic and toxicant measures that can be acquired from scats. We use detection dogs to locate scats with relatively high frequency from target species over large remote areas. We obtained multiple endocrine, diet and toxicant measures from genotyped samples collected over time, examining the physiological and reproductive response to simultaneously co-varying stressors. I will describe two case studies to illustrate these points, where we examine impacts of multiple pressures on killer whales (*Orcinus orca*) in the Salish Sea and caribou (*Rangifer tarandus*) in mid-winter in the Alberta Tar Sands (Canada).

WORKSHOP SUMMARIES

Workshop I: Cryopreservation of gametes and embryos for conservation breeding

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The knowledge on cell-, tissue-, individual- and species-specific constraints concerning the biophysical and biochemical challenges of cryopreservation in general and, in particular, for reproductive cells and tissues but is still very limited. Nevertheless, there are several efforts to cryopreserve valuable biological material with the prospect of future use in conservation, e. g. in a German cell bank for wildlife or a felid gamete rescue project. Cryopreservation of female germ cells of wildlife species is still the biggest challenge, although new approaches of preserving oocytes within ovarian cortex in combination with a (xeno)transplantation are promising. Despite retransplantation, different *in vitro* methods to evaluate the survival of intraovarian oocytes after thawing and culture are discussed. The optimisation of cryoprotocols for semen and embryos is a permanent need in those wildlife species where no experience exists so far, as reported for some rodent and avian species. Also, the lyophilisation of cells, its benefits and restrictions as a preservation technology, are introduced. Considering the fact that most samples are recruited under field conditions, the application of simple cryopreservation methods with low operating expense will be demonstrated.

Workshop II: Using genetic tools for *ex situ* population management

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The success of conservation breeding programmes often relies on intensive management of populations. However, management decisions are usually based on pedigree records, which are frequently incomplete or unreliable. Depending on the quality of a studbook, molecular information can substantially improve the knowledge of a population and contribute to improving the retention of genetic diversity. Fortunately, in recent years, molecular techniques and tools have become readily available to the conservation community, and relatively affordable. This

now opens up a huge range of possibilities for applied conservation genetics, more in particular for the use of molecular tools in the management of *ex situ* conservation breeding programmes. However, both within the zoo community and the conservation community, the proximity of this “Brave New World” seems to cause both excitement and dread, optimism and uncertainty. In this workshop we aim to illustrate how molecular tools can be used for the sustainable management of captive and wildlife populations, but also to introduce some of the opportunities and potential pitfalls, as well as “lessons learned”, both from a scientific and applied point of view, and both from the angle of a conservation scientist and a breeding programme manager.

Workshop III: Urban wildlife ecology

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Urban areas are rapidly increasing worldwide and lead to the transformation of habitat for wildlife. On the one hand, novel ecosystems may arise, e.g. by offering new food resources, while on the other hand the human-wildlife interface increases through habitat fragmentation and expansion of developed areas. These processes not only change the contact zones between humans and wildlife leading to human-wildlife conflicts, but also alter transmission pathways for zoonotic pathogens or emerging infectious diseases. It is therefore of paramount importance to understand the adaptive strategies of wildlife species to urban environments to contribute to a reasonable wildlife management. This workshop aims to provide an overview of current work done in the relatively young field of urban wildlife ecology by focusing on behavioural and physiological adaptations (movement behaviour and habitat selection, genetic structure, resource use) of wildlife to urban environments, stressors and selective pressures to wildlife in cities as well as on infectious diseases of wildlife at the human-wildlife interface.

Workshop IV: Ecophysiology of wildlife

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Ecophysiology studies both the adaptation an organism's physiology to environmental conditions and the reaction to changes in environmental conditions. Availability, assimilation and allocation of food and/or energy as well as the economical management of body reserves in times of food shortage is of vital importance for several aspects of the biology and life-history of animals. Among others body mass is an important factor that determines physiological responses and the adaptability of animals, and comparative analyses often make use of allometric relationships.

This workshop reviews various aspects of ecophysiology such as adaptation to seasonality, management of energy resources and energy reserves, acquisition and processing of food, and the relevance of allometry in wildlife species. Recent findings will be presented of research from field and laboratory studies and new techniques will be introduced, which hopefully stimulates discussion and encourages young scientists to work in this field.

Workshop V: Making the best use of NGS (next-generation sequencing): difficult samples and/or loci

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Advances made in DNA technologies over the past decade have transformed many biological disciplines. Initially it was mainly groups studying model organisms that benefitted most from these technologies. However, disciplines like conservation biology and molecular ecology did not lag behind too long, and these genomic tools are now leveraged for use with non-model organisms – organisms for which genomic data is largely absent or scarce.

In this context, studies will be presented that have adapted genomic tools and techniques to their non-model organism(s) of interest. It will also be discussed which techniques were adopted (or adapted) to prepare and/or modify genetic libraries for NGS, and the decision processes that were involved in choosing an appropriate sequencing platform. A further topic for discussion will be the bioinformatics pipelines used to analyse data.

Workshop VI: Conservation

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Human activities are causing serious degradation of habitats, alteration of ecological processes on a global scale and an alarmingly high rate of biodiversity loss. These detrimental processes seem set to increase in step with the growth in size of the human population and its rising demand for natural resources. Various methods aimed at preventing or minimise these detrimental processes have been implemented but their efficacy has rarely been vigorously assessed. During this workshop a variety of issues in conservation will be presented and the outcome of various conservation projects will be discussed.

Workshop VII: Behavioural rhythms

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The rhythmic organisation of behaviour is genetically controlled on the one hand and on the other hand modified by the actual living conditions of an organism. Thus, the analysis of rhythmic patterns provides insight into both basic ecological interrelations as well as individual adaptations. However, studies on the temporal behaviour of free running animals require special technical-methodological and analytic-theoretical skills.

The long-term and continuously measurement of behavioural parameters on freely moving animals and the analysing techniques of the data obtained are in the focus during the first part of the workshop. Subsequently, results from applied investigations on wildlife, zoo or laboratory animals will be presented and discussed as well as the enormous potential of eco-chronobiology to distinguish between normal behavioural patterns and those of diseased and stressed animals and, thus, for animal welfare and conservation research.

We invite participants to join the workshop to present and discuss new basic concepts or methods of temporal analysis and interpretation of behavioural data.

WORKSHOP INTRODUCTORY TALKS

Workshop III: Urban wildlife ecology

Urban carnivores: special challenges for uneasy neighbours

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Wildlife species vary in their responses to urban areas, with some avoiding urbanisation while others are synanthropic, in that they appear to thrive in urbanised landscapes. As a group, the Carnivora have been largely persecuted by humans, either for perceived or real conflicts, so it is not surprising that only 14 % of terrestrial Carnivora species are associated with urban areas (GEHRT *et al.*, 2010). Despite their association with urban areas, these 'urban carnivores' exhibit widely different responses to urbanisation. Cross-species comparisons reveal that body size and dietary breadth are two parameters that largely explain whether carnivore species are urban residents or urban transients (IOSSA *et al.*, 2010). Mesocarnivores (1 - 15 kg) with omnivorous diets tend to be residents, whereas larger carnivores tend to be transients. However, even among urban resident species, there are substantial variations in response to urbanisation, such that some urban populations are sources, others are sinks, and others are remnants (BATEMAN and FLEMING, 2012). As a case study of the complexities of synanthropy, we present results from a long-term study of the urban ecology of coyotes (*Canis latrans*) in the Chicago metropolitan area, a species traditionally considered an icon of wilderness. Local population densities and reproductive rates of urban coyotes were slightly higher, and survival rates for pups were five times higher compared to rural populations (GEHRT *et al.*, 2011). In contrast to demographic patterns, behavioural responses to urbanisation, including home range size, avoidance of urban land cover, activity budget, and diet, were not consistent with synanthropy, even for coyotes located in the urban matrix (GEHRT *et al.*, 2009, 2011). The success of coyotes in the Chicago area has had important ecological effects as well as challenges for human-wildlife conflicts. As urbanisation continues to have a significant imprint on landscapes worldwide, the story of urban carnivores is evolving, and they continue to exhibit considerable variety in their relationships to urbanisation.

BATEMAN PW, FLEMING PA (2012): Big city life: carnivores in urban environments. *J Zool* **287**, 1 - 23.

GEHRT SD, ANCHOR C, WHITE LA (2009): Home range and landscape use of coyotes in a major metropolitan landscape: conflict or coexistence? *J Mammal* **90**, 1045 - 1057.

- GEHRT SD, RILEY SPD, CYPHER BL (2010): Urban Carnivores: Ecology, Conflict, and Conservation. The Johns Hopkins University Press, Baltimore, MD.
- GEHRT SD, ANCHOR C, BROWN JL (2011): Is the urban coyote a misanthropic synanthrope? The case from Chicago. *Cities and the Environment* 4:Iss 1, Article 3 (online journal: <http://digitalcommons.lmu.edu/cate/vol4/iss1/3>).
- IOSSA G, SOULSBURY CD, BAKER PJ, HARRIS S (2010): A Taxonomic Analysis of Urban Carnivore Ecology Coyotes (*Canis latrans*). Pages 173 - 180 in: *Urban Carnivores: Ecology, Conflict, and Conservation*. (GEHRT SD, RILEY SPD, CYPHER BL, editors). The Johns Hopkins University Press, Baltimore, MD.

Workshop IV: Ecophysiology of Wildlife

The art of allometry: relevance, functional logic and evolutionary history in comparative analyses

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Comparative analyses of datasets that comprise anatomical, physiological or life history characteristics of large numbers of animal species are widespread in life sciences. The scaling of many of such characteristics with body mass in a non-linear (i.e., ‘allo-metric’) pattern is often considered akin to a ‘natural law’, is the foundation of macroecological theory such as the Metabolic Theory of Ecology (SIBLY *et al.*, 2012), and is used to explain species diversification and niche differentiation along the body size axis. A classical example is the presumed increase of digestive efficiency with increasing body mass in herbivores, as part of the so-called ‘Jarman-Bell principle’ (MÜLLER *et al.*, 2013).

Analyses of comparative datasets can be subject to a variety of fallacies. Although the use of comparative methods that account for the effect of phylogeny in such analyses has been advocated for a long time (HARVEY and PAGEL, 1991), their application to comparative datasets can still generate surprising insights. Examples from digestive physiology and from life history do not only show that empirical data can drastically deviate from classic ‘allometric rules’, but that conceptual (and mathematical) problems in deriving or interpreting allometries are easily overlooked.

A typical pattern in such datasets is a similarity in the scaling exponent but a difference in intercept between phylogenetic groups (such as the similar scaling of energy requirements in mammals and reptiles, but at different absolute levels). Such differences in the intercept are usually interpreted as different ‘lifestyles’ or adaptations to different niches (SIBLY and BROWN, 2007). Using examples from digestive physiology and life history, I advocate that under certain conditions, such differences in intercept can rather reflect sequences of ‘key innovations’.

MÜLLER DWH, CODRON D, MELORO C, MUNN AJ, SCHWARM A, HUMMEL J, CLAUSS M (2013): Assessing the Jarman-Bell Principle: scaling of intake, digestibility, retention time and gut fill with body mass in mammalian herbivores. *Comp Biochem Physiol A* **164**, 129 - 140.

HARVEY PH, PAGEL MD (1991): *The comparative method in evolutionary biology*. Oxford University Press, Oxford, UK.

SIBLY RM, BROWN JH (2007): Effects of body size and lifestyle on evolution of mammal life histories. *PNAS* **104**, 17707 - 17712.

SIBLY RM, BROWN JH, KODRIC-BROWN A (2012): *Metabolic ecology. A scaling approach*. Wiley-Blackwell, Chichester, UK.

Workshop V: Making the best use of NGS (next-generation sequencing): difficult samples and/or loci

A brief introduction to the trials and tribulations of studying non-model organisms using NGS (next-generation sequencing)

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Model organisms represented a critical resource in the establishment and development of next-generation sequencing (NGS) technologies. And these models are still the go-to species when advancing methodologies. While they have attributes that make them favourable for these tasks – e.g. genetic uniformity, ease of laboratory breeding – they frequently lack the interesting traits that drive our desire to understand the biological diversity in nature. In other words, we often have to turn to non-model organisms when it comes to answering specific evolutionary and ecological questions.

NGS approaches are now sufficiently refined, and their costs no longer as prohibitive, so that they are used more and more commonly in research involving non-model organisms and wild populations (both extant and extinct). While many of the early promises of NGS are still out of our grasp – e.g. whole genome based phylogenies, environmental sequencing, deciphering the genetic basis for behaviour – others are in easier reach. For example, multiple approaches have been developed to screen many individuals at multiple (100s - 10000s) markers without the need for a reference genome; targeted candidate gene sequencing can be used to identify allelic variation underlying important processes (e.g. immune competence) or to investigate phylogeography and historical demography; screening of SNPs in ancient (>10 ky old) samples can be used to determine phenotypes of these historic animals; environmental samples can be used to track the transmission of diseases; the epidemiological status and co-infections of individuals can be determined by screening their microbiome and virome; just to name a few.

Thus, this introduction will give a short overview over both the most common NGS sequencing platforms as well as the common hurdles researchers will likely face when working with such non-model organisms – with a particular focus on approaches employed to deal with difficult samples and/or loci.

CONTRIBUTED PAPERS

Analysis of distribution of genetic lineages of African rodents – DNA barcoding using next-generation sequencing and museum samples

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DNA barcoding allowed the genetic identification of organisms based on short sequence of DNA. In last years this method has been boosted by continuing advances in sequencing technology. The so-called next-generation sequencing (NGS) delivers massive amount of DNA sequences at a reasonable cost and level of effort. In our study, we used 454 pyrosequencing to genotype ancient DNA (including type material) with the aim to analyse the distributional pattern of genetic lineages of rodents in Eastern Africa. Rodents are very suitable model organisms for phylogeographical study, but material from inaccessible areas is often limited only to old museum collections. The collections of African rodents from museums in Paris (MHNM) and Tervuren (RMCA) provided unique material from large geographical area, including localities that are not feasible to sample today. Even if the DNA was often degraded, minibarcoding based on 136 bp fragment of mitochondrial gene of cytochrome *b* was confirmed as appropriate approach, because it allowed the assignment of museum samples to previously described genetic lineages. Massive parallel sequencing was also able to successfully overcome the contamination by non-rodent DNA.

Reproductive success of wild female common hamster (*Cricetus cricetus*)

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The common hamster (*Cricetus cricetus*) is a typical r-strategist, which is able to reproduce three times in a single active season (FRANCESCHINI and MILLESI, 2005; HARPENSLAGER *et al.*, 2011) with litter sizes up to 11 (WEINHOLD and KAYSER, 2006). Despite this high reproductive potential, its populations in Western Europe are critically endangered. Although reproductive success plays a major role in terms of population dynamics and stability (ULBRICH and KAYSER, 2004), no detailed information on reproductive success in wild hamster populations exist to date for the endangered western populations. Therefore we investigated reproductive success of 17 wild female common hamsters in two wild populations in central Germany. We located females during the whole active season using radio telemetry. Reproductive timing, litter size and offspring development were documented using an automatically controlled device. This device integrates a RFID reader, a weighting scale and video camera. Since the first emergence of juveniles at the natal burrows in mid-June number of juveniles and individual weight were recorded. Litter sizes ranged from 2 to 6. Body mass of juveniles increased about 5 g per day. In comparison to breeding programs, the animals in the study populations exhibit a steeper increase of weight. This may also have important consequences for population dynamics as sexual maturity is reached within a shorter period. In this study we assembled basic data on reproduction of wild hamsters, which now can be compared to findings in conservation, breeding and reintroduction programmes.

FRANCESCHINI C, MILLESI E (2005): Reproductive timing and success in common hamsters. Proceedings of the International Hamsterworkgroup 63 - 66.

HARPENSLAGER SF, LA HAYE MJJ, VAN KATS RJM, MÜSKENS GJDM (2011): Reproduction of female common hamsters (*Cricetus Cricetus*) in Limburg, the Netherlands. Säugetierkd Info **8**, 131 - 138.

ULBRICH K, KAYSER A (2004): A risk analysis for the common hamster (*Cricetus cricetus*). Biol Conserv **117**, 263 - 270.

WEINHOLD U, KAYSER A (2006): Der Feldhamster. Die neue Brehm-Bücherei Bd. 625., Westarp Wissenschaften, Hohenwarsleben.

Assessment of immuno-physiological status of females during offspring growth in domestic cat (*Felis catus*)

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The period of the highest costs for mammalian females is related to lactation and offspring growth, particularly in species with long-term parental care. Reallocation of organism's resources processing in this period can result in significant metabolic stress and loss of immunity. The aim of this study was to estimate immuno-physiological state of females during lactation in domestic cat and to compare it with their litter size.

The study was conducted at the experimental station "Tchernogolovka" of IEE RAS in 2011 and 2012. The objects of study were six females of domestic cat with their litters. We collected blood samples and weighed animals during pregnancy and lactation. The clinical blood analysis was estimated on the automatic hemoanalyser Abacus junior vet 1.22 (Diatron Messtechnik GmbH, Austria). The percentage of different leucocytes' types on the blood smears was counted with microscope Leica DM5000 B (Leica Microsystems Ltd., Switzerland). The cortisol concentration and antibodies concentration to feline panleukopenia virus (FPV) were measured with EIA analysis.

All physiological parameters such as number of white blood cells (WBC), ratio of neutrophils to lymphocytes (N:L) and body mass of females changed significantly in females from parturition to ten weeks of lactation (Friedman ANOVA: $N = 6$, $df = 8$, $T = 19.78 - 27.12$, $p < 0.05$), except cortisol concentration (Friedman ANOVA: $N = 6$, $df = 8$, $T = 8.53$, ns). Cortisol level, WBC number and N:L reached the greatest values (221.20 ± 67.43 ng/ml, $24.34 \pm 3.61 \times 10^9/l$ and 2.48 ± 0.48 accordingly) while body mass was the lowest (3.10 ± 0.12 kg) at the seventh week of lactation when kittens have already eaten solid food. Body mass rose (3.33 ± 0.11 kg) and cortisol level, WBC number, N:L decreased significantly (185.02 ± 92.18 ng/ml, $19.91 \pm 3.11 \times 10^9/l$ and 1.41 ± 0.13 accordingly) to the tenth week of lactation (Wilcoxon matched pairs test: $N = 6$, $Z = 1.99$, $p < 0.05$). All lactating females showed humoral immune response to FPV vaccine comparable with adult males and non-reproducing females and it increased significantly in 23 days after vaccination fivefold (Wilcoxon matched pairs test: $N = 6$, $Z = 1.99$, $p < 0.05$). Moreover, in lactating females, antibodies concentration at vaccination point was twofold lower than in non-breeding females.

Thus, our data indicates that the maximal metabolic stress in lactating females is related to one and a half months of lactation that result in some exhaustion of their organisms. Right after ten weeks of lactation physiological characteristics of females comes to normal levels.

This study was supported by grants of RFBR № 13-04-01465.

Comparative physiological and molecular study of some sheep breeds in Saudi Arabia

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The Arabian sheep *Ovis aries* was subjected to a comparative isoenzymatic and mitogenomic investigation for the first time. Naemi, Heri, Najdi and Sawakni sheep breeds inhabiting the Kingdom of Saudi Arabia were studied physiologically and molecularly. Native polyacrylamide gel-electrophoreses for the two enzymes malate dehydrogenase (Mdh) and malic enzyme recorded five isoenzyme loci from which four were polymorphic and one was monomorphic. Mdh showed three fractions, the first was recorded in Sawakni and Najdi breeds while the second and the third fractions were recorded in all except Heri. Malic enzyme showed two polymorphic fractions, the second was recorded in all breeds while the first was recorded in Heri and Naemi. Both metabolic enzymes were higher in Sawakni than in the native Saudi breeds. Nucleotides of 607 bp, 227 bp, 498 bp and 595 bp from CO1, ND4, cytb genes and d-loop, respectively, were sequenced. Base substitutions among and within breeds were detected for ND4 gene and the d-loop but not for CO1 and cytb genes. The molecular tree clustered the three breeds other than Naemi in one group and Naemi was basal. Therefore, isoenzymes discriminate clearly among the studied breeds although they are not as accurate as molecular tools. This indicates that their applicability was more efficient in physiology than in genetics while the d-loop was efficient in discriminating the studied breeds phenotypically.

AL-HARBI MS, AMER SAM (2012): Preliminary comparative physiological and biochemical study of five different goat breeds inhabiting Saudi Arabia. *Nat Res* **3** (4), 206 - 212.

HIENDLEDER S, LEWALSKI H, WASSMUTH R, JANKE A (1998): The complete mitochondrial DNA sequence of the domestic sheep (*Ovis aries*) and comparison with the other major Ovine haplotype. *J Mol Evol* **47**, 441 - 448.

LALIOTIS GP, BIZELIS I, ROGDAKIS E (2010): Comparative approach of the de novo fatty acid synthesis (Lipogenesis) between ruminant and non ruminant mammalian species: From biochemical level to the main regulatory lipogenic genes. *Cur Genom* **11**, 168 - 183.

From formation to maintenance of luteal tissue – different hormonal and histological profiles of *corpus luteum* in felids

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Formed from residual follicular cells after ovulation, *corpus luteum* (CL) is known to be a key player in pregnancy maintenance. And while the secretion of progesterone is a common characteristic of this gland for all mammals, there are undoubtedly variations in luteal structure and function among different species. To characterise the individual luteal profiles inside the *Felidae*, we performed histological and hormonal analyses of the CL in Iberian lynx (*Lynx pardinus*), lion (*Panthera leo*) and tiger (*Panthera tigris*), in comparison to domestic cat (*Felis catus*). Intraluteal levels of progesterone (P4) and oestradiol (E2) were measured with ELISA. Histomorphology of the CL was visualised by Hematoxylin and Eosin staining.

In Iberian lynx, the intraluteal P4 levels remained comparable from the CL formation [8.4-29.1 µg/g] to its state of maintenance [10 - 19.1 µg/g]. While E2 showed extremely elevated levels on the 7th day after natural mating [2274.1 - 7254.6 ng/g] and dropped down notably with the progression of luteal stage [61.6 - 356.1 ng/g]. This elevation however was not reflected in serum concentrations, proposing the local effect of E2. Indeed, the performed immunohistochemistry for oestrogen receptors showed high receptivity of the CL tissue during formation. The histomorphology of the Iberian lynx CL during maintenance is distinguished by large luteal cells that often appear binuclear. The formation process is comparable to that of domestic cat CL, showing the tissue remodelling with former follicular cells intermixing and undergoing luteinisation. The P4 levels were already visibly high one day after induced ovulation in lion [58.5 - 143.4 µg/g], while the E2 concentrations appeared low [11.7 - 38.8 ng/g] in relation to domestic cat. Expanded vascularisation of the CL was detected by histology, showing prominent vessels occupying large areas between forming luteal cells. These findings suggest more rapid changes in E2/P4 concentrations and vascularisation in lion compared to domestic cat. Almost basal levels of P4 [0.08 µg/g] were noted in tiger during morphologically maintained CL, accompanied by low concentrations of E2 [7.1 ng/g]. The histological analysis detected first signs of luteal degradation as based on domestic cat description - coarse vacuolisation beginning to spread among the tissue, nuclei deforming and cells losing their fine polyhedral structure. In conclusion, our results show and describe high variations in luteal profiles inside the *Felidae*, supporting the individual reproductive approach for each member of this family.

Cryopreservation of Campbell's dwarf hamster embryos as a model for exotic hamster species cryobanking

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Genome Resource Bank (GRB) at the Institute of Cytology and Genetics was established to maintain biodiversity of laboratory, exotic and wildlife species. Along with cryobanking mice and rats, the embryos of exotic hamster species belonging to *Phodopus* genus (*P. campbelli* and *P. sungorus*) were successfully frozen and stored in our GRB. To obtain hamster (*Phodopus*) embryos, the females were mated with conspecific males and humanely killed by cervical dislocation on Day 3 of their pregnancy (presence of spermatozoa in the vaginal smears indicated Day 1 of pregnancy). Uteri and oviducts were removed and flushed with Complete Ultra Flushing Solution (EMCARE, ICPBio Reproduction, USA). Different protocols for embryo freezing and thawing were applied and tested in mice (ICR strain) and Campbell's dwarf hamster (*P. campbelli*). Ethylene Glycol (EG, 1.5 M) was used either as a single cryoprotectant or in a mixture with sucrose 0.1 M. Freezing was performed using a programmable freezer (CL 8800, CryoLogic, Australia) and 0.25mL straws (Cryo Bio System, France): 18 °C to -7 °C with -1 °C/min; hold for 10 min at -7 °C, manual seeding; from -7 °C to -35 °C with -0.3 °C/min; hold for 10 min at -35 °C; transfer to liquid nitrogen. A slow-thawing method (40 sec at RT, followed by 40 sec in a water bath of 30.0 °C) was compared with a rapid-thawing method (10 sec in a water bath of 37 °C). After cryopreservation the embryos were evaluated by fluorescein diacetate/propidium iodide double staining under a fluorescent microscope (Leica M205FA Microsystems, Germany). The other group of frozen/thawed embryos was cultured *in vitro* for 48 hours under mineral oil at 37 °C in 5 % CO₂ with the use of modified embryo culture medium for hamsters and M16 (Sigma) medium for mice. To our knowledge, this is the first successful attempt of *Phodopus* embryos cryobanking and *in vitro* culturing. Viability of embryos of both species thawed by slow method was not different from viability after rapid thawing. However, microscopic observation indicated that slow thawing is beneficial for the integrity of the *zona pellucida* in both species. Adding sucrose to cryoprotectant solution improved the survival rates from 53.6 ± 13.3 to 89.2 ± 5.5 in hamsters and from 71.0 ± 9.0 to 90.5 ± 9.5 in mice, respectively. Our data suggest that the programmed freezing of preimplantation embryos using EG + sucrose and slow thawing may be considered as a method of choice for rodent species including hamsters of the *Phodopus* genus.

Urban Earthworm Project

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There is hardly need to make a case for studying earthworms, as their role within the soil ecosystem has been recognised for more than a century. Earthworms positively affect soil structure development, recycle significant amounts of organic matter, and form a vital component within many food webs. Global earthworm diversity is estimated to 3,000 species and about 25 native species of earthworms live in Belgium. Earthworms inhabit a wide variety of habitats, including habitats with rather extreme environmental conditions, however, species demonstrate different responses to abiotic factors and environmental disturbances. Consequently, earthworm diversity, abundance, and biomass have been considered to be convenient indicators to assess soil fertility, site quality and the impact of land use.

While being vital components of the soil ecosystem, earthworms in urban environments may face harsh living conditions, including limited space, physical isolation, highly disturbed, compacted and/or contaminated soils, and reduced availability of water and organic material. In this study we will screen different urban soils for their earthworm communities, as a first step in gathering baseline information for using earthworms in urban soil quality assessment. We will put forward several research hypotheses to gain insights into fundamental questions relating to urban ecology and earthworms, which can be examined by using non-expensive, low-technology methods. The simple research techniques in combination with the relatively easy taxonomic identification of earthworms allow for reaching a broad public, including children, and involving them as (temporary) participators in urban ecology research.

Experimental reduction in parasite intensity in the context of disease tolerance

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Understanding how organisms protect themselves from infectious diseases is a major question in ecoimmunology and evolutionary parasitology. Besides the well-known role of the immune system protecting organisms from infections, the defense strategy may also rely on the organism's ability to tolerate the presence of the pathogen. This dichotomy between disease resistance and disease tolerance has been largely overlooked in animal studies and is becoming the focus of an increasing number of studies in the recent years. We used naturally infected blackcaps *Sylvia atricapilla*, as a model system to identify physiological parameters involved in disease tolerance, and test predictions about interactions between resistance and tolerance. We treated a group of birds with an anti-malaria drug (primaquine) to experimentally reduce intensity of infection and thus emulate the role of the immune system reducing parasite intensity. Our results indicate that the experimental treatment successfully reduced intensity of infection by *Haemoproteus* sp. We will present the results concerning variation in parameters likely involved in disease tolerance such as acute phase proteins (haptoglobin), and in parameters involved in resistance such as immunoglobulin levels and leukocyte profiles.

Sexual selection and extinction in deer

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By performing a comparative analysis and using phylogenetic relationships of the Cervidae family this study aimed to address whether or not sexual selection may play a role in the extinction of species by making species more vulnerable to extinction. The role of sexual selection in making species more vulnerable to extinction is largely unexplored, and several factors such as ecological and life history traits may increase the risk of extinction.

In all species of the family Cervidae (GILBERT *et al.*, 2006; GEIST, 1998; GROVES and GRUBB, 2011; PRICE *et al.*, 2005) sexually selected characters plays a main role in determining species status and thus potentially their probability of extinction. In this study the intensity of sexual selection (measured as sexual size dimorphism, antler size and mating system) and the rate of extinction (IUCN classification and anthropogenic effect) were counted as factors to determine the role of sexual selection intensity in both species-rich and species-poor clades.

By using the programme MESQUITE and phylogenetic trees, the results show an association between species with larger body size and dimorphism, living in open habitats and having larger antler size expanded to more than three tines; such species are mostly non-territorial and form harems during the rutting season. The small species are territorial, live in closed habitats, are monomorphic and have small antler size limited to two tines or less. Moreover species that are more subjected to habitat degradation and anthropogenic effects tend to become smaller in size.

Extinction risk for the species-rich clades with small sized, territorial and small antler sized species is lower than for those consisting of species with larger antler size, larger body size, living in open habitats and using harems as mating system.

GILBERT C, ROPIQUET A, HASSANIN A (2006): Mitochondrial and nuclear phylogenies of Cervidae (*Mammalia, Ruminantia*): Systematics, morphology, and biogeography. *Mol Phylogenet Evol* **40**, 101 – 117.

GEIST V (1998): *Deer of the World: Their Evolution, Behaviour, and Ecology*. Stackpole Books, Mechanicsburg, PA. pp. 119 - 121.

GROVES C, RUBB P (2011): *Ungulate Taxonomy*. JHU Press. Johns Hopkins University press., Baltimore, ML

PRICE SA, BININDA-EMONDS ORP, GITTLEMAN JL (2005): A complete phylogeny of the whales, dolphins and even-toed hoofed mammals (*Cetartiodactyla*). *Biol Rev* **80**, 445 - 473.

Faecal glucocorticoid metabolite measurements in spectacled bears (*Tremarctos ornatus*) - validation and monitoring

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To measure stress in wild and zoo animals, monitoring faecal glucocorticoid metabolites (fGM) is a widely recognised non-invasive method for many species. Despite the great demand to assess stress in spectacled bears there are so far no procedures validated for this species. To achieve a reliable method the laboratory process had to be analysed and a challenge test had to be set up as available for other species (TOUMA and PALME, 2005; WASSER *et al.*, 2000).

Faeces of 13 bears (5 male, 8 female; 3 – 32 years old) housed in five German zoos were collected weekly and stored at -20 °C until processing. After thawing the samples were extracted with methanol and analysed using radioimmunoassays. Following parallelism, recovery and inter-assay and intra-assay coefficients were determined. During a twelve-day stress provocation test, faecal samples were collected daily and an artificial stressful event was set up at day six to test whether stress causes increased faecal glucocorticoid metabolite levels.

Parameters for validation of the laboratory process showed that our radioimmunoassay provides reproducible and reliable values for the fGM-content of the analysed samples. The minimum detection limit of the assay is 0.176 ng/g faeces. Serial dilutions revealed dilution coefficients of 57.9 ± 4.3 % and the determined recovery is 93 %. Inter-assay and intra-assay coefficients were around 12 %. The stress-provocation test induced increased fGM concentrations two- to threefold after the intervention and documented that these procedures can be used to detect stressful situations.

Using non-invasive methods to identify stress in spectacled bears gives great opportunity to improve knowledge about their physiology and pathology under human care as well as free-ranging. Possible fields of application can be investigations about habitat changes or the Spectacled Bear Alopecia Syndrome.

TOUMA C, PALME R (2005): Measuring fecal glucocorticoid metabolites in mammals and birds: The importance of validation; *Ann NY Acad Sci* **1046**, 54 - 74.

WASSER SK, HUNT KE, BROWN JL, COOPER K, CROCKETT CM, BECHERT U, MILLSPAUGH JJ, LARSON S, MONFORT SL (2000): A generalized fecal glucocorticoid assay for use in a diverse array of non-domestic mammalian and avian species. *Gen Comp Endocr* **120**, 260 - 275.

Balancing the need to feed and the urge to breed

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Bats use behavioural (change in activity patterns or in ingested energy) and physiological (torpor, metabolic compensation, and/or variability in digestive efficiency), mutually nonexclusive mechanisms to balance their energy budget. As small and actively flying mammals, bats have a high (mass-specific) energy demand relative to body mass; therefore, balancing mechanisms should be pronounced in this group. Since the energy budgets of bats exhibit seasonal changes, the combination and use of different mechanisms could vary during times of high and low energy demand. Using a combination of flow-through respirometry, temperature telemetry and behavioural observations in free-flying bats, we found that male *Myotis daubentonii* exhibited marked variation in the relative importance of these different mechanisms during their period of seasonal activity in response to extrinsic (ambient temperature, insect abundance) and intrinsic (reproduction, body condition) factors. Cold ambient temperatures in spring facilitated long and frequent daily torpor bouts, whereas in early summer increased energy intake was the dominant factor in energy balancing. Intake was further increased in late summer, when insect abundance was highest, and daily torpor bouts were shorter and less frequent than in early summer. In autumn, males used metabolic compensation to reduce their resting metabolic rate in addition to daily torpor. Metabolic compensation might be one of the mechanisms that allow males to maintain high body temperature during the day while decreasing the need for foraging time at night, thus maximising their opportunities to mate.

Sibling rivalry and hunger increase allostatic load in spotted hyaena twin litters

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Spotted hyaena (*Crocuta crocuta*) cubs are entirely dependent on and intensively compete for highly nutritious maternal milk in twin litters. In our study site in the Serengeti National Park in Tanzania, regular long-distance foraging excursions by mothers to distant migratory herds profoundly affect the frequency of maternal nursing visits and hence the amount of milk transferred to offspring. Dominance between twin siblings emerges during early competition for milk and involves trained winner and loser effects. Conflict declines with age as behavioural dominance conventions are established. Cortisol mobilises energy and helps animals adapt to environmental and social challenges but reduces health, cognition or reproduction if chronically elevated. Allostatic load represents the cumulative energetic cost of such challenges to the body. We investigated the effects of (1) hunger, (2) within-litter dominance status, (3) age and (4) sex on the allostatic load in terms of faecal cortisol metabolites of both dominant and subordinate siblings in twin litters.

We collected 175 faecal samples from 77 cubs and measured their levels of faecal cortisol metabolites with a previously validated enzyme immunoassay. We found that when maternal nursing visits were rare, both dominants and subordinates had significantly higher levels of faecal cortisol metabolites than when regularly nursed. Young (< 6 months of age) subordinate siblings had higher concentrations of faecal cortisol metabolites than dominant siblings, indicating a higher allostatic load in subordinates than in dominants in the first months of life. Hungry subordinates competing against a dominant sister are particularly assertive. We found that dominants sisters had higher faecal cortisol metabolite concentrations than dominants brothers.

Hunger, trained loser effects and conflict for milk thus increased allostatic load in spotted hyaena twin litters. As elevated cortisol concentrations indicate elevated energy expenditure for the maintenance of homeostasis, early sibling conflict could imply costly long-term consequences in adult life.

The use of long-term and continuous acceleration or temperature measurements in wildlife research

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Modern wildlife collars are commonly used to obtain regular GPS location of animals, thereby providing information on home range size and migration paths. In most studies, only few GPS fixes per day are collected due to the considerable amount of energy GPS fixes need. In contrast, measurements of acceleration or temperature data need little energy, allowing a virtually continuous monitoring of animals.

Nowadays, wildlife research is quickly moving from monitoring animals with one single sensor, usually a GPS receiver, to using multiple, integrated sensors that register spatial (i.e. GPS positions) and non-spatial measurements such as acceleration or temperature. In an overview I will specify the relevance of these kinds of data for answering questions of wildlife research and management, and I will present the potential of continuously measured acceleration data analysis for drawing conclusions to the animals' behaviour.

Firstly I will introduce a procedure for biorhythmic status diagnosis to identify systemic disorders and "stress loads" in wild animals by changes in total daily activity and in day- night relationships as well as a reduced coupling between the behavioural rhythm and the diurnal environmental periodicity. Secondly, we will focus on the development of analysis methods to distinguish between several behaviours (e.g. resting, calving, hunting) by detecting locomotion and activity patterns. Detailed knowledge about what an animal is doing at what time and place is crucial for understanding both, the habitat use of undisturbed animals and for detecting deviations from the norm, e.g. diseases or responses to disturbances or predators.

Furthermore, additional extra-corporal temperature sensors may provide valuable information about close environmental conditions, e.g. ambient temperature, the animal is exposed to. Although these extra-corporal sensors are in some respects affected by the radiation of the sun and the heat of the animals' body, they can provide high-resolution information about the individual thermoregulatory behaviour (i.e. active cooling or sunbathing) and about the ambient temperature. Finally, continuous information about ambient temperature can be related to the spatial position of the animal and provides new opportunity to connect temporal-spatial behaviour of wildlife with climate conditions.

All information of an investigated animal summarised, one can create home-range maps that additionally provide significant information about positions or habitats where certain behaviours – such as resting, calving or feeding - are preferred (functional habitat maps).

The new urban ecology project: European hedgehogs (*Erinaceus europaeus*) in Berlin

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European hedgehogs (*Erinaceus europaeus*) are solitary insectivores and are in Germany protected by law. They are not only found in rural landscapes but also in urban areas of large cities like Berlin with 3.3 million inhabitants. We want introduce the research project “Hedgehogs in Berlin” aiming to examine the distribution of hedgehogs adapted to the urban conditions in their behaviour and life-history strategies.

In this project, we will conduct a long term and comprehensive collection of population data (including kinship analyses) of hedgehogs in Berlin by public enquiries (citizen science) as well as by own data acquisition. In five different study areas that differ in habitat structure and the level of human interference, we will evaluate the population density, the body condition, food availability, reproductive output, mortality causes, parasite loads, and hibernation behaviour of several individual hedgehogs on a long-term scale. Using VHF-transmitters on some individuals we will track the detailed path to get information on habitat use and home range sizes under different conditions. We are planning to investigate the hedgehogs’ hibernation behaviour in response to the warmer urban climate by means of computer tomography and implanted thermal and activity sensors in different climate chambers. The data will give insights into the physiological and behavioural adaptations of the European hedgehog in urban environments.

The project started in summer 2013 with a “Berlin hedgehog workshop” at the IZW and is in close dialogue with Berlin authorities, registered associations and different stakeholders.

The results will be used to enhance objectivity in sometimes emotionally loaded conflicts between different stakeholders and create a synthesis between conservation and urban development and may be used to develop conservation measures and strategies and to provide guidelines for future concepts of structuring urban areas.

Behavioural analysis of captive tigers (*Panthera tigris*) under different zoo managements: preliminary data

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Activity budgets of seven captive tigers (*Panthera tigris*), housed in four different zoological gardens (A, B, C, D), were analysed in order to recognise signs of stress or of good welfare related with enclosure type, management and animal background. A and B were traditional zoos, C and D safari parks. All animals, but one, were housed in pairs.

An instantaneous focal animal sampling was used to record behaviours with an interval of two minutes. An ethogram of 40 behaviours was adapted from literature. Data were collected by five observers. Before beginning the study, the observers reached a within-observer reliability ranging from 0.72 (CI95 %: 0.54–0.9) to 1 (CI95 %: 0.82-1) and a between-observer reliability of 0.95 (CI95 %: 0.9-1). Each institution was visited five times from April 2012 to October 2012 and observations were taken when the animals were on exhibition. To process data, activity budgets were constructed. The behaviours were then categorised into neutral, signs of stress, and signs of good welfare, according to previous literature. A multinomial logistic regression model was carried out.

Over 195 hours of data were collected and an amount of 5,867 observations were recorded. Overall finding was that tigers spent most of their time sleeping (28.14 %). In addition to that, the most frequently occurring behaviours were walking (14.91 %) and resting with open eyes (14.15 %). Active time, considered as the time when the tigers were neither sleeping nor resting, was 45.03 %. All tigers were engaged in pacing only for a small amount of time (0.37 %).

The preliminary data analysis suggests that tigers, subject of this study, do not display consistent signs of stress (i.e. pacing). Tigers housed in zoos have a higher probability to display behavioural signs of good welfare than the ones housed in safari parks, suggesting that welfare status seems better in animals housed in traditional zoos than in safari parks.

Further analysis is required to identify which daily routine aspects of the animals and/or enclosure features have most influence on welfare status of captive tigers. In addition the spread of participation index will be calculated to assess enclosure use by the animals and to highlight potential effects of enclosure design on welfare of tigers.

Space use patterns of red foxes (*Vulpes vulpes*) in settlement area

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The aim of the present study was to investigate activity ranges and movement patterns of red foxes related to a village (size: 40 ha). The study was carried out in the federal state Brandenburg, 20 km northeast of Berlin. Thirteen Foxes were caught within a distance of up to 500 m around the village and equipped with radio collars. Their spatial behaviour was analysed with particular emphasis on the settlement area.

We observed differences in space use of foxes and distinguished three types of spatial behaviour:

- (1) Foxes (“shifter”) using the transition zone between urban and rural areas. The settlement was only used for foraging.
- (2) Foxes (“commuter”) with two separate residence areas roaming between the rural and the urban area which was only used for foraging.
- (3) Foxes (“village foxes”) using exclusively the settlement area. This type of foxes was characterised by very small home ranges and strong adaptation to humans. These foxes seemed to be predestined to form urban fox populations.

The data indicate that the conditions for fox survival are given in settlements. Food is concentrated there and foxes use this area as resting sites during daytime as well as for rearing the offspring. But the establishment of permanent fox populations is difficult there due to the low tolerance of foxes by village inhabitants.

Meerkat (*Suricata suricatta*) contact calls: hormonally mediated?

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Animal vocalisations are characterised by individual differences in production rate and acoustic structure. This variation can partly be explained by the social and environmental contexts that individuals experience and also by their internal state. Thus, they can provide information concerning the producer's age, size, rank, sex and endocrine status. Individual differences in androgens and glucocorticoids have been repeatedly associated with competitive ability, social rank, vigilance behaviour and reproductive success, and with variation in calling behaviour. Meerkats are cooperative breeding mammals that have a highly developed vocal communication system, which they use to coordinate their spatial organisation, social interactions and anti-predator behaviour. Particularly, meerkats produce quiet and close calls during foraging that seem to aid in the maintenance of group cohesion. There is great variation in calling rate with dominant females and young adult subordinate males calling at higher rates than the remaining group members, additionally suggesting a potential role of contact calls in leading the groups between foraging patches. Thus, meerkats are an ideal study system in which to explore links between behaviour, vocalisations and hormones in animal societies. Experimental elevation of glucocorticoids, although having significant effects on vigilance and foraging behaviour, did not affect close calling rate in male but not in female subordinates. In addition, long-term (21 days) blocking of testosterone receptors in young subordinate males had no effect on either call rate or structure. Overall, our results show that, in meerkats, the caller's circulating cortisol and testosterone levels do not mediate close call structure and calling rate.

New future for the largest antelope

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More than 40 experts from seven countries and four continents met in January 2013 in Senegal to create the conservation strategy for the Western Derby eland (*Taurotragus derbianus derbianus*), a critically endangered antelope (ISIS 2012). The last viable population (170 individuals recorded in 2006) of this antelope lives in Niokolo Koba National Park (NKNP) in Eastern Senegal, threatened by poaching and habitat loss. A semi-captive population was established in 2000 from six founders captured in NKNP thanks to the Directorate of National Parks in Senegal (DPN) and the Society for the Protection of Environment and Fauna of Senegal (SPEFS) (NEŽERKOVÁ *et al.*, 2004). This semi-captive population has become the base of the conservation programme led by Derbianus Czech Society for African Wildlife NGO, DPN, and SPEFS. Due to careful breeding management, research and education, the semi-captive population reached 95 individuals in 2013, separated into several herds within two fenced reserves (Bandia and Fathala) in Western Senegal (KOLÁČKOVÁ *et al.*, 2011, 2012). A Species Conservation Planning workshop for the Western Derby eland was organised by Derbianus Czech Society for African Wildlife, DPN and SPEFS, and supported by Czech University of Life Sciences Prague, Knowsley Safari Park, Prague Zoo, Chester Zoo and IUCN. During this workshop, a conservation strategy plan for Western Derby eland was established. Before the workshop, the participants had possibility to visit NKNP and see the original habitat of Western Derby elands, which is woody savannah and lateritic plateaus. We hope that the conservation strategy accepted by all key stakeholders will lead to one plan for the *ex situ* and *in situ* population as the *ex situ* animals may directly contribute to the conservation of the unique ecosystem of West African Savannah.

ISIS (2012): International Species Information System. Available: <http://www.isis.org>. Accessed 1 May 2013.

KOLÁČKOVÁ K, HEJCMANOVÁ P, ANTONÍNOVÁ M, BRANDL P (2011): Population management as a tool in the recovery of the critically endangered Western Derby eland *Taurotragus derbianus* in Senegal, Africa. *Wildlife Biol* 17, 299 - 310.

KOLÁČKOVÁ K, HABEROVÁ T, VYMYSLICKÁ P, ŽÁČKOVÁ M, HEJCMANOVÁ P, BRANDL P (2012): African Studbook: Western Derby eland (*Taurotragus derbianus derbianus*, GRAY 1847). Prague: Czech University of Life Sciences Prague.

NEŽERKOVÁ P, VERNER PH, ANTONÍNOVÁ M (2004): The conservation programme of the Western giant eland (*Taurotragus derbianus derbianus*) in Senegal – Czech Aid Development Project. *Gazella* 31, 87 - 182.

The expression of relaxin-like peptides and their receptors in the corpus luteum of the Iberian lynx (*Lynx pardinus*)

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The Iberian lynx is the most endangered felid species of the world, and to prevent it from extinction the Iberian lynx Conservation breeding program (ILCBP) was initiated some years ago. Assisted reproductive techniques are considered as an essential tool within the breeding programme, but require profound knowledge on the biological basics of reproduction. One specific reproductive feature of lynxes is the physiological persistence of corpora lutea (CL). The aim of this study is to characterise lynx CL stages concerning the occurrence of relaxin-like peptides and their receptors as potential luteal factors. Relaxin plays an important role during pregnancy. Relaxin-3, a related peptide, is mainly involved in neurobiological processes, but was detected in reproductive tissue, too. In dependence of the species pregnancy-related relaxin is produced by either the CL or the placenta.

For animal welfare reasons, an ovariohysterectomy in two Iberian lynx females of ILCBP was performed. The surgeries were performed seven days after natural mating and extirpated oviducts were flushed for embryo collection. The ovaries were inspected for fresh and old CLs, and each CL was isolated and preserved for future analysis separately. In one female, early morulae were obtained; accordingly the respective CLs were classified as pregnant (PR). In case of the other female, only unfertilised oocytes were found, thus the CLs were treated as pseudopregnant (PP). We analysed the mRNA expression of relaxin, relaxin-3 and their receptors RXFP1, RXFP2 and RXFP3 in all CLs by quantitative PCR.

The relaxin expression is much lower in CL than in placenta tissue. Statistically significant differences were observed between old and fresh CLs. Generally, relaxin expression in fresh samples was higher than in old CLs. In addition, we found a significant difference between old PR CLs and old PP CLs, the expression was higher in old PR CLs. The same significant differences were found for relaxin-3 expression although its expression was very low. Regarding the receptors only the expression of RXFP2 shows the same expression tendencies, for the other two receptors higher expressions in old CLs were detected. We conclude that relaxin-like peptides could influence locally the function of the Iberian lynx CLs during early pregnancy as we detected a higher expression in newly formed CLs.

Characterisation of the allele expression of class I MHC homologues in the marsupial yolk sac placenta

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Pregnancy in therian mammals (eutherians and marsupials) requires that foetal and maternal tissues reside in close apposition to each other. How this occurs in spite of differing genetic composition and expression of self-molecules has been the subject of intense scientific scrutiny for some time. In well studied eutherian mammals, there is evidence for silencing of classical class I MHC molecules (transplantation antigens) at the foetal-maternal interface. However, this specific regulation of class I molecules may not be necessary in the Marsupialia where the conceptus is enclosed in a protective shell coat for up to 80 % of gestation, and the period of placental/uterine interaction is relatively short. To better understand this process in marsupials we have characterised mRNA expression of the recently described MHC class I loci of the tammar wallaby (*Macropus eugenii*) from the period of shell coat rupture (day 18) through to the last days (25/26) of pregnancy. We found prevalent expression of class Ia molecules in both tri- and bi-laminar yolk sac tissues throughout the attachment phase of pregnancy in the tammar wallaby. These loci showed similar nucleotide identity and allelic diversity to those previously described for non-reproductive nucleated tissue types in the tammar.

These data suggest that the short-lived placenta of marsupials expresses the same complement of class I MHC molecules as normal nucleated cells such as kidney, liver and skin and that there is no silencing of gene expression during the main period of foetal-maternal interaction. The presence of MHC class I molecules suggests that the foetus is either not affected by the maternal immune system, or that the short pregnancy of marsupials allows birth prior to any maternal immune challenge.

The elaboration of lactation instead of placentation in many marsupials may be a strategy to avoid immunological conflict.

A new marker set for rapid identification of large predators from livestock kills

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Large carnivores such as wolf and lynx currently spread across Central Europe, leading to human-animal conflicts in several areas. Predation of livestock and game species are a key issue here, resulting in a direct financial impact on farmers, breeders, or hunters. While several countries or federal states have launched management plans, which often comprise compensation fees for livestock kills caused by wild predators, implementation of this action requires the reliable distinction from kills caused by wild predators vs., for instance, dogs. In Germany, where wolves currently spread, the lack of a sufficient number of well-trained experts and wildlife managers requires an increasing use of molecular methods based on DNA detection from saliva traces on livestock kills.

In this poster presentation we compare different methodologies (microsatellites vs. newly designed mitochondrial markers) for the sound discrimination of wolf, lynx, and dog from kills and document its increasing application across Germany. Advantages, limitations, and potential for future developments of the method are discussed.

Effects of human disturbance on red deer behaviour: comparing the Bavarian Forest National Park and the Southern Black Forest

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Red deer (*Cervus elaphus*) in Southern Germany is heavily managed. In the Bavarian Forest National Park for instance the maximisation of visibility of species is one essential management aim while the management in the Southern Black Forest is mainly interested in reducing the browsing impact on the forest. In both regions we studied the behavioural response of collared red deer on approaching humans as a disturbance event [Bavarian Forest National Park N = 11 (male = 6, female = 5), Southern Black Forest N = 12 (male = 3, female = 9)] during 2008 and 2009. We computed the Euclidian distance of each pair of adjacent GPS-locations and home range estimates (MCP, LoCoH) based on GPS-locations within three days before and after the disturbance. Our results highlight that both, the Euclidian distance and home range size increased significant after the disturbance event for red deer of the Bavarian Forest National Park while they decreased slightly for red deer in the Southern Black Forest. The latter individuals showed a tendency to hide in regeneration patches of deciduous forest which are very browsing sensitive in the Black Forest. Red deer in the Bavarian Forest National Park increased the distances between adjacent locations which reduce the predictability of deer locations and thus its observability. We conclude that human disturbance has negative consequences for some key management objectives.

Circannual rhythm of salivary cortisol secretion in captive African elephants (*Loxodonta africana*)

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Non-invasive glucocorticoid analysing techniques allow accurate monitoring of stress responses and to assess welfare of captive and free-ranging animals. Cortisol is a glucocorticoid released from the adrenal cortex as result of the activation of the hypothalamic-pituitary-adrenal axis during a stressful situation. In African elephants, cortisol has already been measured in faecal and urinary samples, but not in salivary samples (MENARGUES MARCILLA *et al.*, 2012). However, knowledge of the basal secretory circannual rhythm is necessary to evaluate the significance of fluctuations in cortisol concentrations as a stress indicator during the year. In this study, non-invasive salivary samples from nine non-pregnant African elephant females (ages range between 7 and 25 years), *Loxodonta africana*, were collected every week (536 weeks samples in total) from the first of March 2012 to the end of March 2013. Animals are kept at zoological garden “Bioparc Valencia” under identical circumstances: the herd is maintained in their indoor enclosures until 10:00, and then released to the outdoor enclosures until 21:00 (May/June) and 19:00 (November). Salivary samples were collected using cotton swabs between 07:30 to 08:30, before feeding and cleaning. Samples were centrifuged after collection and stored at -20 °C until the hormonal analysis. Cortisol was measured in unextracted samples by enzyme immunoassay technique, previously validated for this species. Results revealed an overall seasonal pattern for salivary cortisol, and significant differences in cortisol levels among months were found. The highest cortisol levels were reached in November (6.74 ± 0.29 ng/ml), December (6.42 ± 0.22 ng/ml) and January (5.14 ± 0.49 ng/ml) and then decreased until reaching the lowest concentrations in March (0.81 ± 0.22 ng/ml) to September (1.69 ± 0.13 ng/ml). From the results obtained, we can conclude that cortisol in African elephants follow a circannual rhythm, and this should be taken into account when using glucocorticoid measure to assess stress response in captive animals.

MENARGUES MARCILLA A, URIOS V, LIMIÑANA R (2012): Seasonal rhythms of salivary cortisol secretion in captive Asian elephants (*Elephas maximus*). Gen Comp Endocr **176**, 259 - 264.

Thermography during large felids' gestation: preliminary findings

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IR thermography, a non-invasive diagnostic technique, is increasingly applied in the study of physiological and pathological processes in wild animals. We employed it to evaluate superficial body temperature variations during oestrus, pregnancy and early lactational period in four felid species: *Panthera leo* L. 1758, *P. pardus* L. 1758, *P. tigris* L. 1758 and *Puma concolor* L. 1771. Since at the time of study onset we had access to only four captive cycling females, our main aims during this preliminary phase were: i. to establish which anatomical regions (eyes, rhinarium, lateral abdomen, mammae) can be most reliably sampled and ii. to assess most suitable conditions for accurate measurements. Animals were trained to rest in the night shelter for ca one hour at noon and were repeatedly scanned, for a total of 12 sessions each, over six months. Averaged values for each anatomical region were plotted against environmental temperature and analysed. The eyes showed the highest values and lowest variance: mean overall temperature = 32.62°C (range 27.28 - 36.15, St.dev 1.99, Var. 3.96). Compared to eyes', the rhinarium's values were lower ($-2.73 \pm 3.18^\circ\text{C}$ in the lioness, -2.02 ± 4.20 in the leopard, -2.08 ± 1.93 in the tigress, -3.62 ± 4.44 in the puma; mean overall value = 29.99 ± 5.04) and their variance larger (25.41 on average). Similarly, the abdominal and mammary superficial temperatures were even lower than the eyes' ones but less variable than the rhinarium's ($-3.58 \pm 1.78^\circ\text{C}$ in the lioness, -6.25 ± 2.09 in the leopard, -4.72 ± 3.64 in the tigress, -5.44 ± 2.44 in the puma; mean overall temperature = 27.76 ± 4.08 , Var. 16.63). Thus, the eyes yield the most reliable measure, whereas rhinarium's temperature may be frequently altered by mucus and saliva and the abdominal region's temperature is disguised by hair. Although differing, all body values for each animal were significantly positively associated ($p < 0.001$). Since eyes' superficial values and concurrent environmental temperatures showed similar trends and were positively associated ($n = 40$, $r_s = 0.85$, $p < 0.0001$), we reckoned the body residual thermic values by subtracting environmental temperatures from thermographic data: the residual values were not correlated with environmental temperatures (n.s.). All females experienced a drop in superficial temperature shortly before parturition, but the lioness who suffered instead a peak at abortion.

Movements of free-ranging urban domestic cats (*Felis silvestris catus*) and changes in the demographic structure of their population

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An area of approximately 40 ha in the centre of Bologna town (Italy) was sampled in 1982, 1983, 1985, 1997 - 2000, and 2010 for presence of stray cats. A total of 80 adult cats, from a large spatially structured population comprising circa 300 individuals on the whole, were identified and their movements monitored; 23 colonies were defined and five single-living females located. Cats were assigned to a colony on the basis of the amount of time they spent in or near the core area of the colony itself, and consequently the frequency and intensity of interactions with local conspecifics. Due to changes in the amount of vehicle traffic and the urbanisation of the area, the persistence and distribution of all colonies and single-living cats experienced dramatic changes during this period. Further, an extensive trap-neuter-return programme was started in 1997, which rapidly decreased the number of free-ranging intact females, and to a lesser extent of intact toms.

The original structure of the total population was characterised by two major colonies occupying two homogeneous green areas, ca 800 m apart from each other, surrounded by 11 smaller satellite colonies dwelling more patchy environments. Emigration, immigration and even daily commuting were patent, and rates were recorded for both sexes, although road traffic caused ever increasing fragmentation of the habitat thereby limiting movements. Following a change of destination of the two green areas, the two large colonies gradually dispersed until extinction, splitting into subgroups and single individuals that emigrated into smaller adjacent colonies. The resulting 19 colonies (1997) were distinguished by an unusually high rate of transfer and interchange of individuals. All colonies exhibited recruitment of adult individuals of both sexes from other colonies, even those as distant as 1 km; single wandering individuals represented another source of recruits and introduction was usually unobtrusive. Amicable relations as well as active displacements were recorded in three contiguous colonies (distances: 200 and 500 m). Most of their toms visited other colonies daily (84.62 % on average) and fed there to some extent; rates of visits during early mating season further increased. Adult females as well visited other colonies, but tended to do so to a lesser extent compared to males, and to eventually move to the most visited colony. Two colonies merged, constituting a fission-fusion group during 1999 and 2000: the bulk of the group travelled daily to the nursery, where queens and kittens permanently resided, to get additional food but also to rest together.

Modelling habitat quality using the example of European bison (*Bison bonasus*) under consideration of nutritional aspects in a low mountain range working forest

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In the E+E-Project „Wisente im Rothaargebirge“ (“E+E” roughly translates to “proving and development”) a herd of up to 25 European bison shall be reintroduced in the wild. To estimate habitat feasibility and future habitat use in a private working forest of low mountain range (Bad Berleburg, NRW, Germany), investigations have been carried out during phenological spring, summer and autumn in 2012 on 10 defined habitat formations with 10 sample plots respectively in each period.

In chemical analysis dry matter, crude ash, crude protein, crude fat, acid and neutral fibre (ADF, NDF) as well as gas production of the Hohenheim Gas Test were measured for each formation from seasonal mixed samples.

Large differences were found between the formations as well as between the seasons regarding biomass production (kg DM / ha). The most productive formations were game meadows, pastures and storm damaged areas. Comparatively low values were found in the spruce and beech forests that dominate the area.

Forage quality (ME / kg DM) slightly differed between the formations. The quality was on a similar high level in spring and summer and declined in autumn. Highest values were found on game meadows in spring and summer and in young beech forests in autumn. Lowest values were found on the formation other deciduous forest in spring, other coniferous forest in summer and old spruce forest in autumn. Highest qualities were found on game meadows and lowest in other deciduous forests on average.

Biomass production and forage quality were allocated to an area-energy index (ME / ha). The available forage energy on the formations greatly differed throughout the year. Highest energy densities were found on pastures, second on game meadows and third on storm damaged areas in spring and summer. The formation storm damaged area did show higher values than the game meadows only in autumn. Lowest values were found in young spruce forests in spring, in young spruce as well as young beech forests in summer and in autumn.

The prospective habitat use of the European bison presumably depends on several factors and therefore is difficult to predict in detail. Under the assumption that the food supply regarding the energy- and nutrient-content is a relevant factor, it can be concluded that the primary used habitats will be the highly productive areas.

A review and update on the Tasmanian devil MHC and its role in devil facial tumour disease

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The Tasmanian devil (*Sarcophilus harrisii*), an iconic marsupial carnivore endemic to Australia, is currently under threat of extinction due to a contagious cancer – devil facial tumour disease (DFTD). We have intensively studied the major histocompatibility complex (MHC) in this species, not only to provide a better understanding of the Tasmanian devil immune system and the disease, but also to assist the Save the Tasmanian Devil Program in establishing an insurance population that retains the existing genetic diversity.

Four genomic regions containing devil MHC class I and II genes were characterised through bacterial artificial chromosome contig assembly and sequencing. All these regions were physically mapped to the same area on the long arm of devil chromosome 4, indicating the genomic location of the devil MHC. Thirty-four genes and pseudogenes were annotated, including five class I and four class II loci. Comparison between two haplotypes from two individuals revealed three genomic copy number variants within the class I region, causing differences in the number of functional class I genes among individuals. Genetic variability at MHC loci was examined in devils from across Tasmania. Relatively higher heterozygosity values were observed in northwestern subpopulations than in eastern ones, but the overall level of genetic diversity is low. Evidence suggested that the loss of MHC diversity in devils is likely a result of both historical population bottlenecks and purifying selection at MHC loci.

The limited variation in MHC molecules sets a low immunological barrier for DFTD tumour cells to be transferred between unrelated individuals. Skin graft experiments showed that similarity in MHC antigens may contribute to delayed allojection in the devil. However, low MHC diversity alone does not fully explain the spread of DFTD. Recent evidence has demonstrated that the tumour is actively evading the host immunosurveillance by down-regulating cell-surface expression of MHC molecules. Further study is required to determine whether genetic variation at the MHC plays a role in different susceptibility/resistance to DFTD in devils.

Comparison of glucocorticoid levels in droppings of blue-fronted Amazon parrots (*Amazona aestiva*) in different environments

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Measuring glucocorticoid concentrations is one of the most important methods for monitoring the endocrine status, which enables the understanding of animal's physiological responses and their relationship with environmental variables. The goal of the present study was to compare the levels of glucocorticoids in urofaecal samples obtained from blue-fronted Amazon parrots (*Amazona aestiva*) maintained in three different systems of captive management and free-ranging individuals. The samples obtained from free-ranging animals (24 samples) were collected at San Francisco farm, located in the sub-region of Miranda, Pantanal, of Mato Grosso do Sul, Brazil. In captivity, samples were collected from each management system: 20 from a commercial breeder (Criadouro da Brisa, located in Jaboticabal/SP), 22 from a zoo (Parque Ecológico Municipal de Piracicaba/SP) and 20 from pets (residences of Jaboticabal/SP). All the 86 urofaecal samples were collected in August 2011, during the same period of the day. The extraction, dosage and sample analysis were done at Laboratório de Dosagens Hormonais of NUPECCE, Faculdade de Ciências Agrárias e Veterinárias, Unesp Jaboticabal. The samples were dried in an oven (72 h at 56°C) and extracted with 80 % methanol. The hormone assays were performed by EIA using monoclonal cortisol antibody (Munro, University of California, Davis/CA, USA). This assay was validated for *Amazona aestiva* samples by FUJIHARA (2008). Mean values \pm SEM levels of glucocorticoid metabolites (ng/g) of dried urofaecal samples were: free-ranging parrots 158 ± 18 ng/g; breeding centre 84 ± 3 ng/g; pets 67 ± 6 ng/g; and zoo 84 ± 20 ng/g. According to Tukey's test, the results obtained show that the average values of free-ranging animals were significantly higher ($P < 0.05$) than those of the other groups, while none of the captivity systems showed significant differences among themselves. This study shows the differences of urofaecal glucocorticoids levels between captive and free ranging blue-fronted Amazon parrots individuals. The higher levels of free-ranging individuals could be a sign that this species adapts well to captivity. Thus, these results must be considered in the reintroduction programmes of confiscated animals.

FUJIHARA CJ (2008): Validação de método não-invasivo para análise de hormônios ligados ao estresse em papagaio verdadeiro (*amazona aestiva*). Master Dissertation. FMVZ-UNESP Botucatu. Disponible 17th June 2013 in: http://www.athena.biblioteca.unesp.br/exlibris/bd/bbo/33004064022P3/2008/fujihara_cj_me_botf_mvz_prot.

The German cell bank for wildlife – preserving genetic resources, providing versatile biomaterial, promoting cell based applications

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The German cell bank for wildlife collects and preserves cell cultures from wildlife. About 5,000 samples of 300 cell cultures representing 100 species have been generated and cryopreserved so far. Because the cells proliferate over long periods of time a sustainable usability of the collection is ensured. While a core stock of samples of each cell culture is stored in the long term, a working stock is used to make cells available for scientific application. The range of applications of the cell cultures is as diverse as wildlife diversity itself. Different findings and applications presented within this talk illustrate this potential.

Identity, species and sex-specific information is contained in the contact calls of northern and southern white rhinoceros

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Vocal communication of rhinos has been until now studied only very little and although descriptions of vocal repertoire of several species have lately been published, no studies have reported any information contained in specific rhino calls or an ability of rhinos to perceive such information. Northern (*Ceratotherium cottoni*) and southern white rhinos (*Ceratotherium simum*) are the most social from all rhinoceros species and they also have a wide vocal repertoire. Acoustic recognition may therefore play an important role in their social interactions. White rhinos produce a repetitive contact call ‘pant’, which does not have parallel in any other rhinoceros species.

We acoustically analysed 385 pant calls of six northern and 14 southern white rhinos and we conducted playback experiments with pant calls on nine wild southern white rhino bulls. Pant calls were recorded in several zoological gardens and South African wildlife reserves and we investigated if they contain information about individual identity and species of the caller. Discriminant analysis showed that pant calls are highly individually distinctive and calls of individuals also clustered into obviously separated groups according to the species. Both species significantly differed in call duration and in several frequency parameters of their calls. We also examined if adult southern white rhino bulls were able to discriminate between the pant calls of female and male southern white rhinos. Playback experiments were conducted in several wildlife reserves in South Africa. Bulls were able to recognise caller’s sex and showed more intensive reaction to female than male calls. The bulls were more active as they spent more time walking and running after they heard a playback of a female call in comparison to male call. The bulls also showed a shorter latency to mark their territory with urine or dung after a playback of female call.

Pant calls seem to have an important role in the social behaviour of white rhinos and due to their complex structure they might also encode other information than that reported in this study. Better knowledge of vocal communication of white rhinos is important for the improvement of their management in zoological gardens and wildlife reserves. Breeding success of white rhinos in captivity is very low and the use of playbacks of pant calls might be extremely helpful for the stimulation of their social and reproductive behaviour.

Wild southern white rhinos (*Ceratotherium simum*) are able to recognise information about familiarity and sex in the dung of their conspecifics

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Recognition of conspecifics may be important mainly in social species and might allow a creation of network of social relationships through recognition of familiar from unfamiliar animals, particular individuals, relatives, group members or neighbours. White rhinos are known for their sociality; the bulls are territorial while females, subadults and calves live in groups. They have weak eyesight and communicate by means of a wide range of vocal repertoire and by scent messages conveyed by dung and urine. White rhinos defecate at common dungheaps and the dung may provide them with the information about the movements of their conspecifics. The knowledge of processes of olfactory communication in rhinos might have an important use in rhino management and conservation; however, studies on the olfactory communication of free-ranging white rhinos have been until now only descriptive.

We experimentally studied olfactory investigation of dung by wild southern white rhinos in Welgevonden Game Reserve and Lapalala Wilderness in South Africa and examined their reactions (number of sniffing events, duration of sniffing and latency of vigilance posture) to the dung of familiar and unfamiliar adult females and males. The experimental dung was placed near already established dungheaps, where no other fresh dung was present and the experiment started when an animal approached the dung and started sniffing it. The reaction of the animals was video recorded for five minutes. We included the reactions of animals of all sex-age classes including calves older than six months. The rhinos sniffed the dung of unfamiliar animals longer and more often. We did not find any differences in the number of sniffing events or duration of sniffing between the female and male dung. Nevertheless, the rhinos showed shorter latency of vigilance posture to familiar dung of males than that of females while to unfamiliar dung they showed shorter latency of vigilance posture to female than male dung. Information about familiarity and sex contained in the dung of white rhinos might therefore be important for their social behaviour and spatial organisation as the dung can inform the animals about the movements of their conspecifics even in their absence. White rhinos in zoological gardens have a very low reproductive rate and better understanding to their olfactory communication might be extremely helpful in their management.

The importance of wildlife immunology in conservation programmes and methodological challenges

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Within conservation biology, anthropogenic factors such as habitat destruction, climate change or pollution (chemical, light or biological, including pathogens) are considered as major driving forces of biodiversity loss (CHAPIN *et al.* 2000). To better understand the effect of these factors and their contribution in population declines, several physiological markers have been proposed to monitor the health status of different animal populations. These markers include endocrine, oxidative balance or immunological parameters (WIKELSKI and COOKE 2006; BEAULIEU *et al.* 2013). In recent years, several new immunological tools have been developed for wildlife species (BOUGHTON *et al.* 2011), however the lack of species-specific reagents (e.g. antibodies, T-cell markers) prevents the application of many modern immunological tools to wildlife. Besides these considerable obstacles, many of these methods require repeated, invasive sampling, making their usage unsuitable or difficult to apply in field conservation programmes. Under these circumstances the development of new tools are required, preferably based on samples that can be obtained through minimally invasive techniques. New analytical methods can be developed using new molecular approaches and existing resources from closely related model species (e.g. laboratory species, domestic mammalian and avian species). The potential importance of such new immunological markers is considerable as they will both help to determine the health status of different wildlife populations and also provide a better understanding on the short- and long term effects of different pollutants on individuals and populations. Moreover, describing the immunopathogenesis of different parasitic and infectious diseases is essential for the development of efficacious therapeutic and preventive intervention strategies (e.g. vaccination). Using examples from the literature and own research I discuss in detail the importance and the difficulties of immunological measurements in wildlife species, and their significance in providing science-based information for different species conservation programmes.

BEALIEU M, THIERRY A-M, GONZÁLEZ-ACUNA D, POLITO MJ (2013): Integrating oxidative ecology into conservation physiology. *Conserv Physiol* **1**, cot004.

BOUGHTON RK, JOOP G, ARMITAGE SAO (2011): Outdoor immunology: methodological considerations for ecologists. *Func Ecol* **21**, 85 - 100.

CHAPIN FS, ZAVALA ES, EVINER VT, NAYLOR RL, VITOUSEK PM, REYNOLDS HL, HOOPER DU, LAVOREL S, SALA OE, HOBBI SE, MACK MC, DIAZ S (2000): Consequences of changing biodiversity. *Nature* **405**, 234 - 242.

WIKELSKI M, COOKE SJ (2006): Conservation physiology. *Trends Ecol Evol* **21**, 38 - 46.

“Wie man sich bettet, so schläft man” – Flexible hibernation and torpor patterns in Malagasy lemurs

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Of all fundamental principles in biology, energy expenditure is perhaps the single-most important as it is a prerequisite for life itself. In many species life history parameters, such as nutrition ecology, reproductive patterns or even social systems are shaped by energetical constraints. Flexibility in physiology can contribute to the success and persistence of species. In particular, the ability to modify thermal biology via seasonal adjustments in physiological processes can be vitally important. This is especially critical during periods of scarce conditions and/or low ambient temperature. Climatic conditions change not only on a day-to-day basis but also seasonally (and due to global warming), and can do so in an unpredictable manner. To cope with environmental energetic bottlenecks many small mammal species use torpor or hibernation, temporary and controlled physiological states of reduction in metabolic rate and body temperature.

Within the order primates, heterothermy has so far only been found in the family Cheirogaleidae, small Malagasy lemurs, and one species of galagos, all living under tropical, but nevertheless seasonal and energetically demanding conditions. Comparison of the Cheirogaleidae species showed that there is an amazing physiological flexibility in regard to their thermoregulatory adaptations, depending on the climatic parameters of their habitat and choices of hibernacula, between closely related species, between individuals of the same population, or even within the same individual, reflecting ecological and evolutionary forces, and permitting immediate responses to prevailing conditions. These results emphasise that physiological flexibility is particularly important for species living in less predictable habitats.

The DNA variation of amphibian larval from various habitats in Israel

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The molecular DNA variation among *Salamandra infraimmaculata* (GOLDBERG *et al.*, 2007) and *Triturus vittatus* (PEARLSON *et al.*, 2005; PEARLSON and DEGANI, 2007) larvae populations, representing diverse breeding sites in Israel, was analysed by cytochrome b fragment, control region, DNA polymerase chain reaction (RAPD PCR) and amplified fragment length polymorphism (AFLP) methods. Although the molecular polymorphisms in both mitochondrial and nuclear DNA are small, they reflect a sharp ecological separation between DNA variation of seasonal breeding sites and permanent water sources. These are presumably adaptive changes caused by natural selection. Low genetic (cyt b and 12S, and RAPD PCR) variation, was revealed by sequences from specimens of *Hyla felixarabica* (GVOZDIK *et al.*, 2010). *Pseudepidalea viridis* (STÖCK *et al.*, 2006), *Rana bedriagae* and *Pelobates syriacus* populations, respectively, at each location, analysed by Arlequin software. We found that both *H. savignyi* and *P. viridis* are adapted to more unpredictable breeding places than *R. bedriagae* and *P. syriacus*.

GOLDBERG T, PEARLSON O, NEVO E, DEGANI G (2007): Mitochondrial DNA analysis of *Salamandra infraimmaculata* larvae from habitats in northern Israel. *Progrese și Perspective in Medicina Veterinară* - Lucrări științifice, **50**, 23 - 31.

GVOZDIK V, MORAVEC J, KLÜTSCH C, KOTLÍK P (2010): Phylogeography of the Middle Eastern tree frogs (*Hyla*, *Hylidae*, *Amphibia*) as inferred from nuclear and mitochondrial DNA variation, with a description of a new species. *Mol Phylogenet Evol* **55**, 1146 - 66.

PEARLSON O, JACKSON K, DEGANI G (2005): Molecular DNA variation and mitochondrial sequence analysis of *Triturus vittatus vittatus* (Urodela) from breeding sites at various altitudes in the southern limit of its distribution. In: *Fiseb federation of the israel societies for experimental biology.* Eilat.

PEARLSON O, DEGANI G (2007): *Triturus v. vittatus* (Urodela) larvae at various breeding sites in Israel. *Progrese si Perspective in Medicina Veterinara*, **50**, 214 - 226.

STÖCK M, MORITZ C, HICKERSON M, FRYNTA D, DUJSEBAYEVA T, EREMCHENKO V, MACEY JR, PAPPENFUSS TJ, WAKE DB (2006): Evolution of mitochondrial relationships and biogeography of palearctic green toads (*Bufo viridis* subgroup) with insights in their genomic plasticity. *Mol Phylogenet Evol* **41**, 663 - 89.

Deriving animal behaviour from GPS-tracking

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Increasing technological advancements allow us to obtain more information on behavioural ecology, where this was previously not possible or subject to observations that were restricted in space and time. GPS-tracking has proved to be a valuable tool to gather more information on the movements of wildlife. The aim of the present study was to test whether GPS location data can be used to infer which behaviour an animal is performing. Behavioural observations on cattle were linked to movement metrics based on GPS data that was obtained in both an open and forested area, and at a 1-minute and 2-second interval. A permutation ANOVA showed that at a 1-minute interval the four dominant types of behaviour (Foraging, Ruminating, Standing and Walking) differed significantly for both distance and turning angle except for Ruminating and Standing and with the use of a CART tree it was possible to classify the GPS data correctly for more than 70 % of the cases. A 2-second interval did not allow for a better classification of behaviour. Creating larger time steps by using the data at a larger (12-second) interval improved the classification, and we investigated if an optimal time interval exists for the derivation of behaviour. Furthermore, as expected based on findings that forest cover causes poorer GPS performance, it was found that the data from the forested area could not be classified as good as the data obtained from the open field, which may be the biggest obstacle for inferring behaviour from wildlife tracking yet. Nevertheless this study shows very promising results considering the inference of behaviour from GPS data, creating the link between behaviour and individual animal movements, which is a very important step in the integration of behaviour and environmental data. Further development may help to easily obtain and better understand environmental interactions and habitat use of animals, and detect and respond to deviations in behaviour that occur as a result from e.g., diseases.

The effective population size of the arctic foxes of Mednyi Island (*Vulpes lagopus semenovi*)

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What part of a population contributes to the gene pool of the next generations? This information could serve as an important indicator of the viability of populations, because it determines its genetic polymorphism and future existence. Based on that, the concept of effective population size N_e was introduced in population genetics (WRIGHT, 1931, 1938). In practice, population size is measured by the number of breeding males and females as recommended by IUCN, because Guidelines for Using the IUCN Red List (2010) state that "mature individuals that will never produce new recruits should not be counted". However, mature individuals whose descendants are infertile do not contribute to the future gene pool either, nor are non-breeding animals. Long-term individual-based studies of Arctic foxes on Mednyi Island (The Commander Islands, Northern Pacific) show that the lack of information about second-generation litters of the breeding individuals can lead to significant measurement errors in the empirical measurement of the effective population size. According to our findings, about half of all animals who lived up to at least one year will take part in the reproduction ($54.5 \pm 25.6\%$, $M \pm SD$; 95 % CI = 40.3 - 68.2 %). But only $19.8 \pm 14.2\%$ (95 % CI = 11.9 - 27.7 %) will have second-generation litters (N = 15 - the number of years included in the analysis). This means that most of the breeding individuals of the Mednyi Arctic fox population do not contribute to the future gene pool because their offspring die before breeding. It is too early to say whether this situation is typical for mammalian populations but this study suggests that: (1) estimation of effective population size based on empirical measurements of breeding individuals produces a largely overestimated number of individuals affecting the gene pool; and (2) small, isolated natural populations, like the Arctic foxes on Mednyi Island, whose recorded adult population is about 100, can have a "reproductive core" of only two dozen animals. The surveys were financed by grants of the Russian Foundation of Basic Sciences.

WRIGHT S (1931): Evolution in Mendelian populations. *Genetics* **16** (2), 97 - 159.

WRIGHT S (1938): Size of population and breeding structure in relation to evolution. *Science* **87** (2263), 430 - 431.

IUCN STANDARDS AND PETITIONS SUBCOMMITTEE (2010): Guidelines for Using the IUCN Red List Categories and Criteria. Version 8.1. <http://www.nationalredlist.org/files/2012/09/Guidelines-for-Using-the-IUCN-Red-List.pdf>

Chromosome and molecular distinction between the brown brocket (*M. gouazoubira*) and the Amazonian brown brocket deer (*M. nemorivaga*)

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Amazonian brown brocket deer (*Mazama nemorivaga*) was considered a synonymy of brown brocket deer (*M. gouazoubira*), until a taxonomical morphological review showed the existence of significant differences between them. However a genetic assessment was not yet performed. Our aim was to perform a systematic genetic research to analyse both species applying cytogenetic and molecular markers. For cytogenetic analysis blood and skin samples were collected from 23 animals (15 *M. gouazoubira* and 8 *M. nemorivaga*). The chromosomal slides were submitted to banding techniques (G, C and Ag-NOR staining) and to *in situ* fluorescent hybridisation. The brown brocket (*M. gouazoubira*) showed all acrocentric chromosomes including also the sexual pair, with the same diploid and fundamental number ($2n = 70$ and $FN = 70$). The amazonian brown brocket (*M. nemorivaga*) showed three different karyotypes being $2n = 68/69$, $FN = 70$; $2n = 67$, $FN = 70$; $2n = 69$, $FN = 72$, including 2 to 6 B chromosomes and a sexual chromosome system XX/XY1Y2 explained by an autosomic fusion involving the 34 chromosome present in the basic karyotype of the brown brocket *M. gouazoubira*. For molecular studies we sampled 94 individuals (77 *M. gouazoubira* and 17 *M. nemorivaga*). We used two mitochondrial molecular markers (*Cytocrome b* and *Cytocrome Oxidase I*) and three nuclear markers (IL16, a-Lalb and MGF). For phylogentic analysis we used Maximum Likelihood algorithm considering the evolution model GTR+G with 1,000 bootstrap pseudoreplications. Both species showed significant differentiation with the molecular markers. Furthermore the genetic distance is so significative that the two taxa potentially belong to different taxonomic genera. The genetic analysis clearly showed significant genetic differentiation, suggesting reproductive isolation among both taxa as required under the Biological Species Concept. These findings have important implications for conservation and management guidelines.

Nursing effort, milk transfer and sibling conflict affect milk intake in the spotted hyaena

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Lactation is energetically demanding. Investment in lactation in the spotted hyaena (*Crocuta crocuta*) is high because offspring are entirely dependent on maternal milk for at least six months and can be weaned at 18 months of age. In the Serengeti National Park, Tanzania, lactating females are long-distance central place foragers for between 50 – 75 % of the year. They regularly travel approximately 80 - 140 km between their dependent cubs at communal dens in their clan territory and distant, shifting concentrations of migratory herbivores. Maternal nursing patterns are chiefly determined by foraging distance and maternal absence intervals can vary between several hours (when mothers forage ‘at home’) and several days (when they travel long distances). We investigated how maternal nursing patterns influenced milk quality (nutritional composition), the rate of milk transfer to offspring and the quantity of milk obtained by cubs during nursing bouts. To better understand the impact of within-litter dominance relationships on sibling growth, and survival in twin litters, and the phenomenon of facultative siblicide by enforced starvation in this species, we investigated how sibling competition for access to maternal teats impacts milk intake by dominant and subordinate littermates. We expected milk quality, quantity and rate of transfer to be influenced by nursing patterns, litter size, within-litter dominance status and the intensity of within-litter sibling rivalry. We found that spotted hyaena milk has a high gross energy density (9.7 kJ g^{-1}) for a terrestrial carnivore, including a high fat (mean 14.0 %) and protein (mean 14.9 %) content and low lactose (mean 3.0 %) content. Milk quality increased as maternal absence intervals increased and changed with lactation stage (i.e. relative time until weaning). Milk intake volume and intake rate were significantly higher during the first suckling bout after a mother returned from a foraging trip than in subsequent bouts, indicating that milk flow constrains milk consumption. Milk intake per nursing bout by singletons was significantly higher (0.44 kg) than by both offspring in twin litters. Dominants had a higher milk intake (0.34 kg) and intake rate (9.0 g min^{-1}) than their subordinate sibs (0.26 kg and 5.8 g min^{-1} , respectively) during the first nursing bout. These differences between littermates increased as the rate of sibling aggression during a nursing bout increased.

Investigating reproduction and population performance in the European captive population of eastern black rhinoceros (*Diceros bicornis michaeli*)

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With fewer than 5,000 black rhinoceros (*Diceros bicornis*) left in the wild, *ex situ* populations play a vital role in the conservation of this species. However, the European captive population of the eastern black rhinoceros (*D. b. michaeli*) is currently underperforming compared to their *in situ* counterparts, with annual growth rates of only 1 - 2 %, compared to > 5 % *in situ*. In recent years, the primary factor limiting growth of this population has been low rates of reproduction, with only around 11 % of adult females breeding each year. Furthermore, approximately 40 % of reproductive-age individuals are yet to successfully produce offspring, resulting in high reproductive skew in both males and females. To investigate differences in reproductive success, faecal samples were collected from 23 males and 39 females at 13 institutions across Europe, and used to measure reproductive and adrenal hormones by enzyme immunoassay. In females, approximately three-quarters of all oestrous cycles observed were 20 - 40 days in length, but irregular cyclicity was also apparent in both parous and nulliparous females, with short (< 20 days) and extended cycles (> 40 days) often exhibited over a 12-month period. Overall there were no differences in average faecal glucocorticoid metabolite concentration between parous and nulliparous females; however, long cycles were more often observed in nulliparous females, and within females were associated with elevated faecal glucocorticoid metabolite concentration compared to other cycle types. In males, faecal testosterone metabolite concentration was higher in males that had previously sired offspring than those that had not, but this was unrelated to faecal glucocorticoid concentration. Intrinsic differences in reproductive hormone profiles may be related to differential reproductive success observed in both male and female black rhinos in this population, and research is on-going into what other factors may be involved.

Long-term egg-loss-rate in white storks (*Ciconia ciconia*) - an example of a cooperative study between volunteers and scientists

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Long-term datasets, especially on reproductive success, provide a fundamental basis for studies on ecological systems and on relationships between biotic and abiotic variables. The collection of long-term datasets is very labour-intensive and we explore here the value of the inclusion of data collected by committed volunteers for scientific work. For more than 30 years the white stork (*Ciconia ciconia*) nests in the rural district Kalbe (Milde) in Germany (federal state Saxony-Anhalt) were maintained and monitored by a group of volunteers: This dataset provides highly valuable information on the breeding success in white storks: Even though this species is studied intensively, only very few data are available on the number of eggs laid. The analysis of breeding parameters such as the number of pairs and their fledglings, as well as the yearly variation in the percentage of eggs that are not turning into fledglings, enables a more specific quantification of juvenile mortality: On average 3.6 ± 1.5 SD eggs (range 0 - 6) were laid per nest, but only 2.1 ± 1.4 SD juveniles (range 1 - 5) fledged. Thereby the mean egg-loss-rate per year was $42 \% \pm 9.6 \%$, varying from 19 % to 58 % between years. Further statistical modelling will reveal the influence of environmental variables such as weather and habitat on the breeding success and especially on the egg-loss-rate in white storks. We would like to emphasise the role of volunteers in nature conservation and monitoring programmes and to encourage cooperative studies between volunteers and scientists because they can complement each other by sharing expertise and resources.

Spatio-temporal patterns of behaviour in captive Asiatic golden cats (*Pardofelis temminckii*)

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The Asiatic golden cat (*Pardofelis temminckii*) is one of the least known felids (NOWELL and JACKSON, 1996). This species is rarely maintained in captivity and only moderate breeding success has occurred (BROCKLEHURST, 1997). Accordingly, the objective of the research was to examine the spatio-temporal patterns of behaviour of Asiatic golden cats in zoo husbandry by the means of chronoethological methods. Six Asiatic golden cats (4.2) at Tiergarten Heidelberg and two Asiatic golden cats (1.1) at Allwetterzoo Münster were continuously observed on the basis of 24 hour infrared-time-lapse-videorecording. A total of 805 recorded days were selected for detailed analysis and evaluation.

The activity of the Asiatic golden cats and especially the time patterns of behaviour were analysed in detail. The average share of sleep and rest totaled 45.7 % over the 24 hour day. Locomotive behaviour was as high as 23.6 %, and an average share of 3.6 % of the locomotion was displayed as stereotypic pacing. The amount of stereotypic pacing of one male cat increased to 13.9 % due to several aversive stimuli in and adjacent to the enclosure.

The Asiatic golden cats live mainly crepuscular. They try to move to concealed areas of the enclosure and usually avoid social contact. The presence of conspecifics and keepers functioned as external stimuli for the animals (MELLEN, 1991). The activity rhythm of the adult cats usually was biphasic. Two cats (1.1) displayed a deviating monophasic activity rhythm prior to their deaths; these incidents were the result of chronic stress.

The results show how important the application of chronoethological methods can be for the welfare of animals in captivity. The registration of activity rhythms and deviating spatio-temporal patterns can be crucially important, in order to identify suboptimal husbandry conditions.

BROCKLEHURST M (1997): Husbandry and breeding of the Asiatic golden cat (*Catopuma temminckii*) at Melbourne Zoo. International Zoo Yearbook **35**, 74 - 78.

MELLEN JD (1991): Factors influencing reproductive success of small captive exotic felids (*Felis* spp.): A multiple regression analysis. Zoo Biol **10**, 95 - 110.

NOWELL K, JACKSON P (1996): Asiatic golden cat *Catopuma temminckii*. In: Wild Cats: Status Survey and Conservation Action Plan. IUCN/SSC Cat Specialist Group, Gland, Switzerland.

Interaction of social and ecological parameters on offspring survival in a wild primate

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Loss of offspring severely limits parent direct fitness, particularly in species with low reproductive output. In gregarious mammals, both ecological and social variables impact offspring survival and may interact with each other. Although a number of studies have investigated factors influencing offspring loss in mammals, still little is known about the interaction of these factors. We therefore investigated foetal and infant mortality in three large groups of wild crested macaques (*Macaca nigra*) over a period of five years including potential social and ecological causes in a multivariate survival analysis. Infant but not foetal survival was most impaired by a recent take-over of the alpha-male position by an immigrant male. Infant survival was furthermore affected by the interaction between the number of group females and food availability. This interaction also influenced foetal survival, but was additionally a function of maternal rank. Our results show that the interaction of ecological and social variables can influence offspring survival and thus stress the importance of survival analyses using a multivariate approach. They further show that these variables may vary between different offspring stages and thus point out the importance of studies encompassing more than a single offspring stage when investigating parent fitness determinants. Results will be discussed on the background of the socio-ecological model.

The social ecology of male African elephants (*Loxodonta africana*) in Botswana

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The Makgadikgadi National Park (MNP) of Botswana is historically a peripheral elephant range, however in recent years there has been an influx of male elephants into this area with the current population being predominantly bulls with sightings of male groups more than 100 strong socialising together (BRADLEY, *pers. comm.*). Male groups as large as these have not been sighted in Africa in recent history, giving us a unique opportunity to further understand the social ecology of male elephants.

The Okavango Delta is extremely dynamic, relying on a flood pulsing system, which shifts the wet and dry seasons, since 2008 the flood levels have increased dramatically, through necessity, the elephants are periodically forced into new and old ranges. This along with a recent increase and then stabilisation of the elephant population may have caused the recent influx of male elephants into the MNP and surrounding areas, resulting in increased conflict.

Our study focuses on social groupings and individual recognition to further investigate the importance of relationships in male elephant ecology. Data collected on group size, group composition and season will be compared to our data on males in the Okavango Delta, where the largest male group size seen was 17.

Initial findings show that groups as large as 52 male elephants are meeting at the river not only to drink and mudbath but to socialise. These groups are very fluid and there is a lack of <36yr males in the area. This is contrary to what we found in the Okavango Delta, where group sizes were smaller and groups were generally cohesive for longer. Leading us to wonder what role these large social groupings have in male elephant sociality and the implications for elephant conservation and welfare both *in situ* and *ex situ*.

Assessing the edible portion consumed by tigers feeding on wild prey

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Fewer than 3,500 tigers (*Panthera tigris*) remain in the wild. Given this situation, conservation actions must be set in place to help the recovery of tiger populations. Quantifying tiger energetic requirements is a key question that enables the estimation of nutritional carrying capacity, the impact of tigers on prey, and aids in developing science-based conservation recommendations. In order to do that, kill rates as well as prey requirements need to be determined. However, while kill rate is an important ecological parameter, ultimately the consumption rate matters most for tiger conservation. To obtain consumption rates, both the weight of the prey and the percentage of the carcass being consumed need to be assessed. However, because of variation in digestibility and inability to conduct trials in the field, most studies rely on published anecdotal data, gross estimates, other species, or all three of the above. In the present study we systematically assess the edible portion of different prey species consumed by tigers. The study took place at Laohu Valley Reserve (South Africa), where the charitable foundation Save China's Tigers breeds and rewilds captive-born South China tigers (*Panthera tigris amoyensis*) for later reintroduction into protected areas in China. Nine tigers - four males and five females - were fed fresh carcasses of small (springbok, *Antidorcas marsupialis*), medium (blesbok, *Damaliscus pygargus*), and large antelopes (either blue wildebeest, *Connochaetes taurinus* or red hartebeest, *Alcelaphus bucelaphus*) in similar proportions (N = 16). The carcasses were weighted before and after being given to the tigers, and the proportion of carcass eaten calculated. In a parallel test, six animals from each of the above mentioned sizes were weighted before and after removing their stomach contents. Data revealed that tigers consumed, on average, 74.9 % of the carcasses. The 25 % remaining consisted of stomach contents (mean = 14.49 %) and animal parts which usually included some hide, long bones from the legs, horns, lower jaws, pelvis, some (or all) spine, ribs and hooves (mean = 13.51 %). As expected, the larger the species, the higher the proportion not consumed by the tigers (20.08 % from small antelopes, 26.12 % from medium-sized and 3.53 % from large-sized antelopes). Our data provide reliable results that will enable the calculation of accurate annual consumption rates for wild tigers, which will help in planning conservation programmes. Given the scarcity of this kind of data in the literature, our results could also be extrapolated to other large felid species.

A step forward in tiger conservation: rewilded tigers hunt and kill wild prey

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The South China tiger (*Panthera tigris amoyensis*) is the most endangered of the remaining six tiger subspecies; there are probably no more than 30 individuals in the wild while the captive population, most of them in Chinese zoos, number about 100. Given these numbers, conservation of this species can only be achieved by captive breeding and subsequent reintroduction to the wild. However, the success of the reintroduction will in part depend on each tiger's ability to secure prey on its own. Save China's Tigers is a charitable foundation that breeds and rewilds South China tigers for later reintroduction in restored protected areas in China. The tiger rewilding programme, located in South Africa, has developed a rewilding methodology where captive-born tigers are provided with self-taught opportunities to learn to hunt independently. To date all first and second-generation tigers over two years of age (N = 8) have been able to hunt wild animals. To assess their hunting proficiency, six rewilded tigers were fitted with GPS satellite collars and placed individually into two hunting camps of same dimensions but different landscape features to assess their ability to hunt in both conditions. Each camp was stocked with 40 blesbok (*Damaliscus pygargus*), being 10 of them (five per camp) fitted with proximity collars, to determine when tigers came into close proximity with the prey (i.e. less than 100 m). Each tiger spent a 24-day test period in each camp and was then removed. The suspected feeding sites were subsequently visited to confirm the presence of a kill. Data revealed significant differences in hunting performance between camps, where tigers hunted more frequently in the camp with more opportunities for concealment (mean time between kills = 5.16 days) than in the camp with more open areas (mean time between kills = 11.52 days), as suggested in the literature. Nevertheless, while in the camp with less cover tigers adapted by preying on other naturally occurring species such as steenbok (*Raphicercus campestris*), aardvark (*Orycteropus afer*) and Cape hare (*Lepus capensis*) among others, revealing flexibility on their choice of prey depending on environmental factors. These preliminary results indicate that rewilded tigers are able to kill frequently enough to ensure an adequate food intake compared to wild, free-ranging tigers if given the right environment and, therefore, they could be candidates for reintroduction into protected reserves in China. However, additional data are needed in order to confirm the success of the rewilding process for this species.

Measuring glucocorticoid metabolites in pachyderms in zoos and in the wild: opportunities and limitations

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Glucocorticoid metabolites are commonly measured in pachyderms, either in the wild or in captivity. A good example is the evaluation of stress following human interventions (e.g., capture, translocation and release to novel environments in the wild) or the monitoring of reproductive status, as well as responses to environmental changes (e.g., new enclosures, handling procedures, and social conflicts in captivity). Here, we present data from case studies (*in situ* and *ex situ*) using glucocorticoid measurements in elephants and African rhinoceroses under different research objectives. Studies were conducted between 1998 and 2011. *Ex situ* studies were carried out at Zoo Berlin (Asian elephants), Tierpark Berlin-Friedrichsfelde (Asian and African elephants), and Magdeburg Zoo (black rhinos). An *in situ* post-release study on African rhinos took place in a wildlife reserve in north-central Namibia.

Stress measurements related to reproduction has been proven useful to illustrate single events, e.g. mating, post-natal stress in conjunction with handling or separation or integration of mother-calf-dyad into the group (*post-hoc* info). However, measuring glucocorticoids to predict oestrus and parturition in zoo elephants has no sufficient prognostic values, because of the delayed response of glucocorticoid metabolites to physiological changes.

The evaluation of post-release stress of African rhinos in the wild revealed limitations: the large study area and the small number of rhinos prevented collection of basic data on a daily level and allocation of samples to individuals. Additionally, a methodological artefact (clear relation between dry mass of samples and the level of glucocorticoid metabolite concentrations) was found *in situ* and *ex situ*. Two years of data collection of black rhino faecal samples showed lower metabolite concentrations of the pooled data during the second year post-release, which indicates a possible long-term acclimatisation process. A shorter study period (8 months) concerning a white rhino group (pooled data set) and a single white rhino male had shown no such trend.

Moving black rhinos into new housing facilities at a zoo provided the chance to verify the methodology and overcome some of these limitations. There was no difference in the average glucocorticoid concentrations between the wild and the zoo. The response of glucocorticoid metabolites of black rhinos after transfer into new housing facilities in the zoo is focus of another contribution.

Our results highlight the diversity of applications for measuring glucocorticoids but reveal also the importance of developing precise research objectives. Ideally, stress assessment should be combined with complementary methods (e.g. progesterone measurements, behavioural investigations).

Intraspecific variations of energy turnover and body temperature in free-living edible dormice, *Glis glis*

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Many mammals show marked seasonal fluctuations in their metabolic rate and body temperature (T_b). A substantial part of these annual changes can be attributed to different levels of locomotor activity, variations in food intake and the heat increment of feeding. However, in species where food availability varies regularly, MR and T_b may also be endogenously down-regulated to adjust energy expenditure to food availability.

Edible dormice (*Glis glis*) are small arboreal mammals and their whole life history is tightly linked to the irregular seed production of their main feeding trees. Accordingly, edible dormice reproduce in years with high food availability, but entire populations may skip reproduction in years when tree seeds are absent.

One aim of this field study was to investigate energy turnover and T_b in edible dormice during periods of high and low food availability, to understand energy saving strategies, besides the use of hibernation and torpor. Furthermore, we wanted to know if energy consumption during the active period of edible dormice is endogenously controlled or primarily effected by environmental factors like food availability.

We therefore measured resting metabolic rate (RMR) of 37 euthermic individuals with portable gas analysers (Oxbox) and analysed T_b patterns of 118 individuals during years of high and low food supply. All measurements were carried out in the field during the active period of edible dormice between 1996 and 2012 in south western Germany.

Results of this study demonstrate that energy turnover and T_b in edible dormice vary markedly over their active season during years of high food availability. Variations of food intake and the heat increment of feeding are likely to cause a substantial part of these variations together with the reactivation of organs that are atrophied during hibernation. During years of low food availability, however, T_b and RMR were significantly lower than during years of high food supply and did not show seasonal variations. Results of our study reveal that edible dormice are perfectly adapted to the irregular pattern of food supply, as they drastically reduce energy consumption, by slightly lowering their T_b during years when tree seeds are absent.

Applied chronoethology

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The time pattern of behaviour is controlled by genetics and, of course, modified by the actual living conditions (ASCHOFF *et al.*, 1982; BENESCH *et al.*, 2005; DAAN and ASCHOFF, 1975; FLEISSNER and FLEISSNER, 1998; SCHEIBE *et al.*, 2009). As these behavioural patterns reflect the well-being of animals, and, thus, may become an important tool for improving any kind of animal keeping, it is first of all necessary to establish a "reference chronoethogram" under the given maintenance conditions. Comparison of the current time structure of various behavioural categories with this reference chronoethogram may allow for conclusions about the health situation, phase of reproductive cycle, deficits of the keeping conditions, etc., and even a prognosis for major events, e.g., of the day and time of giving birth. By means of studies on more than 50 species of zoo animals like giraffes, elephants, moose and also desert arthropods like scorpions the idea of a "chronoethologic paradigm" will be introduced and discussed. Nowadays, sophisticated development of computer-based data acquisition offers a very optimistic future of applying chronoethology on animals and humans as data sampling and even their interpretation can in large part be taken over by computers.

ASCHOFF J, DAAN S, HONMA KI (1982): Zeitgeber, Entrainment and Masking: Some Unsettled Questions. In: ASCHOFF J, DAAN S, GROOS GA (Eds.), *Vertebrate Circadian Systems*. Springer, New York, pp. 13 - 22.

BENESCH AR, EHLERT K, HOFMANN M, HOLLAND R, KANDLER C, LUEDICKE T, RATZE S, RUCH T, SCHUBERT C, SICKS F, BECKER M, FLEISSNER GU, FLEISSNER GE (2005): The influence of husbandry on the circadian activity rhythms of zoo animals. *Mammal Biol* **70S**, 9 - 10.

DAAN S, ASCHOFF J (1975): Circadian rhythms of locomotor activity in captive birds and mammals: their variation with season and latitude. *Oecologia* **18**, 269 - 316.

FLEISSNER GU, FLEISSNER GE (1998): Natural photic Zeitgeber signals and underlying neuronal mechanisms in scorpions. In: TOUITOU Y (Eds.), *Biological Clocks - Mechanisms and Applications*. Paris: Elsevier, pp. 171 - 180.

SCHEIBE KM, ROBINSON TL, SCHEIBE A, BERGER A (2009): Variation of the phase of the 24-h activity period in different large herbivore species under European and African conditions. *Biol Rhythm Res* **40** (2), 169 - 179.

Population structure and re-establishment of Eurasian beavers in Germany and adjacent regions

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Following its near-extinction in Germany during the first half of the 20th century, the beaver has made a remarkable comeback during the past decades. During multiple reintroduction programmes beavers of various origins have been successfully established in different parts of the country, which leads to complex and regionally different genetic patterns within and among beaver populations in Germany and adjacent regions. We collected samples of various central European beaver populations, including the admixed southern German population, the relict population of *Castor fiber albicus* along the Elbe drainage and introduced beaver populations in Hesse, the Greater Region, and Switzerland. Analyses of nuclear (microsatellites) and mitochondrial (control region sequencing) DNA variation show that genetic diversity within beaver populations is usually highest in regions with repeated introductions from multiple origins. While admixture between different beaver lineages is nearly complete in southern Germany, it is still an ongoing process in populations of the Elbe drainage, between southern Germany and Hesse, and between different introduced lineages in Switzerland. In conclusion we hypothesise that beavers will continuously admix in Germany, eventually leading to the potential disappearance of local forms or traditionally recognised "subspecies".

The use and integration of molecular DNA information in conservation breeding programmes

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Conservation breeding programmes often rely on intensive genetic management of the captive population. However, the relatedness between individuals and the individual mean kinship is often estimated based on pedigree records, which are frequently incomplete or can even be unreliable. Depending on the quality of a studbook (e.g. expressed as percentage of pedigree known), molecular information can substantially improve the knowledge of a population, and therefore contribute to improving the retention of genetic diversity every generation. As the use of molecular data has been largely undervalued, this presentation aims to provide information on the various types of genetic markers that can be used, the estimation of (DNA based) relatedness and pedigrees, their integration in studbooks, the use of molecular information in breeding pair selection, hybridisation issues and population management in general. In this presentation we discuss recent developments in methodology (e.g. next-generation sequencing), theoretical considerations, and software that can aid conservation breeders in each phase of the programme from the founding phase to the (potential) reintroduction, each clarified by various examples from recent literature. Special attention is given to group management since it is much harder to control mating and reconstruct pedigrees.

New mitochondrial DNA primers to identify species from meat in poisoned baits: a contribution to wildlife forensic investigations

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European laws prohibit or restrict the use of poisoned baits. Nevertheless, they continue to be a common, illegal practice in many countries. The laying of baits represents a serious threat for wild animals, when poison is released into nature, while in urban areas baits are highly dangerous for livestock and pets, as well as for humans. A conspicuous number of poisoned bears, wolves, foxes, wild boars, birds of prey and other wild species are delivered every year to “Centro di Referenza Nazionale per la Medicina Forense Veterinaria” for post-mortem examination, together with the poisoned baits found on the crime scene or in the surroundings. Baits and stomach contents of the victims are analysed to search for the toxic, while the species source of the tissues that make up the baits and poisoned food (usually meat) ingested are molecularly identified through DNA testing. The results from species identification can link an alleged poisoner to the offence: for example, the link is found if individuals of the same species as that identified in the meat of poisoned baits, and/or in the stomach content of the victims, are also possessed by the suspect; or if the specific individual used as bait shows kinship relationships with those of the same species possessed by the suspect. In other words, by delineating the perpetrator's “*modus operandi*” you can narrow the investigation and successfully resolve a case. The DNA extracted from baits and stomach contents is often of low quantity and quality. DNA barcoding for species identification is usually based on the sequencing of mitochondrial (mt) fragments longer than 600 base pairs (bp), which are hardly amplifiable in forensic samples. Our DNA analysis was conducted using newly designed primer sets for the identification of species through sequencing of small mtDNA segments. Primer pairs were designed to amplify: 1) a 483 bp long segment in the cytochrome b of mammals and birds; 2) four fragments, which differ in length from 231 to 427 bp, in the 12S gene of mammals; 3) a 387 bp long segment in the ND6 gene, specific to birds. The design step was followed by the setup of amplification protocols. Primers were first tested on reference samples and then used to identify species from tissues in baits and stomach contents of poisoned animals. A wildlife forensic case is presented in which the newly developed primer pairs have been successfully used in a crime of poisoning.

Population genetic structure of the critically endangered Saiga antelope *Saiga tatarica* in Kazakhstan

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While the historic Eurasian distribution of the *Saiga tatarica* (Linnaeus, 1776) ranged from the north of France to the New Siberian Islands, the recent distribution is restricted to fragmented populations in the Eurasian steppe of Kalmykia, Kazakhstan, and Mongolia. Since the end of the last glacial period former distribution ranges were contracted presumably caused by climate warming enhanced by anthropogenic impacts. This resulted in habitat fragmentation and population decline. Further studies showed a reduced mitochondrial genetic diversity in recent populations compared to ancient samples. However, there is still a lack of knowledge about fine scale population patterns, population connectivity and recent gene flow in the current relict populations of the species, although this data is crucially needed to delineate units for conservation management.

Therefore we developed a set of highly variable microsatellite markers and applied it to blood samples of 175 individuals from all three relict populations in Kazakhstan (Ural, Ustyurt, Betpak-Dala). Genetic diversity was relatively low, in coincidence with observed massive population declines during the past century. The analysis of molecular variance (AMOVA) showed a hierarchical structure of the groups with most variation (~97.5 %) within populations. Further analyses revealed generally strong genetic similarities between populations, with a clear genetic differentiation between the western population (Ural) and the eastern ones (Ustyurt, Betpak-Dala).

Using molecular genetic analysis to evaluate the impact of missing pedigree data on small population management

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Small closed populations, such as those found in zoos, risk losing genetic diversity through drift and inbreeding. Contemporary population management programmes aim to reduce this by issuing breeding and transfer recommendations based on relatedness values derived from pedigree analysis. The effectiveness of population management is compromised because many studbooks have missing pedigree data. To address this, population managers historically created analytical studbooks that filled in the gaps in the pedigree with ‘best guesses’ resulting in a complete, but possibly fictional, studbook that can be used for population management. The recent development of new software has allowed the inclusion of multiple sires and dams as parents for individuals with missing parentage data. Whilst both of these approaches address the issue of missing pedigree data, their efficacy and impact on managed populations had not been evaluated.

This study used relatedness values derived from 13 microsatellites (molecular markers) to evaluate the comparative accuracy of the true international studbook with missing parentage data, a traditional analytical studbook, and an analytical studbook constructed with multiple parents for a threatened species of antelope, the scimitar-horned oryx *Oryx dammah*. This international studbook is particularly appropriate to explore these issues because it contains a large data set with substantial amounts of missing pedigree data (69 %), and is representative of many other studbooks.

There was concordance between the true and analytical studbooks, but no relationship between any of the true and analytical studbooks and the molecular data until original pedigree completeness exceeded 87.5 %. However, sample size was too small at this level of pedigree completeness to be conclusive ($N = 9$). The impact of using molecular, true and analytical studbook data for population management decisions was evaluated in both a true and analytical studbook framework. Overall, analytical studbooks performed better, indicating that it is appropriate to use analytical data sets for population management. The results highlight the importance of complete pedigree data for populations under intensive management. When pedigree data are largely missing, molecular analyses may provide an alternative approach to preserving genetic diversity in captive populations. Limitations of the study are discussed along with recommendations for additional research.

Investigation of diet and hunting behaviour of Eurasian lynx (*Lynx lynx*) using location and activity data of Vectronic-GPS-collars

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From a conservation and management perspective predation is an important aspect of large carnivore ecology. In the past decade, technological developments, especially telemetry with global positioning systems (GPS) and global systems for mobile communications (GSM), have provided valuable insights into diet and prey selection of elusive predators. Modern collars (e.g. GPS collars from Vectronic Aerospace, Berlin) record GPS location and acceleration data simultaneously, but data are usually analysed separately in behavioural and ecological studies on large predators. FRÖHLICH *et al.* (2012) were the first to provide data for a novel approach of combining GPS cluster analysis and activity data to study the hunting activity of a single female leopard. Results showed that the combination of these methods provides valuable means for detecting kill sites, predicting kills from non-kills and to get further insight into feeding patterns. We refined the method presented by FRÖHLICH *et al.* (2012) with a larger data set to gain further insight into the behavioural ecology and feeding habits of Eurasian lynx in the Bohemian Forest. During a previous study we identified clustered GPS positions of six lynx (three males and three females) obtained by Vectronic-GPS-collars (Vectronic Aerospace, Berlin). These potential lynx kill sites were checked for prey remains in the field. We compared these data with positions and acceleration data also obtained by the Vectronic-GPS-collars. A total of 250 confirmed kill clusters were distinguished from 57 non-kill clusters and several periods of “normal activity” outside the clusters. We checked for feeding patterns using General Additive Modelling (GAM) and frequency analysis of activity data. The advantages and disadvantages of this method are discussed in order to evaluate how far the collar data can serve as an automatic detection of hunting behaviour in lynx and therefore reduce laborious and time consuming field work.

FRÖHLICH M, BERGER A, KRAMER-SCHADT S, HECKMANN I, MARTINS Q (2012): Complementing GPS cluster analysis with activity data for studies of leopard (*Panthera pardus*) diet. *S Afr J Wildl Res* **42/2**, 104 - 110.

Mating behaviour of Steller sea lion (*Eumetopias jubatus*) females

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It is widely accepted that in eared seals males play a main organising role in reproduction. They are highly territorial, and detain as many females in their territory as possible, thereby restricting access of other males to harem females. Despite of that, many authors have pointed out that in some species of eared seals female mate-choice may be as important for reproduction as male fighting ability and the role of males in the breeding organisation is overstated because the harem mating system did not provide the expected benefits for the males. We investigated the role of Steller sea lion females in the formation of reproductive relationships and the impact of social environment on that role. We analysed video records collected in 2010 (rookery at Kozlov Cape (KC), Eastern coast of Kamchatka), and 2011 (rookery at Medny Island (MI), Commander Islands). We recorded 67 and 115 copulations on KC and MI, respectively. We also used detailed descriptions of 46 copulation events at KC and 21 at MI. In both years from June 10th to 10th July, we determined the maximum number of males and females on both rookeries (peaking between June 16th and June 21th). Most of mated females delivered one pup in present year (KC – 59 %, MI – 83 %). The presence of a pup indirectly restricted the mobility of the female while in oestrus. Females with and without pups used different parts of the rookery and mated with different categories of males (with pups: central areas; without pups: mostly on the edge). Duration of activity and movement prior to mating was a function of pup presence (with pup < without pup) and rookery (with pup: MI < KC; without pup: MI > KC). Differences between rookeries probably are due to differences in the territorial organisation of the males. Duration of female movements after copulation also depends on pup presence on both sites (with pups < without pups). Females without pups moved on the rookery for a longer period. During these movements and while in oestrus they visited territories of several males and were more likely to mate repeatedly compared to females with pups. The maximum number of males that females interacted with during oestrus reached six. Females on average attracted males for 278 minutes. The observed differences in the behaviour of females with and without pup indicate the differences in mechanism of mate choice, and indicate that each group of females has a different role in the formation of reproductive relationships.

Signs for eustress but not distress in black rhinos (*Diceros bicornis*) moved into new housing facilities at Magdeburg Zoo, Germany

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Translocations are invasive and potentially stress-inducing events. Stress may be acute (eustress) or chronic (distress), leading to opposite effects: Acute stress is a punctual response to a short-term stressor, which rapidly wanes and is followed by homeostasis. Chronic stress, however, is a prolonged state with greater potential to negatively affect growth, reproduction and survivorship.

Several studies have used faecal corticoid metabolites (FCM) to assess the stress responses of black rhinos (*Diceros bicornis*) in conjunction with soft-release translocations (capture in the wild, immobilisation, transportation and boma / enclosure management at destination). These procedures lead to ongoing acclimatisation responses in terms of constantly decreasing FCM levels over several weeks. There is, however, little information about the stress level in conjunction with less invasive translocation procedures, e.g. when shifting black rhinos within a zoo between housing facilities.

We measured the FCM concentrations of four black rhinos during a transfer into new housing facilities at the Zoological Garden in Magdeburg (Germany) and one year afterwards using an enzyme immunoassay. The aim was to evaluate the degree of stress responses to the transfer and compare it with FCM profiles from much more invasive *in situ* studies reported in the literature. We give a detailed description of the transfer procedure and housing facilities to highlight the expected lower degree of invasiveness when comparing this study with information from the literature.

As expected, FCM profiles of individual rhinos clearly differed from those described in the literature and showed a moderate and punctual response in conjunction with the transfer but no signs of a period of acclimatisation over several days or even longer. Increased FCM levels of one female one year after the transfer were probably not related to distress caused by the new housing facilities but could be linked to the reproductive status (5 - 6 months before parturition).

Our contribution may serve as a case study for a successful transfer procedure of black rhinos into new housing facilities within zoological gardens, since no signs for distress were detected. Moreover, we assume that moderate eustress may serve as a positive stimulus, which can even increase the reproductive performance of black rhinos in captivity.

Urban red foxes as carriers of antimicrobial resistant bacteria

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Antimicrobial resistant bacteria are a growing threat in human and animal medicine. The role of wildlife in the spread of these bacteria in urban wildlife is widely unknown (GUENTHER *et al.*, 2011). As red foxes (*Vulpes vulpes*) in many cities reach high population densities (BOERNER *et al.*, 2011), have an opportunistic lifestyle and are already subject to several investigations of zoonotic pathogens, we assumed them to be a good study population for antimicrobial resistant bacteria. A total of 512 red foxes, collected from April 2010 to December 2012 in the Berlin city area were investigated for cephalosporin resistant *Escherichia coli* (crEc). Obtained isolates were characterised and compared to those from other animals and humans. Furthermore the pathogenic potential of the crEc was determined to estimate the possible impact of these bacteria on wildlife. For spatial correlation analyses the location of crEc positive foxes was related to different factors, like hospitals, large streets, or number of restaurants in the close proximity that might stand for the availability of garbage food resources.

We found the proportion of red foxes carrying crEc similar to that found in humans and companion animals (KRESKEN *et al.*, 2013), with a wide variety of clonally different isolates. The crEc harboured different patterns of virulence associated genes, some of which suggesting pathogenic potential also for the host animal. The finding sites of crEc positive animals were evenly distributed compared to those of negative animals. There was no significant correlation of the finding sites to the different spatial factors.

Our results point to a frequent exchange of resistant bacteria between humans, companion animals and wildlife in urban areas. Additionally they confirm the red fox as a good indicator species for this kind of investigations.

GUENTHER S, EWERS C, WIELER LH (2011): Extended-spectrum beta-lactamases producing *E. coli* in wildlife, yet another form of environmental pollution? *Front Microbiol* **2**, 246.

KRESKEN M, HAFNER D, KÖRBER-IRRGANG B (2013): PEG-Resistenzstudie - Abschlußbericht 2010, Editor: PEG, Rheinbach, ISBN 978-3-00-040996-7.

BOERNER K, SCHNEIDER R, WITTSTATT U, METZ A (2011): Ausgewählte Parameter zur Populationsbiologie und dem Krankheitsgeschehen des Rotfuchses (*Vulpes vulpes*) in Berlin. Workshop "Wildtiere in Deutschland – ein Überblick zur Ökologie- und Infektionsforschung". 11th to 12th November 2011, Berlin, Germany.

Nutrient and energy content of zoo diets of giraffes and effects on intake in groups of giraffes

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In giraffe diets proportions of lucerne hay, browse and high energy feeds (concentrates and produce) can vary considerably, obviously resulting in diets of different nutritional quality. From the background of diet recommendations and concerns related to nutrition, dry matter intake (DMI) and nutritional quality of diets were quantified for groups of giraffes (*Giraffa camelopardalis*) in six German zoos.

The DMI of the groups was estimated on five consecutive days, for zoo 1, 2 and 3 in winter and summer respectively, for zoo 4, 5 and 6 in summer (n = 9). To consider the heterogeneity of the groups in terms of energy requirement, mean DMI (g/kg metabolic body size [BM^{0.75}]) and mean energy intake (MEI) (MJ ME/kg BM^{0.75}) were standardised to the level of maintenance energy requirement by using factors depending on the individual status of performance (gestation, lactation, growth) of each animal. Feed samples were analysed for chemical composition. Gas production was measured at 24 hours in the Hohenheim gas test for estimating metabolisable energy (ME) for ruminants. Correlation coefficients were tested with SAS 9.2.

Mean DMI was 56.8 g/kg BM^{0.75} (± 8.33). MEI was observed to be on average 0.58 MJ ME/kg BM^{0.75} (± 0.06) and thus likely sufficient to cover assumed requirements (0.40 - 0.60 MJ ME/kg BM^{0.75}). Roughage content ranged from 46 to 61 % of DM, partly not meeting recommendations of at least 50 % roughage in diets. Content of concentrates and produce showed wide ranges of 31 to 53 % and < 1 to 18 % of DM, respectively. Crude protein content in diets was 168 g/kg DM (± 10.9) and fibre (aNDFom) content 454 g/kg DM (± 33.7). A significant negative correlation could be shown for ME content and DMI (p = 0.0017) as well as for ME content and MEI (p = 0.0367). By trend there was a negative correlation between fibre content and ME content (p = 0.0979), whereas fibre content and DMI showed a positive correlation by trend (p = 0.0814). For crude protein content no effects could be determined.

Following a traditional concept of feed intake regulation a negative correlation for ME content and DMI and no significant relation between fibre content and DMI indicate a mainly energy-regulated feed intake in the observed giraffes. Therefore the chemical diet characteristics seem to be more important regarding a decrease in DMI than the structural characteristics of the present diets.

The impact of visitors to a wildlife park on a wild population of red squirrels (*Sciurus vulgaris*)

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As the grey squirrel continues to spread, red squirrel populations are becoming severely contracted and in many habitats are dying out. This could result in red squirrel populations becoming isolated to managed parks, where grey squirrels access can be controlled. However, recreation and public presence can often have a negative effect on the presence of wildlife. This study took place in Fota Wildlife Park, Ireland, an island currently free of grey squirrels. The study aimed to investigate the effect of visitors to Irelands 4th biggest attraction to the existing red squirrel population, as well as investigate whether this park could successfully sustain a healthy, viable red squirrel population. Red squirrels are monitored through monthly trapping and eight squirrels (4♀, 4♂) have been fitted with radio tags. Hair samples are also obtained to examine genetic variability and dispersal throughout the island. These squirrels are monitored twice a week, to obtain information on habitat use and behaviour. When a fix is obtained the number of visitors visible from that location is recorded. In addition daily visitor numbers are obtained from staff operating the gates. A questionnaire is allocated to visitors as they enter the park to record whether they had seen a squirrel during their visit. Squirrel counts are also conducted in areas of public and non public areas at different portions of the day. Provisional results have found that the park supports a healthy squirrel population. However, visitors do appear to impact on habitat use. Tagged squirrels have been observed to move further and explore public access areas to a greater extent when the park is not open to visitors. At times when the park is open, squirrels restrict themselves to areas outside the public domain and constrict their activity to smaller, quieter areas of the park. This study therefore indicates that while public parks can support viable healthy squirrel populations, areas have to be provided where public access is prohibited.

Seasonal age effect in glucocorticoid levels of free-living mouse lemurs

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Glucocorticoids are essential for numerous physiological processes and elicit appropriate responses to stressors; yet chronically elevated levels can lead to impaired health and survival. Studies in humans and mainly captive animals have found that ageing can elevate glucocorticoid levels (GCL) in both sexes. Furthermore, females often show higher basal GCL than males, possibly due to the effects of sex hormones. We examined GCL in relation to animal age and sex in free-living grey mouse lemurs, *Microcebus murinus*, via cortisol metabolite analysis from faeces. GCL were predicted to increase with age and be higher in females. Seasonal patterns were also analysed because of the pronounced seasonality of the habitat.

Faecal samples were collected from individually marked, aged and sexed individuals in Western Madagascar in two dry seasons (mating season, low food availability) and two rainy seasons (end of breeding, high food availability) and GCL were determined with a previously validated enzyme immunoassay.

Adults and old individuals had significantly higher GCL in the dry season than in the wet season. Moreover, the old age class showed significantly higher GCL than juveniles and adults in the dry season, while no age differences were seen in the rainy season. Contrary to our predictions, we found no sex differences in the GCL in any age class or season.

Previous studies have demonstrated that seasonality and ageing can influence GCL. Our results further indicate that in a natural population, senescence and chronic stress may interact to cause a significant GCL raise in aged animals. Seasonal GCL peaks may have negative implications for the health and survival of old individuals.

Multiplex capture of gorilla MHC using DNA from noninvasive samples

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The major histocompatibility complex (MHC) genes play a central role in the vertebrate immune response and thus are expected to influence an individual's fitness. However, comparison of MHC variation and fitness in representatives of endangered species living in natural environments is challenging due to the typical reliance on one or few MHC loci and the use of low quality DNA obtained from noninvasive samples. Inspired by target enrichment strategies employed in the study of ancient DNA, we are using long-range PCR products as "bait" to capture complete genomic sequences of all functionally-relevant MHC genes from DNA derived from wild gorilla faecal samples. We will highlight numerous challenges encountered, including amplification of specific MHC loci as bait. Data generated are being used in conjunction with observational data from a long-term study of wild living mountain gorillas (*Gorilla beringei beringei*). Long-term demographic data will enable us to examine whether this population has maintained high overall patterns of MHC diversity over the last three generations and look for associations between particular MHC variants and individual fitness-related traits such as reproductive success and survival. In sum, this study highlights an approach for MHC analysis in non-model organisms as well as provides fundamental data on the extent of immunity-relevant genetic variation present in a wild animal population.

Safe and sound? Investigation of the immune system in an obligate hibernator

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Hibernation and torpor represent the most extreme physiological adaptations of small mammals to reduce energy expenditure during environmentally unfavourable conditions. During hibernation heart and metabolic rate (MR) are drastically reduced and body temperature (T_b) can reach values around the freezing point. In hibernating species studied so far it could be shown that these extreme physiological changes encompass a severe decrease in circulating leukocytes (~ 90 %) and an impairment in a variety of immune functions during torpor, recovering immediately afterwards.

The edible dormouse (*Glis glis*, 120 g), is a small arboreal mammal inhabiting the deciduous European woodlands. It hibernates about eight months in underground burrows. Meanwhile its survival is highest during winter and mortality reaches highest values in early summer, directly after emergence from hibernation. One aim of this study was therefore to investigate whether hypothermia influences the immune system at the beginning of the active period of edible dormice, which could explain high mortality rates.

Furthermore, immune function is known to be affected by stress which, for example, can be caused by high population densities. Hence, a second aim of our study was to comparably analyse immune and blood characteristics of animals from populations which strongly differ in density.

We therefore captured-marked-recaptured edible dormice in five different study sites in South-Western Germany between June and September 2012 and 2013. We collected blood samples of adult males and females and determined leukocyte and differential blood cell counts as well as several erythrocyte parameters.

On the one hand, our results revealed a clear seasonal pattern in proportions of circulating leukocyte subtypes. While lymphocytes clearly dominated (> 90 %) at the beginning of the active season, proportions of monocytes and neutrophils recovered in the course of the year. A delayed onset in the production of innate immune cells may cause this phenomenon and make edible dormice susceptible to pathogens after hibernation is terminated in early summer.

On the other hand, variations related to population density could be detected in red blood cell parameters. Accordingly, erythrocyte numbers and haematocrit were significantly higher in individuals inhabiting sites of high population density, whereas mean corpuscular haemoglobin was significantly lower in these individuals, indicating anaemia in high density populations.

Summarising, our results reveal that extreme physiological changes during obligate hibernation as well as population densities are reflected in the immune system and other blood parameters in this small mammal.

Ecosystem service of European bats in an anthropogenic landscape

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Bats are known to provide important ecosystem services like the distribution of seeds, the pollination of tropical plants and the consumption of insects (reviewed in GHANEM and VOIGT, 2012). In the temperate zone, bats are particularly relevant for humans by feeding on pest insects, thus reducing insect populations that are detrimental for agriculture (reviewed in KUNZ *et al.*, 2011).

In this study we investigate species richness and foraging activity of bats on three crop types (corn, rapeseed and wheat) in an intensively used agricultural area in the North of Germany. Additionally we assess if and how factors like the crop type, the relative insect abundance and the landscape structure have an effect on bat activity and species richness. Using a genetic approach, we investigate the diet of two common aerial-hawking bat species. We aim to estimate the extent of ecosystem services provided by European bat species and are specifically interested in answering the question whether they feed on economically relevant pest insects, and whether this translates into a monetary benefit for the agricultural industry.

This study is embedded in a large-scale project (AgroScapeLabs: www.scapelabs.org) which aims at exploring land use effects on biodiversity and its links to ecosystem functioning in an agriculturally used landscape.

GHANEM SJ, VOIGT CC (2012): Increasing awareness of ecosystem services provided by bats. *Adv Stud Behav* **44**, 279 - 302.

KUNZ TH, BRAUN DE TORREZ E, BAUER D, LOBOVA T, FLEMING TH (2011): Ecosystem services provided by bats. *Ann NY Acad Sci* **1223**, 1 - 38.

Social distances and association indexes - what can they tell us about the sociality of giraffes?

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Many studies claim that there are no permanent ties and social preferences among giraffe individuals. Giraffes live in the fusion-fission system, groups are temporary and their size depends on the season. The only stable bond in the wild is described between mother and her calf; however there are social bonds among female giraffes in captivity. We aimed to prove that social bonds and preferences among giraffe females exist also in the wild, according to the association index (AI) and inter-individual distances (IID). Twenty-eight introduced giraffes (seven of them adult females) were observed in Bandia reserve in Senegal. In total 144 contacts (88 group and 56 individual sightings) and 70 hours of measuring IID (10h for each female) were recorded in 34 days. We expected that stronger relationships would occur among two females with $AI > 0.4$. These females were considered as “friends”. Simultaneously three hypotheses were postulated. (i) The females with higher AI will have shorter IID than the females with lower AI. (ii) The females with higher AI will be the nearest neighbour more often than the females with lower AI and (iii) the females with higher AI will be among the three nearest individuals more often than the females with lower AI. The mean AI was 0.16 (0 – 0.76). The highest AI was recorded for mother-calf pairs as expected. Three pairs of female giraffes met the criteria of $AI > 0.4$. The mean IID was 50.4 (1 – 200m). (i) The IID was shorter for animals with higher AI (Spearman's coefficient: $= -0.184$, $p < 0.05$). The same result was found also among females but not significant. (ii) The females with higher AI were more often the nearest neighbour (MW U test: $U = 20535$; $Z = -2.432$; $p = 0.01$) (iii) and were also more often among three nearest individuals than the females with lower AI ($U = 29416$; $Z = -2.858$; $p < 0.01$). We proved the social preference for particular female. Therefore, we suppose the existence of social preferences and bonds among wild giraffes.

The research is supported by the Grant Agency of Czech University of Life Sciences Prague CIGA 20135010, CIGA 20134217 and IGA FTZ 51120/1312/3110 and by project Postdok ČZU (ESF/MŠMT CZ.1.07/2.3.00/30.0040).

Quantitative genetics in conservation breeding

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Preserving the genetic architecture of populations over time is an important objective in sustainable conservation breeding. In order to maximise the retention of genetic diversity and minimise inbreeding, *ex situ* population management is essentially based on selective breeding. As such Zoos maintain species specific databases (studbooks), which not only include pedigree information but also contain valuable information on the individual level (e.g. phenotypic, housing, medical and reproductive data). Recent advances in quantitative genetic tools (e.g. mixed-effects models) reinforced the interest in these databases as being “ideal” systems to study evolutionary processes. More specifically, animal models have been put forward as a potentially valuable instrument in a conservation genetic framework to: (i) assess the preservation of additive genetic variance of traits, (ii) evaluate heritabilities and (iii) reveal potential evolutionary responses to selection in captivity. However, concerns on the use of this methodology in carefully managed populations and the role of epigenetics awaits thorough evaluation. In this contribution we will outline recent advances in quantitative genetics focusing on its use in conservation breeding.

Plasma leptin and ghrelin are associated with crib-biting in horses

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Crib-biting in horses is classified as oral stereotypy. A crib-biting horse (*Equus ferus caballus*) grasps a fixed object with its incisors, pulls back and emits a characteristic grunt while drawing air into the cranial oesophagus. Crib-biting is a highly motivated behaviour but its aetiology is poorly understood. Management, gastrointestinal function and genetic susceptibility have been suggested as causal factors. Leptin and ghrelin are orexogenic hormones that regulate appetite and modulate the reward mechanism.

The aim of this study was to determine ghrelin and leptin plasma concentrations in crib-biting horses. The hypothesis was that ghrelin and leptin are associated with crib-biting. Three plasma samples were collected for plasma leptin and ghrelin assay before and during the first morning feeding in customary environments of 15 horses with stereotypic crib-biting and 15 matched controls. Crib-biting intensity was scored in three 5-min phases, and a subgroup of verified crib-biters (n = 8) was defined as horses that were seen to crib-bite during this study.

Plasma leptin concentrations (mean, 95 % confidence interval, CI) were lower in horses seen to crib-bite (1.2, CI 0.8 - 1.7 and 1.0, CI 0.6-1.7 ng/mL) before and after feeding of concentrate, respectively, than in controls (2.3, CI 1.6 - 3.4 and 2.3, CI 1.6 - 3.4 ng/mL) and correlated negatively with crib-biting intensity. Crib-biting intensity was significantly higher shortly after the concentrate than before or 30 min after it. Plasma ghrelin concentrations were significantly higher before feeding on concentrate than before hay feeding or after concentrate consumption but did not differ between groups.

These findings suggest that leptin is associated with crib-biting behaviour in horses. Lower leptin concentrations in verified crib-biters may be attributable to differences in preferences for palatable food or differences in reward mechanism modulation. Decreased leptin concentration may be a predisposing factor for crib-biting, crib-biting bouts may decrease the leptin concentration, or there may be a third, unknown factor affecting both crib-biting and plasma leptin concentration. In our recent study, plasma ghrelin concentrations were higher in crib-biting horses than in their controls. Both ghrelin and leptin have been associated with feeding, sweet sensitivity and reward behaviour, and thus interaction of leptin and ghrelin with the reward system in feeding behaviour is likely.

Hatching failure in wild and captive endangered birds

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In many critically endangered birds, more than half of all eggs laid never hatch. This represents a huge reduction in the reproductive success of many struggling species. Most studies fail to distinguish between infertility (due to a lack of sperm) and embryo mortality as the cause of hatching failure, yet doing so is crucial in order to understand the underlying reproductive problem. Using newly developed techniques, which involve using fluorescence microscopy to visualise sperm and embryonic tissue (BIRKHEAD *et al.*, 2008), we are now able to determine unequivocally whether unhatched eggs were fertilised or not. Across over 300 eggs from five endangered species, including both wild and captive birds, we found the majority of unhatched eggs had been fertilised and numerous sperm had reached the ovum (HEMMINGS *et al.*, 2012). This finding indicates that infertility is not a major problem for endangered birds; instead, high levels of embryo death contribute to their low reproductive success. Eggs of captive birds had fewer sperm and were more likely to be infertile than those of wild birds. Our findings have important implications for bird conservationists and raise interesting questions regarding the management of captive breeding programmes.

BIRKHEAD TR, HALL J, SCHUT E, HEMMINGS N (2008): Unhatched eggs: methods for discriminating between infertility and early embryo mortality. *ibis* 150: 508 - 517 (doi:10.1111/j.1474 - 919x.2008.00813.x)

HEMMINGS N, WEST M, BIRKHEAD TR (2012): Causes of hatching failure in endangered birds. *Biol letters* (doi:10.1098/rsbl.2012.0655)

Aggressiveness and the ability to manage a problem situation – testing the coping styles hypothesis in two house mouse subspecies

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The coping styles concept describes the association between behavioural strategies and the level of aggression. By this paradigm, two approaches can be defined: proactive – more aggressive, active and less flexible; and reactive – less aggressive, likely to be passive, but more flexible. It is also suggested, that proactive type is successful in stable conditions, while reactive type have advantages in dynamic situations. Two house mouse subspecies, *Mus musculus musculus* and *Mus m. domesticus*, which hybridise along a contact zone across Europe, are known to differ in the level of male aggression, as well as in several other behavioural parameters. The aim of our study was to investigate how males of both subspecies cope with aversely motivated test in the Morris water maze, and to reveal if their behaviour corresponds with the coping styles concept. We tested the first generation offspring of wild mice and homosubspecific F₁ crosses between wild-derived strains. There was no significant difference in basic swimming capacities, although there were some signs of species-specific swimming patterns. Interestingly, in agreement with the coping styles concept, less aggressive *M. m. musculus* males performed significantly better in solving the Morris water task. This suggests that *M. musculus* subspecies are more flexible and act better under stressful and/or dynamic situations, which can appear during dispersal. We conclude that this advantage may play a role in selection-dispersal dynamics of the house mouse hybrid zone.

Financial support: Czech Science Foundation grants Nos. 206/08/0640 & P506-11-1792.

Seasonal response to low protein in wild cavies (*Cavia aperea*)

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Herbivorous animals are well adapted to adjust their energetic and nutrient (protein, fiber) requirements to food availability and food quality. During phases of high energy/protein requirement such as growth or reproduction they increase food intake and selectively ingest high quality food, whereas during phases of low demands intake and quality might decline. This synchronization of energy demanding processes with food availability is particularly important in temperate zone animals facing pronounced seasonal changes in habitat quality. In our study with wild cavies (*Cavia aperea*) we aim at understanding how this small sized herbivore copes with dietary changes and protein-poor diets and whether the physiological response is influenced by season. We hypothesise that a decrease in dietary protein content in autumn, when facing winter time, provokes different reactions compared to a challenge in spring, when cavies start their reproduction phase.

Ten male cavies were housed under semi-natural conditions i.e. natural temperature and photoperiod in our field research station near Berlin. They were fed ad libitum a maintenance cavies diet (pellets, protein content 15.6 %) and hay (protein content 12.3 %), and had ad libitum access to water and indoor- and outdoor enclosures. In either spring or autumn two subgroups with each five cavies received a pelleted low-protein diet (protein content 6.6 %) and hay for two months. Digestion parameters such as intake and digestibility of dry matter, energy and protein, respectively were recorded before and after dietary treatment as well as six times during treatment.

In spring cavies lowered the intake of dry matter energy and protein but body mass remained constant. Compared to ad libitum intake rates in summer their energetic demand was met but protein was in deficit. However, during autumn treated animals showed a different response. Although dry matter intake and energy intake was increased they not completely compensated the protein deficit. Animals lost body mass at the beginning but recovered until the end of treatment.

Our results show that cavies are able to at least short-term cope with low-protein diets, but responses differed between seasons: in spring animals tolerate protein deficiency and feed energy orientated. In autumn cavies compensate protein deficiency by increasing dry matter intake, and by this increase body mass. We conclude that the phenotypic plasticity of cavies allows them to handle at least short term protein shortage and make them less prone to changes in food quality associated with, for example, climate change.

Accurate estimation of genome-wide heterozygosity using high-throughput sequencing

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Laboratory studies suggest that inbreeding can be detrimental to the fitness of individuals, but the effects of inbreeding depression in natural populations remain largely unstudied due to a paucity of deep pedigrees (PEMBERTON 2004). Alternatively, inbreeding can be estimated from the heterozygosity of genetic markers, but thus far it has not been practical to genotype the thousands of markers required for accurate estimation. Instead, molecular studies have largely relied on proxy measures of heterozygosity based on typically around ten polymorphic microsatellites (HANSSON and WESTERBERG 2002). We therefore used Illumina sequencing of Restriction Site Associated DNA (RAD) tags (DAVEY and BLAXTER 2011) to estimate genome-wide heterozygosity; an approach that is in principle transferrable to any organism. As a proof of concept, we first RAD genotyped 36 Oldfield mice (*Peromyscus polionotus*) from a semi-natural pedigreed population, and find good agreement between the inbreeding coefficient and heterozygosity based on 13,198 RAD markers ($r^2 = 0.75$). We then revisit a study reporting a heterozygosity-fitness correlation for lungworm burden in a natural population of harbour seals, *Phoca vitulina* (RIJKS *et al.* 2008). The original relationship based on 27 microsatellites strengthened considerably when 14,585 RAD markers were deployed, providing strong support for the underlying mechanism being inbreeding depression. We believe this to be the first convincing example of inbreeding depression in a natural system lacking a detailed pedigree, with implications for the way in which ecologists, evolutionary and conservation biologists study inbreeding depression in the wild.

DAVEY JW, BLAXTER ML (2011): RADSeq: next-generation population genetics. *Brief Funct Genomics* **9**, 416 - 423.

HANSSON B, WESTERBERG L (2002): On the correlation between heterozygosity and fitness in natural populations. *Mol Ecol* **11**, 2467 - 2474.

PEMBERTON J (2004): Measuring inbreeding depression in the wild: the old ways are the best. *TREE* **19**, 613 - 615.

RIJKS JM, HOFFMAN JI, KUIKEN T, OSTERHAUS ADME, AMOS W (2008): Heterozygosity and lungworm burden in harbour seals (*Phoca vitulina*). *Heredity* **100**, 587 - 593.

The highs and lows of blending molecular genetics with pedigree data to preserve a critically endangered species

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The orange-bellied parrot, *Neophema chrysogaster*, (OBP) is a critically endangered Australian parrot. The OBP is one of two species of parrot that migrates, wintering on the coastal saltmarsh of southern Australia before migrating to Tasmania to breed in the austral summer. In 2010, it was estimated that there were only 50 birds remaining in the wild despite a long-term recovery programme being in place. The OBP has been part of a zoo-based breeding programme since 1986 and over 470 birds have been released over a 15 year period. In the early days of the programme, multiple birds were held in flocking aviaries and so definitive pedigree information is lacking, with 172 parental assumptions made in the studbook. In 2011, 21 new founders were brought in from the wild to supplement the current zoo-based breeding programme. Blood samples collected from the new founders, along with blood collected from 140 captive birds in 2011, were analysed using the markers described in MILLER *et al.* (2013). All of the 14 markers described were found to be heterozygous and used for this analysis.

We have been conducting an extensive review of the OBP programme using a number of new tools, including the MULT capacity of SPARKS 1.6 and its incorporation into PMx, in addition to the molecular genetic data from 160 birds. The highs of this review to date include the resolution of some earlier unknown pedigrees, the ability to allocate possible parents; and the ability to understand the differences in gene diversity and inbreeding of both the current captive and the current wild populations. The lows have been the difficulty in determining which is the best relatedness estimator to use, and how to best incorporate the data into the zoo-based breeding recommendations. The crude method developed so far has allowed us to make significantly better breeding recommendations in 2012 and 2013. Work on streamlining the method continues. The long-term goal is to develop a simple, replicable method which can be used by zoo-based breeding programmes to incorporate molecular genetics and unknown pedigrees into PMx which allows for better management decisions.

MILLER AD, GOOD RT, COLEMAN RA, LANCASTER ML, WEEKS AR (2013): Microsatellite loci and the complete mitochondrial DNA sequence characterized through next generation sequencing and de novo genome assembly for the critically endangered orange-bellied parrot, *Neophema chrysogaster*. Mol Biol Rep **40**(1), 35 - 42.

Do vomeronasal receptor genes of two sympatric mouse lemur species show signals of divergent evolutionary history?

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Most terrestrial mammals possess functional vomeronasal receptors that are used in intraspecific communication and predator recognition. The two types of vomeronasal receptors, V1Rs and V2Rs, bind smaller ligands or larger peptides, respectively. Among primates, mouse lemurs possess the largest V1R repertoire and it has evolved under pervasive and ongoing positive selection.

The aim of this study is to analyse and compare the evolution, genetic diversity and demographic history of selected vomeronasal receptor genes in two sympatric mouse lemur species (*Microcebus murinus* and *M. ravelobensis*) in northwestern Madagascar. A total of 40 mouse lemurs (20 of each species) from one study site in the Ankarafantsika National Park were sequenced at 15 different V1R loci and the two recently discovered V2R genes. All selected genes had been shown before to be expressed in the vomeronasal organ of *M. murinus*.

M. ravelobensis showed a higher genetic diversity as expressed by a higher haplotype and nucleotide diversity than *M. murinus*. A comparative analysis of the respective haplotype networks, mismatch distributions and demographic and spatial modelling will be used to reconstruct the demographic history of both mouse lemur populations and to relate those results to possible Pleistocene colonisation scenarios that were previously developed on the basis of non-coding loci.

Funded by Volkswagen Foundation (VolkswagenStiftung).

Play or fight? Social interactions and ontogeny of dominance relationships in young grey mouse lemurs (*Microcebus murinus*), a primate with female dominance

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Similar to other mammals, young primates can develop social behaviour and fighting skills through play. Nonhuman primates typically show high rates of play in late infancy and early juvenility, but the rates of play decline towards adolescence and adulthood. The development of play and establishment of dominance relationships have been investigated in some primate studies, but mainly focused on group living primates and the integration of youngsters into the adult's hierarchy. This study aims to investigate for the first time the ontogeny of play and dominance relationships in a nocturnal and non-gregarious primate species by investigating same-aged grey mouse lemurs with a longitudinal approach. Although males usually represent the dominant sex in mammals, the opposite phenomenon (female dominance) is known from some exceptional cases, among them some Malagasy lemur species including the grey mouse lemur. However, nothing is known about the ontogenetic development of this rare trait in this species. Therefore, play, agonistic behaviours and dominance relationships were observed under controlled captive conditions in different age categories (AC) among juveniles (ACI: 4 - 5 months, n = 6), adolescents (ACII: 8 - 9 months, n = 8) and young adults (ACIII: 12 - 13 months, n = 8). Adults of two years or older (n = 8) were used as a control group. Data was collected during encounter experiments between one male and one female lasting for 45 minutes with three encounters per dyad and age class (total observation 67.5 hours). Results show a statistical trend for a decrease in the proportion of playing dyads from ACI to ACIII, with no dyad in the control group showing play behaviour. Conversely, agonistic interactions increased in frequency from ACI to ACIII with even more agonistic encounters occurring in the control group. Results indicate that mouse lemurs in ACIII, which were previously considered as mature and can conceive and rear offspring successfully, do not yet show the conflict rates and agonistic intensity of fully adult individuals. Clear dominance relationships were not observed in ACI and first indications of female dominance were only found from ACII onwards with an increasing number of dominant females in ACIII and even more in the control group. In conclusion, this study provides a first indication that social maturation lags behind sexual maturation in a non-gregarious primate and that play, agonistic behaviour as well as dominance relationships, including female dominance, jointly develop over time.

Founded by Bayer Science & Education Foundation.

From worker to royalty – on naked mole rat reproduction

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The naked mole rat (*Heterocephalus glaber*) is in the spotlight of science due to a variety of highly interesting attributes, amongst which the most noteworthy probably are resistance to cancer, extreme longevity, and eusociality. Naked mole rats live in colonies of up to 300 individuals. Of these, usually, only one female, the queen, and one to three males, termed pasha(s), reproduce. The gonadal activity of the remaining working cast individuals is suppressed, primarily due to stress exerted on them by the queen (i.e. by biting and shoving). However, on principle, any individual within the colony retains the capacity to reproduce if the suppressive influence is withdrawn. Naturally, such opportunity arises e.g. in case of the queen's death. However, a new colony may be established artificially by pairing workers of both genders, separated from their colonies.

Using the latter approach, we newly established seven naked mole-rat colonies, consisting of one single female and one male worker each. Under such controlled circumstances, we were able to thoroughly follow the transition of the female and male working cast members to queens and pashas, respectively. This allowed for a detailed study on several aspects of naked mole rat reproduction: (i) As the animals were continuously monitored via a custom-built camera system, we observed the exact date of mating. Thereby, for the first time to our knowledge, we determined the exact gestational duration. (ii) The physical transition of external genitalia, teat and skin morphology was documented photographically, using a digital microscope (KEYENCE VHX-1000, Osaka, Japan). (iii) Ultrasound biomicroscopy was employed using a high-resolution ultrasound system (Vevo 2001, Visualsonics, Canada; 70 MHz linear transducer; maximal resolution ~20µm). Thereby, we closely observed the transition of the inner reproductive organs of both sexes, documenting changes in gonadal activity traits as well as in size. Successively, the different stages of pregnancy, especially embryonic and foetal development were monitored in regular intervals. We also assessed the further abdominal organs for alterations that may be attributable to the changes in social or reproductive status or health.

Thereby, we were able compare and link the alterations of male and female individuals and to set them in correlation to changes in other organs, such as spleen and adrenal glands, which may be indicative of e.g. chronic stress levels associated with social status, or immunologic challenges the animal is subjected to (e.g. during implantation and pregnancy).

Ontogeny of immune function in blackcap (*Sylvia atricapilla*)

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Variation in ontogeny and strength of immune defence mechanisms can be integrally related to life history strategies and determined by trade-offs during development. Although the domestic chicken has served as a model species for the study of the immune function in vertebrates, little is still known about the ontogeny of immune function in wild birds, especially in birds with an altricial mode of development. The immune function of juvenile birds was traditionally assumed to be little developed in the first weeks posthatching and instead developing later in life. However, recent studies have shown that nestlings of wild birds are able to produce their own antibodies few days after hatching. In this study we compared immune parameters of juveniles and adults of blackcaps (*Sylvia atricapilla*) captured in the wild. Our aim was to determine whether the immune parameters of juveniles are similar to those from adults by the time they abandon the nest and become independent. We will present estimates of white blood cell counts, acute stress proteins and IgY levels. Our results will help to understand the ontogeny of immune function in passerine birds and the factors determining susceptibility to infection during the nestling period.

Influence of the season on the mating behaviour in wild guinea pigs (*Cavia aperea*) in captivity

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Reproduction in the wild guinea pig (*Cavia aperea*) is described as moderate seasonal with reduced pregnancy rates during very cold winters (ROOD and WEIR 1970) but independent of photoperiod (TRILLMICH 2000). In this study, we aimed at characterising reproduction behaviour (number and duration of copulations) during three different time periods of the year: July – August 2012 (Jul - Aug), November – December 2012 (Nov – Dec) and April – May 2013 (Apr - May). The animals were kept in groups consisting of one male and one to five females in combined indoor-outdoor enclosures and were monitored by cameras with infrared diodes. Oestrus state (open or closed vaginal membrane) was determined visually during daily handling. Reproduction occurred exclusively during the evening, the night or at the early morning and this period of repeated copulations lasted on average 40 - 70 min in all three observation periods. Copulation was restricted from 6:30 pm to 3:30 am in Jul – Aug, from 4:16 pm to 7:09 am in Nov – Dec and from 4:42 pm to 06:07 am in Apr - May. Duration of each single copulation was not significantly different (Jul – Aug: 3.7 ± 1.9 s; Nov – Dec: 2.7 ± 1.1 s and Apr – May: 2.7 ± 0.7 s), whereas the number of copulations was higher in Nov-Dec (9.0 ± 4.5) than in Jul - Aug (6.2 ± 3.5 , $p = 0.047$). While copulations occurred either at the day before the first signs of oestrus were detected (day -1) or at the first day of oestrus (day 1) in Apr – May, copulations were observed until day 4 of oestrus in Jul - Aug and until day 7 in Nov – Dec ($p = 0.011$). Also, oestrus length was significantly different ($p = 0.024$) between the different time periods and shortest in spring (Jul - Aug: 5.1 ± 1.4 days; Nov - Dec: 5.2 ± 2.9 ; Apr - May: 3.7 ± 0.8). These observations show that despite the wild guinea pig is able to reproduce year-round, changes in reproduction behaviour between different seasons are pronounced and reproductive activity peaks during spring compared to summer and winter months regarding the shorter oestrus length and the restriction of copulation to day -1 and 1 of oestrus.

The project is funded by the Leibniz-Gemeinschaft (SAW-2011-IZW-2).

ROOD JP, WEIR BJ (1970): Reproduction in female wild guinea-pigs. *J Reprod Fert* **23**, 393 – 409.

TRILLMICH F (2000): Effects of low temperature and photoperiod on reproduction in the female wild guinea pig (*Cavia aperea*). *J Mammal* **81**(2), 586 - 594.

Fin-printing great white sharks *Carcharodon carcharias*: a fully automated computer vision system for the identification of individual animals

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Studies in conservation biology and behavioural ecology rely heavily on data relating to the whereabouts and movement of individual animals, with photographic identification methods providing a non-invasive alternative to capture-mark-recapture protocols. And yet, manual identification schemes require enormous amounts of time and effort on the part of a typically small number of highly trained experts, limiting the density of observations that can be made in this way. In order to overcome this limitation, we aim to exploit state-of-the-art computer vision techniques to design systems to automatically identify individual animals. Here, we present results from a prototype system focussing on one of our test-bed species, the great white shark *Carcharodon carcharias*.

Individual shark identification relies on uniqueness encoded in the jagged morphology of the posterior edge of the sharks' dorsal fin. This pattern is stable over decades, making it an ideal machine-recognisable biometric identifier. Taking as input high-quality, high-resolution images of a side view of the fin, we first combine fin-contour and species shape models to automatically extract and recognise fin regions, before using points of high curvature to partition the trailing edge contour, and produce a spectral bag-of-words representation of individual identity. Individuals are identified by matching these spectrally represented contour sections against a pre-computed database of known individuals. Using this approach, and on a test dataset of 132 images, we are able to identify the correct individual in 85 % of cases, 100 % of the time.

Solute and particle retention in captive blackbucks (*Antelope cervicapra*)

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Ruminants have been classified as grazers and browsers according to their feeding habits. These have been hypothesised to be related to passage kinetics of digesta. The pattern observed is that grazers are characterised by a wide ratio of mean retention time of particles vs. fluid ($MRT_{\text{Particle}}/MRT_{\text{Fluid}}$). For the whole GIT, this ratio (the selectivity factor SF) is in the range of 1.9 for grazers and 1.3 for browsers. Among the grazers investigated are cattle, sheep and different antelope families. Being a strict grazer of a different systematic unit (gazelles) with a body mass at the very low end of grazing ruminants, the Indian blackbuck is appropriate to test generality of this relation. In this study, five individuals (3 females, 2 males) with an average body mass (BM) of 26 kg (range: 22 - 32 kg) were investigated. The animals had *ad lib* access to grass hay and in addition were given some (small) amount of alfalfa. Cr-mordanted fibre (1 - 2 mm) and Co-EDTA were used as markers for MRT estimation. The animals ingested on average 40 ± 8.2 g/kg $BM^{0.75}$ (mean \pm SD). Chemical composition of the diet was crude protein 12.4 % DM and neutral-detergent fibre 67 % DM. Retention time was calculated as 60 ± 6.1 h for MRT_{Particle} and as 29 ± 4.1 h for MRT_{Fluid} , resulting in SF of 2.1 ± 0.16 . Based on estimations from data on ruminants available so far, a high SF of 1.9 - 2.0 was expected for blackbucks based on their feeding habit and on their intraruminal papillation gradient. In conclusion, the view that grazing ruminants are characterised by high SF is supported. The advantage of large SF remains to be finally established, but maximisation of microbial harvest from foregut by increasing fluid throughput while at the same time keeping up retention time of grass particles (due to less lignification on average a more fermentable material as browse) represents a coherent explanatory approach.

Out of Africa we presume? Origins and history of admixture among chimpanzees in European Zoos

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Despite ample focus on this endangered species, conservation planning for chimpanzees residing outside Africa has proven a challenge because of lack of ancestry information. Here, we analysed the largest number of chimpanzee samples to date, examining microsatellites in >100 chimpanzees from the range of the species in Africa, and 20 % of the European zoo population. We applied the knowledge about subspecies differentiation throughout equatorial Africa to assign origin to chimpanzees in the largest conservation management programme globally. A total of 63 % of the genotyped chimpanzees from the European zoos could be assigned to one of the recognised subspecies. The majority being of West African origin (40 %) will help consolidate the current breeding programme for this subspecies and the identification of individuals belonging to the two other subspecies so far found in European zoos can form the basis for breeding programmes for these. Individuals of various degree of mixed ancestry made up 37 % of the genotyped European zoo population and thus highlight the need for appropriate management programmes guided by genetic analysis to preserve maximum genetic diversity and reduce hybridisation among subspecies.

Cryopreservation of ovary tissue from wild felids and xenotransplantation

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Cryopreservation of ovarian tissue has a great potential to preserve female germ cells of endangered mammals after death or castration. In the present study, a freezing protocol successfully used for human tissue was adapted for preserving ovarian cortex of felid species. Ovaries from non-domestic felid species were obtained from seven freshly euthanised and two recently deceased cats kept in different European Zoos. Ovarian cortex was dissected and uniform sized pieces of 2 mm diameter were obtained, frozen (slow freezing with -0.3° per min, in 1.5 mol/L ethylene glycol, 0.1 mol/L sucrose) and cultured before and after cryopreservation for seven days. The integrity of primordial follicles was assessed by histology determining morphology and maximum follicle diameter on serial cuttings (every 30 μ m). In addition, the number of follicles per piece (CFN) was extrapolated from the number of sections needed to find 40 primordial follicles. Histology demonstrated a high quantity of early follicles within the cortex in each felid species (CFN: 100 – 500 per 2 mm piece) independent of age and health status. After 7d culture CFN was reduced by 20 to 50 %, but no impact of cryopreservation was detectable in both, CFN and percentage of primordial follicles. Follicle loss during culture was more pronounced in young females (1 yr-old Amur leopard, 2.5 yr-old North-Chinese leopard). Cryopreservation of ovarian cortex was shown to be successful in this study, but for induction of growth and, finally, for oocyte retrieval we propose to perform xenotransplantation into immune-deficient mice.

Food availability influences adaptive flexible responses in the striped mouse, *Rhabdomys pumilio*

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Natural selection is the most important process leading to genetic adaptation. However, many organisms can adapt in a rapid way to drastic environmental changes via phenotypic flexibility. These adaptive responses could imply changes in morphology, physiology and behaviour. For example desert living small mammals display modifications of digestive system and diet preference and reduction of resting metabolic rate as an adaptation to the dry season. Certain species adapt by modifying their behaviour (increase huddling, increase exploratory behaviour to find food) and even sometime the social structure of the population (group living during the dry challenging environment). Such mechanisms of adaptation and their interactions have been well-documented in controlled environment but more integrative studies in natural conditions are missing to fully understand the evolutionary consequences of phenotypic flexibility and the fitness costs of such responses. Here we conducted an integrative study to explore how variation in food availability in a dry and challenging natural environment could influence physiological, morphological and behavioural plastic responses of the South African striped mice (*Rhabdomys pumilio*). We want to know in a first time if reproduction could be maintained during the non-breeding dry season by providing food to a natural population of striped mice. In a second time we will look at how resource availability modifies body mass, metabolic rate and home range size in a natural population and how it could be linked to investment in reproduction.

During the dry season we show that mice from the control group (no food supplementation) did not reproduce whereas mice from experimental groups (food supplementation) did, resulting a higher fitness. This increase in reproductive activity was associated with an increase in resting metabolic rate and a diminution of the home range size. In addition, the growth curves show that control individuals stopped growing whereas the experimental ones continued which led to a large difference in weight between the two groups at the end of the season. Our study suggests that food availability is an important factor which regulate fast phenotypic plastic responses (within a season) however further analyses are needed to integrate all the relations between morphological, reproductive and metabolic changes with endocrines and behavioural ones.

Development of molecular markers for population genetic studies of the black stork (*Ciconia nigra*)

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After more than twenty years of bird genome studies (KOCHER *et al.*, 1989; LUIKART *et al.*, 1998; ZINK and BARROWCLOUGH, 2008) considerable amount of specific microsatellite knowledge for quite a few species has been accumulated (TOMASULO-SECCOMANDI *et al.*, 2003; SEPHARD *et al.*, 2009; HUANG and ZHOU, 2011; SOUZA *et al.*, 2012) and for new species it could be possible and easy to use them for cross-species analysis. We have initiated a large-scale molecular analysis of Black Stork populations. The idea of the project is to ascertain the genetic diversity and structure across a wide range of countries and regions both historically and at the present moment. With cooperation of our colleagues we have been able to put together representative collection of Eurasian contemporary DNA samples; museum access grants have made possible the sample collection from historical specimens.

Overview of the current situation according to our experiences with cross-species microsatellites and also preliminary data of mtDNA sequence analysis in the case of black storks will be presented.

HUANG Y, ZHOU L (2011): Screening and application of microsatellite markers for genetic diversity analysis of Oriental White Stork (*Ciconia boyciana*). *Chinese Birds* **2**(1), 33 - 38.

KOCHER TD, THOMAS WK, MEYER A, EDWARDS SV, PÄÄBO S, VILLABLANCA FX, WILSON AC (1989): Dynamics of mitochondrial DNA evolution in animals: Amplification and sequencing with conserved primers. *Proc Natl Acad Sci* **86**, 6196 - 6200.

LUIKART G, SHERWIN WB, STEELE BM, ALLENDORF FW (1998): Usefulness of molecular markers for detecting population bottlenecks via monitoring genetic change. *Mol Ecol* **7**, 963 - 974.

SEPHARD JM, GALBUSERA P, HELLEMANS B, JUSIC A, AKHANDARF Y (2009): Isolation and characterisation of new suite of microsatellite markers in the European White Stork, *Ciconia ciconia*. *Conserv Genet* **10**, 1525 - 1528.

SOUZA ASM DE CASTRO, MINO AI, DEL LAMA SN (2012): Polymorphic heterologous microsatellite loci for population genetics studies of the white-faced ibis *Plegadis chihi* (Viellot, 1817) (Pelecaniformes, Threskiornithidae). *Genet Mol Biol* **35**, 1, 74 - 80.

TOMASULO-SECCOMANDI AM, SCHABLE NA, LAWRENCE BRYAN A, JR, LEHR BRISBIN I, JR, DEL LAMA SN, GLENN TC (2003): Development of microsatellite DNA loci from the wood stork (Aves, Ciconiidae, *Mycteria americana*). *Mol Ecol Notes* **3**, 563 - 566.

ZINK RM, BARROWCLOUGH GF (2008): Mitochondrial DNA under siege in avian phylogeography. *Mol Ecol* **17**, 2107 - 2121.

The behavioural and physiological response of the increased corticosterone level in a small Arctic seabird, the little auk *Alle alle*

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The little auk *Alle alle* is a small, long-lived seabird breeding in large colonies in the high Arctic. Energy demands of little auk chicks are very high in comparison to other seabird chicks of similar body mass. As a result of observed and predicted climate warming, the increasing inflow of the warm Atlantic water to the Arctic shelf will deteriorate the feeding conditions for the planktivorous seabirds. In response to food deprivation birds increase the production of corticosterone, which may change behaviour and stimulate their foraging activities. The aim of the study was to investigate the effect of the increased corticosterone level on the begging performance, growth and development of chicks and food provisioning strategy of parent birds. It has been hypothesised that levels of corticosterone are associated with increased begging rate, which may act as a signal of hunger for parent birds. To test this on little auks we experimentally increased levels of circulating corticosterone in little auks and investigated the behavioural responses of nestlings and parent birds. We found that the increased corticosterone influenced the chicks' begging behaviour. Moreover, the experimental chicks had higher body mass than control chicks. This is the first study describing such effects in the little auk – the keystone species in the high-Arctic ecosystem of Spitsbergen. Since environmental changes are slow and difficult to predict, an artificial enhancing of corticosterone level will simulate the decrease of trophic conditions. Measuring the behavioural and physiological response of the little auks can be useful to predict their reaction on the individual and population level to gradually changing environmental conditions.

Time budgeting of orang-utan in zoo winter pavilion

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Zoos should continually assess their management practices to reduce stress in animals and enhance quality of life. The goal of our work is to study time budget of orang-utan behavioural activity during the winter period. The studies were conducted in Novosibirsk Zoo. The object of observation was a male Sumatran orang-utan named Zahar (*Pongo pygmaeus abelii* Linnaeus, 1760). Zahar was born in captivity, he is 14 years old. He is housed alone in the enclosure of 50 m². In the neighbouring enclosure one more male orang-utan is housed. Orang-utans are separated from visitors by a glass front. In order to record all behaviours, we have chosen the method of "time slices" with behaviour scanned and recorded every two minutes.

Our observations have shown that the orang-utan allocated most time to sleeping (19.8%) and playing with stimuli - clothing, plastic bottles, and cardboard (18.3%). Food consumption took 17.6% of the time, considerably less than it takes in the wild (60%). This is due to availability of food and absence of food enrichment.

The orang-utan allocated to interaction with visitors 12.2% and 9.9% of the time. The animal spent less time resting (8.4%) and in comfort activity (7.6%). Social activity (interaction with the orang-utan in neighbouring enclosure) took 3.8%. The animal was characterised also by a very low percent of physical activity (1.5%). In the wild, orang-utans spend time on trees, moving from branch to branch while searching for food most of the day. Thus, perhaps the low physical activity is associated with the wrong enclosure design in which little or no ability to move is presented. The tendency of reducing passive behaviour (lying) with increasing of the number of visitors was revealed. The animal has attracted the attention of the audience with facial expressions and gestures. Overall, however, range of behaviours remained limited, while his activity stayed low.

Addressing koala conservation management needs: applying novel genomic methods and assessing ecological exchangeability across the species range

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The koala, *Phascolarctos cinereus*, is undoubtedly an Australian iconic species of immense national importance, yet its numbers continue to decline across many regions in Australia. Although many koala populations are now classified as vulnerable, very little information is available to be able to effectively manage these and other threatened populations. Complicating this problem further, there is a great deal of variability among koala populations throughout their range with regards to morphology, disease susceptibility, habitat and environmental heterogeneity. All of these factors can dramatically effect the survival and persistence of populations. Presently, critical information on koala populations is largely restricted to local governmental regions and there is a distinct lack of broad-scale information spanning the entire species range. For example, koalas are currently divided into three allopatric sub-species: *Phascolarctos cinereus victor* (Victoria and South Australia); *Phascolarctos cinereus cinereus* (New South Wales) and *Phascolarctos cinereus adustus* (Queensland). This sub-species distribution curiously aligns with state borders and there is very limited data supporting their current classification. A species-wide approach to researching factors such as genetic diversity, adaptation, gene flow and exchange is essential to the development of an effective long-term conservation and management strategy. Our project aims to utilise whole-genome RAD-Tag SNP technology on 1000s of koalas distributed across their range to generate detailed information on population dynamics, adaptive variation and sub-species delineation that will contribute to the better management and understanding of the koala in Australia. An overview of our integrated programme and the progress of RAD-tag genotyping and genetic analysis will be discussed as part of this presentation.

Non-invasive measurement of faecal glucocorticoid metabolites in male European mink (*Mustela lutreola*) – validation and limitations

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The application of faecal glucocorticoid metabolite (FGM) measurement has become a valuable non-invasive tool to assess the adrenocortical activity in wild and captive endangered animals. Chronic stress in a population can reduce fitness, *i.e.* by an increase of disease susceptibility or poor reproductive performance. The endangered European mink (*Mustela lutreola*) is difficult to breed in captivity due to adverse reproductive behaviour of the males. By measuring glucocorticoid metabolites we aim to determine whether elevated stress hormone concentrations in non-breeding males are correlated to the development of passive or aggressive breeding behaviour. Metabolism and excretion of glucocorticoid hormones differ significantly between species; thus it is necessary to validate the methods for the measurement of FGM for each species. We conducted an ACTH (adrenocorticotrophic hormone) challenge test in four males. The collected samples were analysed with different Enzyme Immunoassays (EIA) to identify the FGM assay reflecting the increase of cortisol concentration best. The assay using an antibody against 5 α -pregnane-3 β , 11 β , 21-triol-20-one-CMO:BSA was found to be well suited. The species-specific lag time between ACTH injection/stress exposure and the FGM increase in male European mink was 4 to 6 hours. We also tested the stability of the measured glucocorticoid metabolites in fresh faeces. Faecal samples were homogenised and then divided into portions to be frozen at -20°C immediately, after 1, 2, 4 and 8 hours, respectively. In faeces exposed to sunlight the metabolite concentration doubled during the first hour, and reached up to a five-fold increase after 4 - 8 hours. In faeces placed in the shade (at about 20°C ambient temperature) minor, non-significant fluctuations were observed, with concentrations both increasing and decreasing slightly over time. The results emphasise the importance of collecting faeces for the measurement of FGM in this species soon after defaecation. The application of this method in conditions where faecal samples are exposed to sunlight (temperature, UV-light) is restricted, especially during warm and sunny summer days.

The spread of porcine endogenous retroviruses among different populations of wild boar and domestic pig

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The differences between wild and domestic *Sus scrofa* forms by spread of porcine endogenous retroviruses (PERV), a part of the Suiformes genomes has been investigated previously (NIEBERT and TONJES, 2005). We identified the three types of PERV (A, B and C) by DNA testing of 471 animal blood samples from populations of wild subspecies, *S.s. scrofa* (Central Russia), *S.s. attila* (South of Ukraine) and *S.s. nigripes* (Kirgizstan), and domestic pig breeds (Large White, Landrace, Duroc, SM-1, Minipigs). The frequency of PERV-positive chromosomes was statistically analysed (NIKITIN *et al.*, 2008). Domestic pigs were shown to have a higher frequency of PERV and their haplotypes than wild boars. Specific features of the frequency of chromosomes carrying PERV among wild and domestic populations are demonstrated in maps of two principal component coordinates. Among wild subspecies, the European *S.s. scrofa* is the closest to the domestic pigs, and the Central Asian *S.s. nigripes* is the farthest. Domestic pigs of modern meat breeds are the closest to the wild boar; meat-and-lard swine breeds are farther related to wild boar, and miniature pigs are the farthest. It has been shown that microevolution processes associated with PERV have two vectors: the vector of fat deposition and the minus selection vector. Thus, PERV types may cause differences in pig physiology (NIKITIN *et al.*, 2010). It appears that PERVs were not neutral elements in the evolution of the pig genome.

NIEBERT M, TONJES RR (2005): Evolutionary spread and recombination of Porcine Endogenous Retroviruses in Suiformes. *J Virol* **79**, 1, 649 - 654.

NIKITIN SV, YUDIN NS, KNYAZEV SP, AYTNAZAROV RB, KOBZEV VF, BEKENEV VA, SAVINA MA, YERMOLAEV VI (2008): Frequency of chromosomes Carrying Endogenous Retroviruses in the populations of domestic pig and wild boar. *Rus J Genet.* **44**, 6, 686 - 693.

NIKITIN SV, YUDIN NS, KNYAZEV SP, AYTNAZAROV RB, BEKENEV VA, DEEVA VS, GONCHARENKO GM, KOBZEV VF, SAVINA MA, ERMOLAEV VI (2010): Differentiation of wild boar and domestic pig populations based on the frequency of chromosomes carrying endogenous retroviruses. *Nat Sci* **2**, 6, 527 - 534.

Dominance effects on foraging behaviour in a goose flock – first results using accelerometers and high accuracy GPS

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Animals that forage in groups optimise their food intake in relation to food availability, predation risk and competition. Competition within the group is usually minimised by a social hierarchy, and several hypotheses have been examined how the rank of an individual in a group influences its foraging behaviour. The spatial position of the dominant individuals within the group differed between studies (central vs. at the edges) and the time spent foraging seemed to depend on the individual's group status.

In previous studies behaviours have been scored manually or generalised in model simulations. Here, we use novel, high accuracy GPS (Global Positioning System) and tri-axial accelerometer tags to remotely determine the behaviour of adult males in a foraging flock of Canada geese (*Branta c. canadensis*) during moult. In preliminary work accelerometer data patterns have been ground-truthed to observational data, providing criteria to distinguish goose behaviours like sitting/standing, walking/running and foraging.

We show how the behaviours and times of foraging differ between geese of different levels of dominance within the group, and set this into relation to their spatial position in the flock during three full days. The dominance hierarchy of the tagged geese is obtained by observations of agnostic encounters, positions are determined by EGNOS (European Geostationary Navigation Overlay Service) - enhanced GPS, and accelerometer data indicate the geese' time budgets, i.e. times of foraging. This provides insight into mechanisms of risk taking in relation to dominance and foraging preferences at all times of the day and night.

Our study aims to uncover temporal-spatial foraging decisions of group living animals in relation to dominance. Beyond that, it is also an important step towards remote behavioural studies using GPS, leading to a better understanding of foraging decisions of wild animals in inaccessible regions or during migration.

This work is carried out in the framework of the EU FP7 project E-Track (www.etrack-project.eu).

Innate immunity receptors in tropical and temperate zone passerines

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Innate (unspecific) immunity creates the first barrier against pathogens and parasites occurring in the environment and helps to activate the adaptive immune response in vertebrates. One of its most important receptors is a multigene family of toll-like receptors (TLRs), which bind a wide spectrum of invariable pathogen-associated molecular patterns (PAMPs). Although TLRs are generally conservative molecules, intra- and interspecific differences of individual receptors have already been described by several studies, especially in birds. Thus, knowledge of structure and variability of TLRs in various avian species throughout passerine phylogeny may be of great importance in an evolutionary and ecological context.

In this study, we have collected a unique set of samples covering tropical (Cameroon, Nigeria) and temperate zone (Czech Republic, Norway) bird species representing the main taxa of Passeriformes. It was hypothesised that the diversity of pathogens increases towards the equator, therefore the variability of TLRs should also increase with lower latitudes. In our analyses (using methods of next-generation sequencing as well as traditional Sanger sequencing) we are focussing on TLRs recognising conserved bacterial molecules; i.e. TLR 4 with lipopolysaccharide (LPS) from cell walls of Gram-negative bacteria as a ligand, and TLR 5 important for binding flagellin from flagella of motile bacteria. Our study provides the first description and comparison of TLR molecules in non-model passerine species.

Genetic structure of the Amur tiger's (*Panthera tigris altaica*) population in southwest Primorye

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An isolated Amur tiger group in southwest Primorye is separated from the primary population by an anthropogenic barrier between Vladivostok and Ussuriysk. According to the latest estimates (SIGUMOTO *et al.*, 2012), group size does not exceed 19 individuals. We used faecal DNA to determine the group size and genetic structure of the isolated group. DNA was extracted from 128 faecal samples, five hair samples and two blood samples. PCR was performed with nine microsatellite primer pairs: e7, fca304, fca43, e21b, pun935, fca5, fca161, fca91, fca441 (ROZHNOV *et al.*, 2009; MENOTTI-RAYMOND *et al.*, 1999; KARMACHARYA *et al.*, 2011) and one sex marker (BHAGAVATULA and SINGH 2006) for each sample. The value of polymorphism information contents (PIC) for our loci varied from 0.360 to 0.655. Probability of identity for sibling P (ID)sib for all loci was 0.001436. From December 2011 to March 2012 we identified 16 individuals (9 females and 7 males) in the isolated southwest group. Spatial distribution analysis of home ranges for seven tigers showed high levels of overlap of individual areas between males and females, where male territories were larger than female home ranges.

This study was supported by the Russian Geographic Society and by the grant of the President of the Russian Federation № MK-2553.2012.4

BHAGAVATULA J, SINGH L, (2006): Genotyping faecal samples of Bengal tiger *Panthera tigris tigris* for population estimation: A pilot study. *BMC Genetics*7:48, 1 - 12.

KARMACHARYA DB, THAPA K, SHRESTHA R, DHAKAL M, JANECKA JE (2011): Noninvasive genetic population survey of snow leopards (*Panthera uncia*) in Kangchenjunga conservation area. Shey Phoksundo National Park and surrounding buffer zones of Nepal. *BMC Research Notes* 4, 516, 1 - 8.

MENOTTI-RAYMOND M, DAVID V, LYONS LA, SCHAFFER A, TOMLIN J, HUTTON M, O'BRIEN S, (1999): A genetic linkage map of microsatellites in the domestic cat (*Felis catus*). *Genomics* 57, 9 - 23.

ROZHNOV V, SOROKIN P, NAIDENKO S, LUKAREVSKIY V, HERNANDEZ-BLANCO H, LITVINOV M, KOZLYAR A, UYDIN V (2009): Noninvasive individual identification of the Amur tiger (*Panthera tigris altaica*) by molecular genetic methods. *Doklady biological sciences* 429, 518 - 522.

SUGIMOTO T, NAGATA J, ARAMILEV VV, MCCULLOUGH DR (2012): Population size estimation of Amur tigers in Russian Far East using noninvasive genetic samples. *J Mammal* 93(1), 93 - 101.

Involving stakeholders to solve the problem of lead poisoning in white-tailed sea eagles caused by fragments of hunting ammunition

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Our previous studies in Germany demonstrated that lead poisoning is the main cause of death of white-tailed sea eagles and other scavenging birds. Lead was suspected to originate as fragments of hunting ammunition embedded in scavenged carcasses from wildlife shot by hunters. Here, our objectives were to identify the sources of lead and to investigate the behaviour and ecology of white-tailed sea eagles which facilitated the ingestion of lead ammunition. Following our standard practice for such projects, we invited all relevant stakeholders (hunters, hunting association officials, foresters, the ammunition industry, conservationists) to an “expert” meeting before the study began and thereby established the questions important to stakeholders in their debate on how best to manage this issue (KRONE and HOFER, 2005). We therefore studied the home range size, habitat use, foraging behaviour and feeding patterns of eagles, modelled the impact of lead poisoning on population development and evaluated the killing efficiency of lead-free ammunition alternatives. Our results demonstrated where and how eagles ingest bullet fragments and that lead-based ammunition was undoubtedly the source of lethal poisoning (NADJAFZADEH *et al.*, 2013). Moreover, we found that lead poisoning reduced population development (SULAWA *et al.*, 2010) and that lead-free alternatives were equally efficient at killing as lead-based ammunition (TRINOGGA *et al.* 2013). Additional research since confirmed that lead-free ammunition alternatives are safe for hunting practice.

Our research findings were communicated and discussed with stakeholders at three workshops, and via a leaflet, three brochures and a web page (<http://www.seeadlerforschung.de>). We also organised an international conference to present our results and advised decision makers (ministerial civil servants, politicians, managing directors of protected areas, forestry personnel, ammunition industry) on best practise methods (KRONE, 2008, 2011).

The systematic and strategic involvement of stakeholders ensured (1) their participation in the research (but did not determine its outcome!), (2) that the research was relevant to the political and societal discourse, (3) widespread recognition of the research results, and (4) a forum for managed discussions. After being sceptical at first, the problems caused by lead poisoning were accepted by all stakeholders – even if they differed on appropriate management measures.

As a result, Berlin, Brandenburg, North Rhine-Westphalia, Rhineland-Palatinate, Saarland, the Müritz Nationalpark and Rostock banned the use of lead-based

bullets, and with the beginning of the next hunting season (2013-14) the administration of the federal forests and the states of Lower Saxony and Schleswig-Holstein will follow.

- KRONE O, HOFER H (2005): Bleihaltige Geschosse in der Jagd – Todesursache von Seeadlern? Institut für Zoo und Wildtierforschung, 42 pages.
- KRONE O (2008): Bleivergiftungen bei Seeadlern: Ursachen und Lösungsansätze – Anforderungen an bleifreie Büchsen Geschosse. Zusammenfassung der naturwiss. Vorträge des Fachgesprächs vom 05. Mai 2008 im Henry-Ford-Bau der Freien Universität Berlin, IZW, Berlin, 95 pp.
- KRONE O (2011): Bleivergiftungen bei Greifvögeln. Ursachen, Erfahrungen, Lösungsmöglichkeiten. Der Seeadler als Indikator. Proceeding of the Conference „Bleivergiftungen bei Seeadlern: Ursachen und Lösungsansätze“ from April 16th 2009 in Berlin, IZW, Berlin, 127 pp.
- NADJAFZADEH M, HOFER H, KRONE O (2013): The link between feeding ecology and lead poisoning in white-tailed eagles. *J Wildlife Manage* **77**, 48 - 57.
- SULAWA J, ROBERT A, KÖPPEN U, HAUFF P, KRONE O (2010): Recovery dynamics and viability of the white-tailed eagle (*Haliaeetus albicilla*) in Germany. *Biodivers Conserv* **19**, 97 - 112.
- TRINOGGA A, FRITSCH G, HOFER H, KRONE O (2013): Are lead-free hunting rifle bullets as effective at killing wildlife as conventional lead bullets? A comparison based on wound size and morphology. *Sci Total Environ* **443**, 226 - 232. <http://dx.doi.org/10.1016/j.scitotenv.2012.10.084> (open access)

Non-invasive genotyping for the conservation of pine marten (*Martes martes*) in fragmented landscapes

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After heavy persecution during the early 1900's, Pine marten (*Martes martes*) are slowly recovering their former range in Scotland. Although generally viewed as a forest specialist in mainland Europe, evidence suggests that the Scottish population may differ in their behaviour, favouring more fragmented habitats (CARYL *et al.*, 2012). It is important to monitor their progress and gain a better understanding of their requirements, not only for their own conservation, but also to inform stakeholders of their possible impact on prey species.

As an elusive animal, pine marten are difficult to monitor and estimates of pine marten population numbers are very inaccurate at present. Surveys have traditionally involved counting scat; this method suffers several drawbacks such as individual heterogeneity and seasonal variation in diet which can have a strong effect on scat production. We have addressed this problem by using microsatellite markers to identify individuals from hair samples collected using baited hair tubes from four forest sites in the Cairngorm region of Scotland. We then used SECR (Spatial Explicit Mark Recapture) modelling to gain accurate population estimates without the need to trap or disturb the animals.

A total of 115 hair samples were collected across all study sites over 784 trap nights. We did not retrieve samples from one of the sites, but obtained 31 to 53 samples from all others. Results of the SECR models estimate populations of between 6 (95 % CI: 6-7.3) and 17 (95 % CI: 12-37) individuals at each site.

As well as providing information for the management of pine marten in the study sites themselves, the population estimates gained through this method will also be used to shed further light on the relationship between fragmentation and population size in this unique landscape.

I will present the data collection and genetic methods used for this study, the results of the SECR models and some potential applications of the hair sampling method for further research into this and other elusive species.

CARYL FM, QUINE P, PARK KJ (2012): Martens in the matrix: the importance of nonforested habitats for forest carnivores in fragmented landscapes. *J Mammal* **93**, 2, 464 - 474.

Using PMx to apply molecular genetic data on kinships to pedigree management: opportunities and challenges

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Pedigree analysis and management tools allow detailed calculation of kinship structure and the proportion of gene diversity retained within a managed population. Methods have been developed to guide optimal selection of animals for pairing, culling, or transfer between populations. These methods have been extended to accommodate partial pedigree information (data gaps), probabilistic pedigrees (multiple possible parents), alternative modes of reproduction (cloning, selfing, polyploidy), and non-autosomal patterns of inheritance (sex-linked loci, mtDNA). However, traditionally the use of pedigree analysis to guide management of wildlife conservation breeding programmes has started with the assumption that the only information available for genetic management is the documented or assumed pedigree. It has been difficult to integrate information provided by molecular genetics into pedigree calculations.

The PMx software that is used globally for the management of conservation breeding programmes in zoos allows a user to replace the default pedigree assumptions with molecular genetic data on kinships. However, the tool has not yet been applied or tested widely to determine when it does or does not improve genetic management of breeding programmes, and initial attempts to integrate molecular-based kinships into pedigree analyses have raised a number of questions. Which estimate of kinship from molecular data is the appropriate metric for combining with pedigree data? How should imprecision in molecular estimates be accommodated in the calculations and management? How should contrasting estimates from reported parentage and molecular genetic estimates be weighted or otherwise reconciled? How can kinship estimates from molecular data be merged into pedigree calculations when only a part of the population has been analysed? What are the conceptual differences between managing a breeding programme based on maximising genome-wide diversity vs maximising diversity at a small number of sampled loci?

New features within the PMx software provide tools for exploring these issues, but the optimal uses of the tools to resolve the challenges are still to be determined. Alternative methods for integrating molecular-based kinship information with pedigree data might be added to PMx, but only after the new algorithms are developed and tested to confirm that they help achieve conservation goals.

Ways to measure body temperature in the field

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Body temperature (T_b) represents one of the key parameters in ecophysiological studies which focus on energy saving strategies. In our research project, we comparatively analyse intraspecific variations of energy consumption in edible dormice (*Glis glis*) and hazel dormice (*Muscardinus avellanarius*). Both species are obligate hibernators and use hypothermia during their active period to reduce energy consumption. As already slight decreases in T_b can considerably reduce energy consumption in endotherm organisms, simultaneous recordings of T_b and metabolic rate are needed for this comparative approach.

Nowadays, there are different devices available to measure T_b in the field. Accordingly, T_b can be recorded with temperature-sensitive radio transmitters, data loggers or passive transponders. While radio transmitters and loggers can be either implanted or mounted onto a collar, transponders are generally implanted subcutaneously.

In this study we evaluated two types of temperature-sensitive passive transponders (IPTT-300 Transponder; BMDS, Netherlands; 120 mg and Bio Thermo Transponder, Destron Fearing, USA; 120 mg) and one data logger mounted onto a collar (modified Thermochron iButton, DS1922L-F5; Dallas Semiconductor, USA; 1.5 g). First of all, we tested the accuracy of all three devices in a water bath with water temperature ranging between 10 and 40 °C. Secondly, we evaluated the usability of the Bio Thermo Transponder and the modified iButton under field conditions. We therefore subcutaneously implanted 16 edible dormice with temperature-sensitive transponders, and equipped 16 edible dormice and 16 hazel dormice with data loggers to simultaneously record T_b and oxygen consumption with a portable oxygen analyzer (Oxbox). In some individuals we additionally recorded T_b with both devices and comparatively analysed recorded data.

While Bio Thermo Transponders measured temperature within the smallest range of all three devices (25 - 40 °C), their accuracy was highest (+/- 0.3 °C). IPTT-300 Transponders, on the other hand, measured temperature between 10 and 40 °C, but accuracy decreased drastically at values below 30 °C. An individual calibration of each transponder is therefore needed, before using them for the measurement of low T_b s. The accuracy of the data loggers was comparatively high (+/-0.5 °C) and stable over the whole temperature range tested.

An investigation of the combined T_b and MR measurements under field conditions revealed that data loggers as well as Bio Thermo Transponders produced reliable results, within their temperature range.

Our comparative study demonstrates that for measuring T_b in the field, the system of choice depends on the range of T_b to be investigated and the specific question to be answered.

Using animal behaviour data for validating corridor model predictions

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Corridors are popular conservation tools because they are thought to allow animals to safely move between habitat fragments, thereby maintaining landscape connectivity. Nonetheless, few studies show that mammals actually use predicted corridors and their model assumptions are rarely validated with field data. Fishers (*Pekania pennanti*, formerly *Martes pennanti*) are semi-arboreal members of the Mustelidae family that once occupied much of the boreal and northern forests of North America, yet are currently threatened in much of their western range, despite recently colonising suburban landscapes in parts of the eastern range. We used GPS tracking collars to collect high-resolution movement data from fishers inhabiting a fragmented, suburban landscape near Albany, New York, USA. We used these movement data to predict within home range corridors for our fishers using two cost-based corridor models: least-cost path analysis and circuit theory. We then validated the performance of these two models by developing a novel corridor model that identifies clusters of “corridor use behaviour” and then validated each corridor model with an independent data set of camera trap detections. Our corridor model suggests that six of the eight fishers we tracked used corridors to connect forest patches within their home ranges; however, the locations of these observed corridors were not well predicted by the two cost-based models, which together identified only five of the 23 used corridors. Further, camera traps placed within cost-based predicted corridors detected fewer fishers and mammals than nearby habitat patches (i.e., randomly located cameras within suitable fisher habitat), whereas camera traps within our observed corridors recorded more passes made by fishers, carnivores, and all other non-target mammal groups. Our results suggest that (1) fishers use corridors to connect disjunct habitat fragments, (2) animal movement data can be used to identify corridors at local scales, (3) camera traps are useful tools for testing corridor model predictions, (4) that corridor models can and should be improved by incorporating animal behaviour data, and (5) that suburban landscapes can support diverse carnivore communities. Our work highlights the value of green space within developed landscapes and emphasises the importance of corridors and connectivity for allowing native wildlife to move between these spaces. However, given the conservation importance and monetary costs of corridors, improving and validating corridor model predictions is vital.

The long-term mother-offspring associations in the Steller sea lion on the two North Pacific reproductive rookeries

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Females of the Steller sea lion (*Eumetopias jubatus*) can maintain the bond with pups born in previous years, continuing to lactate and feed them. Obviously, it is important for offspring survival.

Our analysis is based on the long-term monitoring of individually marked females on the Kozlova Cape (Kamchatka Peninsula) and Medny Island (Commander Islands) rookeries. From 170 females who gave birth on Kozlova Cape from 2002 to 2012, and were encountered on the rookery in the next reproductive season, 68 females maintained bonds with their yearlings (40 %). On Medny Island, 55 of 199 females maintained bonds (28 %). Both rookeries demonstrated a high level of long-term associations, but on Kozlova Cape it is significantly higher. The mother-juvenile bonds can be clearly divided into two types: a stable connection, when a mother-juvenile pair is observed over all reproductive period and female feeds offspring; and an unstable connection, when a mother-juvenile pair is observed occasionally, only a few times per season, usually without milk feeding. The frequency of stable connections on the both rookeries is the same: 49 of 199 females on Medny Island (25 %) and 45 of 170 females on Kozlova Cape (26 %). The rookeries are clearly distinguished by the rate of unstable connection: 23 of 170 females on Kozlova Cape (14 %) and 6 of 199 females on Medny Island (3 %). We can explain the difference by environmental parameters of these rookeries. Kozlova Cape is a small rocky island in the ocean, all animals must lie on the rookery very close to each other and the possibility for mother-yearling meeting is very high. The Medny Island rookery is wide and flat, so yearlings can use more place and the probability of such meeting is lower. We should also consider the distance at which the animals migrate from these two rookeries during the winter. It is more likely that the females from Medny Island migrate for a greater distance. The connection with their offspring can be broken far away from the natal rookery, and the juveniles may not return to the natal rookery with females in present year. Our results show that the differences in ecological conditions are not reflected on the stable connection between mothers and their offspring.

Dietary plasticity of generalist and specialist ungulates in the Namibian desert revealed by stable isotope analysis

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Desert ungulates live in adverse ecosystems that are particularly sensitive to degradation and global climate change. Here, we asked how two ungulate species with contrasting feeding habits, grazing gemsbok (*Oryx g. gazella*) and browsing springbok (*Antidorcas marsupialis*) respond to an increase in food availability during a pronounced rain period. We used a stable isotope approach to delineate the feeding habits of these two ungulates in the arid Kunene Region of Namibia. Our nineteen months field investigation included two time periods of drought when food availability for ungulates was lowest and an intermediate period with extreme, unusual rainfalls. We documented thirteen isotopically distinct food sources in the isotopic space of the study area. Our results indicated a relatively high dietary plasticity of gemsbok, which fed on a mixture of plants, including more than 30 % of C3 plants during drought periods, but almost exclusively on C4 and CAM plant types when food was plentiful. During drought periods, the inferred gemsbok diets also consisted of up to 25 % of *Euphorbia damarana*; an endemic CAM plant that is rich in toxic secondary plant compounds. In contrast, springbok were generalists, feeding on a higher proportion of C3 than C4/CAM plants, irrespective of environmental conditions. Our results illustrate two dietary strategies in gemsbok and springbok which enable them to survive and coexist in the hostile Kunene arid ecosystem.

Artificial light at night deters frugivorous bats from dispersing seeds

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The entire world population growth of the forthcoming decades will concentrate in urban areas, particularly in less developed countries. Urban areas will sprawl and introduce artificial light at night (LAN) into formerly dark rural habitats. Consequently, light pollution is spreading fast all across the world, which might be deleterious for light sensitive wildlife. Obligatory nocturnal animals such as bats can be expected to be particularly affected, since LAN is present in urban as well as in many rural habitats during their nocturnal activity period.

Among bats, a large diversity of feeding habits evolved. In the tropics many bat species are specialised on nectar and fruits. Those frugivorous bats are particularly important for forest regeneration in the Neotropics, since they are among the most effective seed dispersers during early succession. Short-tailed fruit bats (genus *Carollia*), for example, constitute the main disperser of many *Piper* species - pioneer plants in the Neotropics that grow at forest edges or gaps and thus are key to reforestation. However, due to this habitat preference, *Piper* plants are predisposed to become affected by LAN, for example if street lights become installed along roads. If bats avoid illuminated areas, human encroachment into natural habitats may compromise bat-mediated seed dispersal due to an increase in light pollution. However, the effect of LAN on frugivorous bats has not yet been studied experimentally.

We asked whether LAN is reducing the visitation rate, and thus the dispersal of seeds by *Carollia* bats. In a dual choice experiment with captive bats, *C. sowelli* explored a dimly illuminated compartment less often than a dark compartment, and were less likely to harvest fruits in the illuminated than in the dark compartment. Also in free-ranging bats, we observed that *Piper* infructescences were less likely to be harvested when plants were illuminated by a street lamp than under natural darkness.

We conclude that succession and forest regeneration may suffer heavily from urban sprawl when nocturnal seed-dispersers, such as bats, reduce their activity in areas illuminated by street lamps. This might be particularly relevant in the tropics, where ecosystem services of bats are ecologically important for ecosystem functioning, and where at the same time the potential for light pollution to increase is very high.

Urbanisation in the recent co-evolution of *Toxoplasma gondii* and the house mouse

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Urbanisation following the invention of agriculture around 10,000 BC created a dramatic change in the life cycle of the ubiquitous protozoan parasite, *Toxoplasma gondii*. The sexual cycle of *T.gondii* occurs only in the intestine of felids. Oocysts are excreted in faeces and scavenged from the environment by many species, among them prey species of cats, in which the parasite forms long-lived cysts. The cycle is completed when infected prey are eaten by a cat. Since 10,000 BC the domestic cat, *Felis catus*, has come to outnumber all other cat species world-wide by many orders of magnitude. At the same time, the commensal rodents, the house mouse, *Mus musculus*, and the Norway rats and black rats, have increased vastly in number with increasing human population. In the urban but not the rural environment, these species are strictly sympatric with domestic cats, and thus represent by far the most important vector species by which the parasite is transferred from cat to cat. We will discuss the implications of this situation for genetic diversity and for human infection.

Fragmented woodlands in the urban matrix: The influence of woodland character and landscape context on bat abundance and activity

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Urbanisation reduces native biological diversity by reducing the amount and quality of habitat available for wildlife, and by the fragmentation of remaining habitats. Areas of semi-natural habitat (e.g. gardens, parkland) within urban areas can, nevertheless, contain relatively rich wildlife communities. It is well documented that woodland is an important habitat for bats due to foraging and roosting opportunities. Within urban areas, however, woodland is of variable quality, subject to invasive species encroachment, a lack of or over-management and consists of small, fragmented patches which may be very isolated. Little is known about how bats utilise woodland fragments in urban environments and recommendations for woodland management for bats are scarce. The aim of this study was to evaluate the relative importance of woodland characteristics and the surrounding habitat matrix in order to assess the importance of local- vs. landscape-scale woodland management for bat populations. In 2011, we surveyed 34 urban woodlands in Central Scotland to assess their use by foraging bats. Relative bat abundance was assessed using mist nets, a harp trap, and an acoustic lure in the interior of the woodland. Bat activity was quantified using a bat detector within the woodland interior, edges, and surrounding urban matrix. Results suggest that bat abundance and activity were influenced by both local and landscape-level attributes. Higher bat abundance levels were found in woodlands with less vegetation clutter. This suggests that highly managed woodlands, which are often lacking in structural complexity for public safety and aesthetic reasons, may remain suitable habitats for those bat species regularly found in the urban matrix. Higher bat activity levels were found in small and isolated woodland fragments; these apparent positive effects of woodland fragmentation may reflect a more intensive use of woodland in landscapes where this habitat is scarce.

Non-invasive evaluation of testosterone in faeces from guanacos (*Lama guanicoe*)

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Hormone analysis is a precise and widely accepted tool for monitoring reproductive function and responses to stressors. Non-invasive methods have gained popularity over the past 30 years as a more practical approach for assessing ovarian, testicular and adrenocortical activity in wildlife species. Non-invasive hormone monitoring also has been key to understanding biological mechanisms related to observed behaviours of captive and free-ranging animals (GANSWINDT *et al.* 2012). The aim of this study was to establish a non-invasive method to evaluate the testosterone levels of guanaco (*Lama guanicoe*) males to check the efficiency of treatments for inhibition or reduction of testosterone secretion to diminish the extent of aggressive behaviour.

Three adult guanaco from Vigo Zoo (Spain) were studied: a 10 years old male which was housed alone, and two younger males (3 and 7 years old) which were housed together. All three males were vaccinated with Improvac® (Pfizer) with a priming dose and a second dose one month later. Faecal samples were collected twice a week for the assessment of testosterone and stored at -21°C until analysed. The samples were then dried at 60°C and crushed to obtain a homogenous powder. Methanol was used to extract the testosterone metabolites, which were measured using a commercial competitive ELISA kit (Neogen Europe, Ayr, UK) as per the manufacturer's instructions. The assay was validated by determination of assay specificity (dilutional parallelism), accuracy from spike recovery (92 %), precision from intra- assay variability (6.5 %), and sensitivity (0.002 ng/ml).

Results show that Improvac® vaccination induced, even after the priming dose, a significant increase in faecal testosterone levels in all three animals. Testosterone secretion significantly decreased over the following months in the youngest male (which showed highest initial testosterone levels). By contrast, elevated faecal testosterone levels were still present in the remaining two males three months after the second vaccine dose.

A transient increase in testosterone levels is an expected effect of GnRH vaccination, and careful management of the animals is recommended at this period. These results validate the use of a commercial ELISA kit for measuring faecal testosterone concentrations in male guanacos. Such analyses are useful to identify biologically meaningful treatments, as well as to identify hormone fluctuations in relation to behavioural conducts and management procedures.

GANSWINDT A, BROWN JL, FREEMAN EW, KOUBA AJ, PENFOLD LM, SANTYMIRE RM, VICK MM, WIELEBNOWSKI N, WILLIS EL, MILNES MR (2012): International Society for Wildlife Endocrinology - the future of endocrine measures for reproductive science, animal welfare and conservation biology. *Biol Lett* **8**, 695 - 697.

Physiological traits of kittens of different social status in domestic cat (*Felis catus*)

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Majority of cat species have secretive life style and so study of them in the wild is almost impossible. The domestic cat (*Felis catus*) is used as a model species for most of the investigations. Felidae live mainly solitarily and in many species females with their litters are the only long-term groups for many species. There are hierarchical relationships between littermates in ontogeny of some mammal species including domestic cat and Eurasian lynx. Intralitter hierarchical structure should be related to the kittens' physiological characteristics. The aim of our study was to estimate the relations between features of kittens' behaviour (mainly the play) as well as their physiological characteristics and kittens' social status in the litters. As physiological parameters we compared growth rates, steroid hormones level, immune response to the non-replicated antigen and neutrophil/lymphocyte ratio. Twelve domestic cat litters (2 - 5 kittens in each) from the experimental station "Tchernogolovka" of A.N. Severtsov Institute of Ecology and Evolution of RAS were used in our study. We observed kittens' play behaviour and took blood samples for the following EIA during the second and third months of kittens' life in 2011 and 2012. We determined kittens' hierarchical status basing on the order of kittens' approach to the food. The kitten that started to eat first during the feeding sets was considered as a dominant. We found that the dominant kittens initiated play interactions more frequently than their low-rank littermates. Also dominant kittens demonstrated higher average daily increase of body mass and more powerful immune response to the vaccination against feline panleukopenia virus than their subordinate littermates. These differences may be explained by the energy benefits of the dominant kittens. There were no significant variations in the cortisol, testosterone and androstendione levels between kittens of different social status. This may be related to the fact that kittens' endocrine system is still underdeveloped in this age. Comparison of the neutrophil/lymphocyte ratio did not indicate the significant differences between dominant and low-rank kittens, but it was clear tendency that this ratio was higher in subordinate kittens that may suppose their higher stress level.

This study was supported by RFBR 13-04-01465.

Energy reserves and androgenisation explain home range size variation in a wild rodent population

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This study tested the relationships between both individual-level and predation-risk factors and the size of two home range regions, defined as areas of different intensities. Using a novel method of implanted PIT tags and mobile recording stations we collected localisation data from each individual and, from trapping sessions, collected data on sex, body mass, and two previously ignored individual-level factors; androgenisation and subcutaneous fat. The study was conducted in a well studied population of wood mice (*Apodemus sylvaticus*) at Silwood Park, Ascot, England. Sixty-eight home ranges were split into two regions, core and periphery (HRR). Generalised linear models were constructed for each HRR for three seasons: non-breeding season, early and late breeding seasons. Body fat was negatively associated with HR periphery size and interacted with sex on core size in the early breeding season. Body mass also had a significant interaction with sex on core size in the early breeding season. Males with larger anogential distance had larger HRRs in the late breeding season and females in the non-breeding season. Males showed larger periphery sizes than females in both early and late breeding seasons. Shrub cover was negatively associated with each HRR size in both the early and late breeding seasons. Our results show that individual differences in physiology relate to variation in space use during certain seasons and that habitat features that reduce predation risk are important throughout the breeding period.

Testosterone and not body size predicts social interactions in a wild rodent population

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In the polygynous mating system of wood mouse (*Apodemus sylvaticus*), establishing dominance and territoriality is critical to gain copulations and increase reproductive success. The drivers of the underlying social interactions are not fully understood. We used social network analysis to examine phenotypic and hormonal effects on social interactions in a wild population of *Apodemus sylvaticus*. Using a novel system of mobile data loggers we were able to record individual social interactions in a wild population of PIT-tagged mice. Interactions were highest during the breeding season. In males, anogenital distance (AGD) was positively related to interactions during the breeding season. In females, this relationship was only detected during the non-breeding season. In both cases, body size effects on social interactions were negligible as compared to AGDs. These results show that individual level factors are important drivers of social interactions, that androgenisation is far more relevant than body mass in determining these, and they emphasise the need of better understanding physiological drivers of behavioural traits.

Inbreeding and adaptation to captivity depress the response to stress

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In *ex situ* captive breeding programmes, inbreeding and genetic adaptation to captivity of fitness-related traits can reduce the chances of successful reintroductions back into the wild. Here we use white-footed mouse (*Peromyscus leucopus*) from a captive breeding programme experiment to test how baseline corticosterone levels change as the wildlife species adapts to the captive environment. This includes effects due to the inevitable loss of genetic diversity and inbreeding occurring concomitantly with captive breeding. We account for a variety of potentially confounding factors – such as seasonality, sex, and age – which can also influence corticosterone levels. Overall generation and inbreeding had a significantly strong and consistent effect on corticosterone levels. We also tested the effects of three genetic breeding protocols -minimising mean kinship (MK), random breeding (RAN) and selection for docility (DOC)- on corticosterone levels. In DOC artificial selection for docility was practiced by pairing the males and females with lowest scores for flipping behaviours. Our results suggest that inbreeding and increasing number of generations in captivity decrease baseline corticosterone levels. This reduction on stress responsiveness in captivity also has implications for conservation programmes that might be considering releasing animals from long-term captive populations back into the more stressful wild environment. Lastly, the inbreeding depression on corticosterone levels detected has implications for the debate regarding the relationship between fitness and corticosterone response to stress, suggesting that higher baseline corticosterone are adaptive in the wild.

Non-invasive gonadal sex determination in white rhinoceros (*Ceratotherium simum*)

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White rhinoceros are under constant threat due to illegal poaching. Moreover, the low reproduction rate found in this species in captivity is a subject of interest and concern to many research groups. An appropriate management of every rhino population is essential to ensure a future for the species. Although sex determination is mainly visual in rhinoceros, sometimes it might be useful to have a tool to determine sex non-visually, for example when it is difficult to identify the sex, as might be the case in free-ranging rhinos. Androgens and oestrogens proportion seem to determine gonadal sex in all the species. Since a correct identification of the individuals of a rhino population is essential for a proper management, our main objective was to develop a statistical model to determine the sex of the rhinos based on faecal oestrogen and androgen concentrations. A total of 572 faecal samples from 15 white rhinoceroses were collected in three different habitats: captivity (Zoo of Madrid; n = 3); semi-captivity (Bioparc of Valencia; n = 4) and wild population (South African Reserve; n = 8). We have used a non-invasive enzyme immunoassay to analyse androgens (A: 4-androsten-17 β -ol-3-one) and oestrogens (E: oestrone sulphate). Assay sensitivity was 4.9 pg/well and 2.9 pg/well for androgens and oestrogens respectively. The variation coefficient for androgens was 4.32 % (intra-assay) and 7.87 % (inter-assay), and 8.89 % and 10.22 % for oestrogens. Assay precision was determined by 86.70 % androgens recovery and 89.50 % oestrogens recovery. The results obtained did not show a statistical difference between males and females in regard to mean hormone concentrations (A (ng/g): males = 128.20 \pm 22.15; females = 85.39 \pm 7.18; E (ng/g): males = 200.02 \pm 14.90; females = 285.06 \pm 29.71). We modelled individual gonadal sex using mean androgen and oestrogen concentrations of each animal by a logistic model. We compared sensibility and sensitivity in three models: model I: included oestrogens/androgens ratio; model II included oestrogen and androgen values and model III included oestrogen, androgen, and the interaction between both variables. Our results showed that model II had the best balance identifying the sex in rhinos from hormonal faecal concentrations (“when A > 1.46E – 222 ng/g it is a male”), with a 74.6 % of success. We conclude that androgen and oestrogen faecal concentrations are powerful tools to predict the sex in white rhinoceroses.

Niche modelling and GIS integration for black bearded sakis (*Chiropotes satanas*): support for threatened species to better plan protect areas

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Chiropotes satanas is an endemic primate species from the Amazon, which was classified as threatened by extinction by IUCN. Its occurrence is restricted to an endemic core area called Belem Center. This region suffers from intensive deforestation and other anthropogenic impacts (ASNER *et al.*, 2005). To predict the species geographic distribution, a maximum entropy algorithm available on MAXENT software was used (PHILLIPS *et al.*, 2006). In addition, GIS and MAXENT integrated ecologic niche modelling together with species ecologic data (VEIGA, 2001) was applied to increase our understanding of the preferred habitat of the species and to use to develop planning strategies to protect the remaining suitable areas. The land-use based modelling for *Chiropotes satanas* was based on 27 geo-referenced points taken between 1995 and 2007. We used a threshold of 53 % relative probability to distinguish suitable from unsuitable areas. Based on the species' ecology, suitable areas for *Chiropotes satanas* were identified. These suitable areas were overlaid on maps of the Amazon's Protected Areas and protected areas of indigenous people. The results indicate that upland forests and degraded forests (with selective cutting) are favourable areas for this species, corresponding to 75 % of the suitable areas identified by the model (> 53 %). We also observed a loss of 9.45 % of the *Chiropotes satanas* habitat because of human activities, representing approximately 1,719 km². Suitable habitat for *Chiropotes satanas* represented around 10 % of the Belem Endemic Centre, i.e., about 18.197 km². Only ~9 % (1,606 km²) of the total area of suitable habitat identified by our models is within the protected areas. A further 2 % (361 km²) are within integral protection areas and ~90 % (16,595 km²) are completely outside of any kind of protected area, so these areas are further exposed to fragmentation effects.

VEIGA LM (2006): Behavior and ecology of cuxiú preto (*Chiropotes satanas*) in fragmented landscape in Oriental Amazon. Doctoral thesis, UFPA. Belem. Brazil.

ASNER GP, KNAP DE, COOPER AN, BUSTAMANTE MMC, OLANDER LO (2005): Ecosystem structure throughout the Brazilian Amazon from landsat data and automated spectral unmixing. *Earth Interact* **9**, 1 - 31.

PHILLIPS SJ, ANDERSON RP, SCHAPIRE RE (2006): Maximum entropy modeling of species geographic distributions. *Ecol Model* **190**, 231 - 259.

How continuous stakeholder involvement adds value to conservation research and stimulates new research projects – lessons learnt from Namibia

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Research findings generated in projects that focus on human-wildlife-conflicts are sometimes difficult to implement in management plans of local land users. One reason might be that local stakeholders were not involved in the projects from the beginning on or did not have the opportunity to give their input on a continuous basis. This might have led to a dismissive attitude towards new management suggestions. Continuous interactions with stakeholders are likely to generate identification with the project and develop management suggestions that are practical and accepted by stakeholders. Here we present a study on free-ranging cheetahs (*Acinonyx jubatus*) in Namibian farmland that considered these aspects. Most cheetahs in Namibia occur on commercial farmland where farmers perceive them as threat to their livestock. Therefore, many farmers kill cheetahs indiscriminately to protect their livestock. However, such cheetah eliminations do not solve the conflict, because killed cheetahs are quickly replaced by others. Due to this, farmers were ready to collaborate with us and provided us with detailed information on their livestock losses. We set up two research stations on their farmland and collared cheetahs with GPS collars. We agreed with the farmers that they do not kill collared cheetahs and that we provide them regularly with data on cheetah movements. We detected particular areas with very high cheetah activity. These “hotspots” are high risk areas for livestock losses and we showed that shifting cattle herds with calves outside of hotspots can reduce the losses drastically. This conflict solution spread quickly through the farmer community and we were contacted by farmers outside of our study site to identify the hotspots in their areas. The interest was so strong, that farmers and farmer associations provided money for GPS collars and assisted in capturing cheetahs. This close cooperation resulted in additional research questions from the farmers’ side. They discussed with us their ideas and took the initiative to develop and write a research proposal for a study on leopards, the other large carnivore on Namibian farmland, and kudu, an important trophy species. We gave our scientific input on the proposals and the farmers submitted them to national and international foundations. With the money raised we started these projects and have recently collared six leopards and six kudu bulls. This example shows how a close cooperation with stakeholders and the mutual compliance with agreements can build up a bond of trust that is a solid basis for further joint research projects.

Who is who? – Investigating the gut-associated microbial community of the black-backed-jackal (*Canis mesomelas*) of central Namibia

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The relationship between individuals and their gut-associated microbial inhabitants is shaped by numerous intrinsic and extrinsic factors and changes in relative abundances or the appearance of certain pathogenic bacteria can cause serious health issues. For samples of interest, even when these are difficult to work with (e.g. non-invasively collected samples), advances in next-generation sequencing (NGS) technologies make it possible to analyse overall bacterial diversity and bacterial community changes, and elucidate their underlying causes. However, most studies that have investigated gut-associated microbial communities using NGS were carried out on humans or domesticated animals, while studies on wildlife species are still rare. Here, we present a gut microbial community analysis of the black-backed jackal (*Canis mesomelas*) of the central Namibian cattle ranching area using NGS and investigate which factors shape the relationship between this host and its microbial inhabitants. We consider intrinsic variables such as sex and age, and extrinsic factors such as geographical distribution and habitat type (i.e. livestock farm or game farm) in our analyses. Our results show that Fusobacteriaceae, Bacteroidaceae, Clostridiaceae and Lachnospiraceae were the most sequenced bacterial families among all black-backed jackals and that gut-associated microbial communities were in many cases more similar between individuals sampled at the same geographical location than between individuals from different localities. Overall, our results emphasise that further studies in wildlife species are required to obtain a clearer picture about these complex relationships and how they affect wildlife health.

Food habits of arctic fox (*Vulpes lagopus*) in the north-western part of Kolguev Island

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Kolguev Island in the Barents Sea (Russia) is a unique place with very high numbers of geese and with total lack of rodents. White-fronted goose (*Anser albifrons*) and bean goose (*A. fabalis*) nest on the whole island with high density (on average - 40 nests per km² and up to 15 per km² respectively) (KONDRATYEV *et al.*, 2012). Barnacle goose (*Branta leucopsis*) forms breeding colonies. Arctic foxes (*Vulpes lagopus*) and red foxes (*Vulpes vulpes*) are the only terrestrial predators on the island. We studied food habits of arctic foxes in June and July 2012 in the north-western part of the island (249 km²). We counted prey remains at 14 arctic fox dens (adult animals were absent during counting) located at a distance more than 1 km from barnacle goose colonies, and we set trail cameras at five dens. We found out that white-fronted geese were the main prey of arctic foxes; remains of arctic geese were present at all dens and represented 80 % (± 13 %) of all prey remains. Previous studies found that arctic foxes living near geese colonies only rarely hunt geese females during incubation eggs. In our study population, remains of adult geese during incubation period we found at 80 % of dens and they represented 51 % (± 14 %) of all prey remains. In period of gosling hatch and exodus arctic foxes fed mostly on goslings (93 \pm 11.4 %). Cameras at dens recorded adult foxes bringing food for pups, in 90 % cases there were geese remains (in 33 % of cases - eggs, in 61 % - goslings, in one case - adult white-fronted goose). The index of geese frequency of occurrence in arctic fox diet in our study is more than twice higher, than that in Svalbard (Norway; EIDE *et al.*, 2005), where rodents also do not play a great role in arctic fox diet. Thus, arctic foxes in our study during summer feed mostly on white-fronted geese. Further studies are needed to know more about arctic fox foraging on Kolguev Island.

The study was supported by Institute for Waterbird and Wetlands Research (IWWR) e.V.

EIDE NE, EID PM, PRESTRUD P, SWENSON JE (2005): Dietary responses of arctic foxes *Alopex lagopus* to changing prey availability across an Arctic landscape. *Wildl Biol* **11**, 109 - 121.

KONDRATYEV AV, ZAYNAGUTDINOVA EM, KRUCKENBERG H (2012): Recent status and biology of geese on Kolguev Island. *Casarca* **15** (2), 31 - 70.

Collection and vitrification of embryos in Iberian lynx (*Lynx pardinus*)

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The Iberian lynx Conservation breeding program (ILCBP) is an essential part of a coordinated action plan to conserve this highly endangered species. Besides ensuring the existence of the species in captivity, the *ex situ* program allows to study various aspects of the species' biology and physiology. Assisted reproduction techniques (ART) as artificial insemination, cryopreservation of gametes and embryos have already been proven to be very useful in integrated species conservation programs. Vitrification is becoming the first choice method of oocyte and embryo cryopreservation, in both human and animal ART.

The ILCBP was successful in breeding Iberian lynxes since it started in 2005 with more than 80 cubs produced. With increasing age of the animals used within the breeding program, however, problems occur, particularly, in relation to aging of females. Thus elder females are not able to breed without risking their own health. In case of two prime breeding females, Azahar (9 years) and Saliega (11 years), a permanent gonadectomy was considered because of repeated caesarean sections and mammary tumour risk, respectively. Both females were allowed to mate during breeding season and mating was monitored by camera surveillance. Then, seven days after observed first mating an ovariectomy was performed. Directly after surgery, oviducts and uteruses were flushed with 20 ml BoviPRO medium (Minitüb GmbH) using a buttoned cannula.

In both females, embryos or non-fertilised oocytes, respectively, were flushed exclusively from the oviducts. From Azahar three ovulation scars were visible on the ovarian surface. Correspondently, three morulae were obtained (~32 cell stage, before compaction) and immediately vitrified by the use of a commercial Kitazato Vitrification Kit applying the cryotop method. All procedures were performed according to the manufacturer's protocol. In Saliega, the mating was not successful, because no fertilised oocytes were obtained. In this case, only two unfertilised oocytes were flushed, although on the ovaries five ovulation scars were

identified.

In conclusion, the approach of ovariectomy after observed natural mating can be recommended for embryo preservation in the lynx. Seven days after the first mating the embryos were not yet transported to the uterus, thus in future a simple salpingo-oophorectomy will be sufficient to obtain embryos for ART.

What makes a blackbird tick? Impacts of sex and the city on behavioural and testosterone responses

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Many animal species that colonised urban areas show differences in their behaviour. For instance it has been observed that urban and rural individuals of the same species may differ in aggressive behaviour. However, little is known about the underlying mechanisms generating such differences in behaviour between urban and rural animals. Testosterone, a sex steroid hormone which may play an important role in the regulation of aggressive interactions, could be one potential factor behind the differences in agonistic behaviour in urban animals.

In the present study, we investigated behavioural and hormonal responses of hand-raised European blackbirds (*Turdus merula*) from an urban and a rural population to simulated territorial intrusions (STI), and assessed their physiological capabilities of producing testosterone via GnRH challenges.

Rural male and female blackbirds were bolder and more aggressive than urban conspecifics when confronted with a stuffed blackbird. However, this difference in aggressive behaviour between urban and rural blackbirds during the STIs was not accompanied by a difference in plasma testosterone concentrations. Nevertheless, in spring (when free-living blackbirds defend a territory), males who attacked the decoy had higher initial testosterone levels than non-attacking males, and in females the intensity of the attack was positively correlated with initial testosterone levels.

Both males and females increased testosterone in response to the physiological challenge with GnRH. Urban males achieved significantly higher testosterone levels after the GnRH injection than rural males, and a similar trend was observed in females.

The differences in aggressive behaviour and maximum testosterone secretions between the rural and the urban population argues in favour of intrinsic differences and is likely a result of microevolutionary changes following the urbanisation process, although early developmental influences cannot be excluded.

Nothing but a rat race? Pup ontogeny in naked mole rats

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Naked mole rats (*Heterocephalus glaber*) exhibit a complex social system related to their specific reproductive organisation, making them extremely difficult to breed in captivity. Their colonies may contain up to 300 individuals, yet, reproduction is monopolised by a single dominant “queen”, and one or two males. The social system is further characterised by a division of labour, overlapping generations and co-operative care for the offspring. The progeny usually remains in the natal burrows and has to fight for their position in the colony hierarchy. On the way there, both sexes face different physical challenges which we hypothesise to be reflected in developmental differences.

We quantitatively evaluated survival, sex ratio, growth pattern, development based on captive naked mole rat pups at the Leibniz Institute for Zoo and Wildlife Research (IZW). The offspring of three queens was assessed during four consecutive years: a total of 273 pups in 23 litters were born with a mean litter size of 11.87 and an inter-birth interval of on average 103.55 in a range from 72 to 203 days. Infant mortality generally is high in captive naked mole rat colonies; in average only 42 % of offspring survived.

At birth, 56 % of the offspring were male; a male biased sex ratio was found throughout all age classes. This may reflect the queen’s interest to produce more male workers which will not become a threat to her reign; a possible underlying mechanism may be resorptions, which we frequently observed during ultrasonographic monitoring of gestational development and selectively killing female offspring. Within the first 80 days postpartum, in contrast to their male littermates female pups gained body weight faster, although they weighed significantly less than their brothers at birth (t-test, $t = 0.66$, $p = 0.02$, $N = 243$). However, surprisingly, there was a large variability in birth weight within as well as between litters of the three queens during the four years of monitoring. Additionally, these weight differences of the individuals, independent of gender, remained unchanged throughout the whole lifespan. How and when individuals are attributed to different work tasks and if they may change between them is still unknown and subject of further research.

Testes and sperm production in alternative reproductive tactics of the African striped mouse

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The complex process of sperm production is costly in terms of time and energy. Males that follow alternative reproductive tactics (ARTs) might differ in their investment into testes development and sperm production. The resource-allocation hypothesis predicts that males following a sneaker tactic should invest more into sperm production than dominant territorial males, which should invest more into mate guarding. This hypothesis is supported by studies in species where individual males cannot switch between tactics (fixed tactics). In species with plastic ARTs, individual males can switch between tactics. Here we present the first data for a species where males have plastic tactics, the African striped mouse (*Rhabdomys pumilio*). In captivity, we mimicked three tactics observed in the field: philopatric group-living males, singly-housed males representing solitary roaming males, and group-living breeding males. We measured quantitative (testis/epididymis weight, testis volume, spermatogenetic activity, testicular/epididymal sperm number) and qualitative (sperm motility (SpermVision), morphology, mitochondria activity) reproductive traits, as well as hormone concentrations (testis and serum testosterone, serum corticosterone). We found no support for the resource-allocation hypothesis, since breeding and singly-housed males invested similarly in testes and sperm while philopatric males invested less. Further, we tested the hypothesis that philopatric males traded investment into sperm production against growth. Philopatric males became scrotal at an older age and greater body mass than their singly-housed brothers, but philopatric males did not reach a larger body mass at the end of the study than their singly-housed brothers. Interestingly, testosterone synthesis (testis testosterone concentrations) of philopatrics did not differ to those of other males, but serum testosterone levels did. These data suggest (i) that the reduced investment into testes and sperm production by philopatric males indicates reproductive suppression by the breeding male rather than a trade-off between growth and reproduction, and (ii) that philopatric males might be ready to increase their serum testosterone levels when social and environmental conditions allow for this physiological switch accompanying the behavioural switch between tactics.

Analysis of wild Assamese macaque MHC-DRB from faecal samples

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The major histocompatibility complex (MHC) plays a unique role in linking social behaviour to the genetic make-up of social partners with potentially huge effects on fitness. Due to its role in the immune reaction information on the MHC is also relevant in wildlife conservation and evolutionary ecology. Detailed knowledge on the genomic organisation, polymorphism and diversity of MHC has a narrow taxonomic focus though and among macaques is only available for rhesus and long-tailed macaques, the species most commonly used for biomedical research. One reason for the lack of data on wild populations is the difficulty to obtain blood or tissue samples necessary for genotyping approaches. Here, we aimed to analyse MHC-DRB from non-invasively collected faecal samples in wild Assamese macaques (*Macaca assamensis*) from Thailand. Assamese macaques are an interesting study species for the investigation of genetic impacts on fitness due to their mating system allowing for pronounced female choice. We analysed the highly diverse microsatellite marker MHC-DRB-STR (D6S2878) and obtained results from 43 individuals including 35 members of previously identified families. We detected 28 distinct STR lengths, with individual genotypes containing one to nine MHC-DRB-STRs. Four haplotypes segregating among families in Mendelian fashion and further four potential haplotypes could be defined. Our results indicate that variability and diversity of MHC-DRB in Assamese macaques is comparable to that of other macaque species, each haplotype containing one to five STRs. As expected due to the DNA source, there were a number of problems with the analysis. We have to assume that incomplete genotypes for additional individuals and members of known families presented here are likely, calling for further improvement and evaluation of the current methods. As a first step to do so, we developed a new primer for the amplification of the marker D6S2878 based on Assamese macaque sequences. Our results indicate that faecal samples can be used for non-invasive analysis of MHC genes after thorough method optimisation, opening a number of opportunities for further MHC research on natural populations.

Long-term consequences of birth season in Asian elephants

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In highly seasonal environments, many species maximise offspring survival by reproducing at the time of year with peak resource availability. However, Asian elephants (*Elephas maximus*) do not have a single breeding season, rather females undergo reproductive cycles throughout the year. Whether females concentrate most births on periods of maximum offspring survival is unknown, as are the long-term effects of birth season on patterns of mortality and fertility. These topics are of particular importance in elephants, which are extremely long-lived and endangered, as understanding variation in mortality and reproductive success could contribute towards conservation of the species. We use individual-based longitudinal data for 2350 semi-captive logging elephants from Myanmar that occupy regions with a tropical monsoon climate, to investigate immediate and long term fertility and mortality responses to season. We supplement this long-term data with a one year subsample of 70 elephants for which monthly measurements of body weight, body condition and stress hormone (cortisol) levels were collected, to investigate the physiological correlates of seasonal conditions. Our results show that there is variation in birth rate across the year, with 41 % births occurring between December and March. These months correspond to cool, dry period and the beginning of the hot season and to conceptions occurring during the resting, non-logging period between February and June. Individuals born in during the high birth rate period experience odds for mortality between the ages of one and five years that were seven times lower than those conceived during working months. Our results suggest that maternal workload, through its effects on maternal stress, oestrus cycles or access to males, limits conception rate and calf survival in this population. Individual cortisol levels were highest in the monsoon months of July to September, which also coincides with the fewest conceptions. In addition, we found long-term reproductive consequences birth season with individuals born in the hot season having earlier age at first reproduction and those born in the monsoon experiencing an earlier and faster declining process of reproductive senescence. This is a rare test of effects of early life conditions on a semi-captive species.

Effects of climate on survival of Asian elephants

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Climate change has intensified interest in understanding how climatic variability affects animal life histories. Despite this, little is known of their effect on survival in those species. Asian elephants (*Elephas maximus*) are endangered across their natural distribution, and inhabit regions often characterised by high seasonality of both temperature and rainfall. We investigated the effects of monthly climatic variation on survival and causes of death in Asian elephants of all ages and both sexes, using a unique demographic dataset of 839 semi-captive longitudinally monitored elephants from four sites in Myanmar between 1965 and 2000. Temperature had a pronounced effect on survival, with the lowest predicted survival during the hottest and coldest months in both sexes across all ages. Elephants spent twice as long in temperatures above the optimum of 24°C than below it, therefore of all the deaths recorded, more occurred in hotter than optimum months than in colder than optimum months. Decreased survival at higher temperatures resulted partially from increased deaths from heat stroke and infectious disease, whilst the lower survival in the coldest months is associated with an increase in non-infectious diseases or poor health in general. Variation in survival was also related to rainfall with the highest survival rates during the wettest months. Our results show that even the normal-range monsoon variation in climate can exert large impact on elephant survival in Myanmar leading to large absolute differences in mortality, particularly among the youngest age classes. The persistence of a long-term trend towards higher global temperatures combined with the possibility of higher variation in temperature between seasons may pose a growing challenge to the survival of species such as the endangered Asian elephants.

Serum prevalence to different pathogens of cat species at the Russian Far East: implication for conservation

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Infectious diseases are very dangerous for small isolated population of animals and may result to their decline or extinction. Knowledge of pathogen transmission and the main threats they pose to wildlife host species may contribute to animal conservation. Many free-ranging felids species are typically solitarily and have large home ranges. However, habitats are often of low quality resulting in geographically isolated and small populations. The aim of this study was to determine seroprevalence of antibodies against various pathogens in five wild Far-East felids (Amur tiger *Panthera tigris altaica* (n = 18), Pallas cat *Otocolobus manul* (n = 20), Far-East leopard *P. pardus orientalis* (n = 6), Eurasian lynx *Lynx lynx* (n = 2), Far-East wildcat *Prionailurus bengalensis euptilura* (n = 2)). The study was conducted in Prymorskii and Zabaikalskii krai. Blood sampling was conducted during animal capture. Serum was separated and stored under -20° C until analyses. The presence of antibodies to 11 pathogens was determined using commercially available ELISA kits validated for domestic cats. Immunochromatography tests were used to detect antibodies to feline immunodeficiency virus, feline coronavirus, *Dirofilaria* sp. and antigen of feline leukaemia virus. All tests were conducted in the veterinarian lab of Institute of Ecology and Evolution, Moscow. We found that wild Asian felids had developed antibodies against twelve of the pathogens we screened for. Canine distemper virus is considered as the most dangerous pathogen for Amur tiger (3 tigers were seropositive of 17 that were screened for CDV). Feral and domestic dogs were also tested and considered as the main reservoir of this pathogen (11 seropositive animals of 21 tested). Total vaccination of domestic dogs is suggested to be conducted to prevent CDV epizooties. Amur tiger showed seropositive reactions significantly more often than Pallas cat to *Toxoplasma gondii*, pseudorabies virus, *Trichinella* sp., *Candida* sp. High occurrence of these pathogens in Amur tiger might be related to habitat differences between the two species or feeding specialisation of the cats. Far-East leopard also showed high level of seropositivity to *Trichinella* sp. and *Candida* sp. Feline leukaemia virus was detected in serum of one Amur tiger (of 18 screened tigers), one Far-East leopard (n = 6), one Pallas cat (n = 18). Animals capture as well as control of pathogens distribution is necessary to decrease risk of mortality of endangered felids. This study was supported by RFBR 04-13-01465 and Russian Geographical Society.

Detecting animal behaviour from GPS data: towards integrated hardware-software solutions

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Tracking animals with Global Navigation Satellite Systems (GNSS), of which GPS is the most commonly used, has become an important research method for studying wildlife behaviour. Frequently this is for studying large-scale movements such as migration or resource use within a territory. Technological developments have opened up possibilities to get more information out of positioning data. Augmentation systems such as Europe's EGNOS service give better spatial accuracies, to within one meter. Development in hardware (especially power use, batteries and data storage capacity) mean that GPS tags are getting smaller, lighter and more durable all the time. Other sensors can provide additional information, such as accelerometers, magnetometers, heart pulse sensors and ambient temperature sensors. This increases the number of animal species and applications these tags can be used for. Collecting more data also requires improved data handling and analysis tools. Developments in software mean that it is possible to gain much more detailed information from such data than previously. Automatic classification of behaviour is a way to reduce the amount of data into meaningful information. However, there is not currently an end-to-end solution available that can integrate all these developments. In this paper, we will present a new solution which is being developed in the E-Track project whereby new EGNOS-enabled GPS hardware tags and new software (TrackLab) can be used to analyse close-range movement and identify behaviours of animals. Different aspects of data acquisition, visualisation and analysis will be discussed, illustrated with results obtained from various species of birds and mammals.

The work described in this paper was carried out as part of the E-Track project (www.etrack-project.eu). E-Track is carried out in the context of the Galileo FP7 R&D programme supervised by the GSA (Nr. 277679-2).

SNP or STR? A comparison of marker systems for noninvasive genetic wolf monitoring

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Genetic wildlife monitoring largely relies on the use of microsatellite markers (Short Tandem Repeats; STR). The ongoing advances in next-generation sequencing, however, have facilitated the application of genomic marker systems, such as SNP (Single Nucleotide Polymorphism) chips, even for large sample numbers. The difficulty in applying genomic technologies to forensic samples has so far limited the applicability of these new tools in the field of genetic wildlife monitoring and conservation genetics. In this presentation we compare the efficiency of traditional microsatellite analysis vs. a newly developed panel of SNPs designed for noninvasively collected sample material. Using samples from the ongoing genetic wolf monitoring in Germany, we show that the new SNP tool allows for rapid and cost-effective simultaneous screens of >> 100 loci from tissue, blood, hair, scat, or urine samples. We compare both methods in terms of marker resolution, reliability, work load, and costs per sample.

Applying molecular genetic tools across conservation management: examples, limitations & challenges

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The basic concepts of conservation genetics and their importance in the management of small populations are now well recognised. In many cases, management decisions will rely on the application of appropriate population genetic theory, which will be sufficient to determine best practice in a given situation. However, for a wide range of issues, a lack of information regarding the evolutionary history, population structure, or individual relationships within species, limits our ability to effectively manage populations of conservation concern. The use of molecular genetic techniques has long been proposed as a solution, but arguably molecular conservation genetic studies have often failed to deliver the type of data required for management applications. This presentation will focus on how this situation is starting to change, providing examples of applied conservation genetics across the conservation spectrum, before identifying the challenges that remain to be overcome.

Conservation genomics of the Eurasian beaver: from RAD to reintroduction

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Following its historic population decline and subsequent widespread recovery during the 20th century, the Eurasian beaver, *Castor fiber*, has been the subject of conservation and research interest across Europe for many years. Several studies on the molecular ecology and phylogeography of the species have been undertaken (ELLEGREN *et al.*, 1995; DURKA *et al.*, 2003) and used to support conservation management or understand past translocations. However, until now, a lack of molecular markers with sufficient resolution to evaluate individual genetic diversity or fine scale population structure has limited our knowledge of this species. This has affected the implementation of the Scottish Beaver Trial, a high-profile UK reintroduction of beavers from continental Europe to Scotland (HALLEY, 2010).

In response to this situation, a two-phase project was initiated in 2011 with the aims of: i) applying RAD sequencing to the discovery of large numbers of informative SNP markers in Eurasian beaver, and ii) subsequently applying a panel of these markers to investigate population genetic structure and diversity throughout the species range. Since this project plan was announced at IZW 2011, the two phases have been completed through two consortia projects involving over 20 European researchers.

The work resulted in the discovery of many thousand candidate SNPs (SENN *et al.*, 2013) of which 384 were used to screen 384 individual beavers using an Illumina veracode genotyping assay. The subsequent data has been analysed to investigate genetic diversity and population structure and to develop methods for establishing individual identification, relatedness and the geographic origin of beavers. This presentation will highlight the key findings of the work of relevance to molecular ecologists, conservation geneticists and reintroduction programme managers.

DURKA W, BABIK W, DUCROZ J-F, HEIDECKE D, ROSELL F, SAMJAA R, SAVELJEV AP, STUBBE A, ULEVICIUS A, STUBBE M (2005): Mitochondrial phylogeography of the Eurasian beaver *Castor fiber* L. *Mol Ecol* **14**(12), 3843 - 56.

ELLEGREN H, HARTMAN G, JOHANSSON M, ANDERSSON L (1993): Major histocompatibility complex monomorphism and low levels of DNA fingerprinting variability in a reintroduced and rapidly expanding population of beavers. *PNAS* **98**, 8150 - 8153.

HALLEY D (2011): Sourcing Eurasian beaver *Castor fiber* sock for reintroductions in Great Britain and Western Europe. *Mammal Rev* **41**, 40 - 53.

SENN S, OGDEN R, CEZARD T, GHARBI K, IQBAL Z, JOHNSON E, KAMPS-HUGHES N, ROSELL F, ROSS MCEWING (2013): Reference-free SNP discovery for the Eurasian beaver from RAD paired-end data. *Mol Ecol*, doi: 10.1111/mec.12242

Thermoregulation during pregnancy in temperate forest-dwelling bats

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The reproductive state has a great effect on thermoregulation as foetal growth is energetically costly and undelayed parturition can only be assured by high body temperatures. Foetal growth, and, therefore, high energy requirements, starts in early spring. A reduction of body temperature during pregnancy is likely to result in reduced rates of embryonic development and prolonged pregnancy, whereas a constant and elevated body temperature during pregnancy might ensure undelayed foetal development and parturition. Therefore, we hypothesised that with ongoing pregnancy skin temperatures should remain at normothermic levels.

In 2011 and 2012, we tagged seven Bechstein's bats (*Myotis bechsteinii*), seven Natterer's bats (*M. nattereri*) and seven brown long-eared bats (*Plecotus auritus*) with temperature-sensitive radio transmitters during pregnancy and compared recorded skin temperatures. To be able to account for yearly fluctuations we corrected days of data acquisition with ambient temperatures.

With ongoing pregnancy torpor phases were avoided and skin temperatures remained high. Moreover, skin temperatures were significantly correlated with undelayed days of pregnancy (Spearman Rank correlation, $n = 41$, $R = 0.672$, $P < 0.001$).

The results support our hypothesis that with ongoing pregnancy skin temperatures remained at normothermic levels. This suggests that close to the end of pregnancy thermoregulation is restricted despite the fact that pregnancy is an energy demanding process.

A wolf family pack in captivity: social dynamics and hierarchy

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Animal behaviour might be affected by captivity as well as social dynamics, which can vary during time (HOSEY *et al.*, 2009). The social system of wolves (*Canis lupus*) has very high levels of social complexity and relationships within the pack are established through a clear dominance hierarchy (PACKARD, 2003). Most research on the social dynamics of wolf packs has been conducted in captivity. Captive packs were usually composed of an assortment of wolves from various sources placed together (RABB *et al.*, 1967; ZIMEN, 1975, 1982) whereas in nature, the typical wolf pack is a family (PACKARD, 2003). The purpose of this study is to assess whether and how captivity could influence the social behaviours of wolves in a family pack. Furthermore, we aim at investigating the social relationships and the dominance hierarchy within the pack. The study was carried out over a period of three years (2010 - 2013) with a wolf family pack hosted at Parco Natura Viva (Italy). Data were collected using focal animal continuous sampling method. Affiliative and agonistic behaviours (in particular dominant and submissive behaviours) were collected. Non-parametric tests were used for statistical analysis. Results highlight that the wolves seem to perform species-specific social behaviours. Furthermore, our research suggests that the dominance hierarchy of this pack seems to be linear and dynamic. In conclusion, the captive wolf family pack seems to have a well-developed social system, which establishes well-defined relationships between individuals.

HOSEY G, MELFI V, PANKHURST S (2009): Zoo Animals: Behaviour, Management, and Welfare. Oxford University Press: Oxford.

PACKARD JM (2003): Wolf behavior: reproductive, social, and intelligent. In: MECH LD, BOITANI L (Eds.), Wolves Behavior, Ecology and Conservation. The University of Chicago Press: Chicago and London.

RABB GB, WOOLPY JH, GINSBURG BE (1967): Social relationships in a group of captive wolves. *Am Zool* 7, 305 - 312.

ZIMEN E (1975): Social dynamics of the wolf pack. In: FOX MW (Ed.), *The Wild Canids: Their Systematics, Behavioral Ecology, and Evolution*. Van Nostrand Reinhold: New York.

ZIMEN E (1982): A wolf pack sociogram. In: HARRINGTON FH, PAQUET PC (Eds.), *Wolves of the World: Perspectives of Behavior, Ecology, and Conservation*. Noyes Publications: Park Ridge.

The evolution of primate handedness: a comparative study

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Humans show a consistent right-hand preference for manual activities (ANNETT, 1985) and that asymmetry could be related to a lateralisation of brain functions (ROGERS and ANDREWS, 2002). Despite extensive studies, the evolution of primate handedness is still unclear (SCHEUMANN *et al.*, 1985). The Postural Origins Theory (POT) states that in the ancestral primate the left hand became preferred for reaching whereas the right hand was used to provide postural support (MACNEILAGE *et al.*, 1987). This study aims to find evidences of handedness in 9 adult ring-tailed lemurs, 15 Barbary macaques and 10 chimpanzees housed at Parco Natura Viva (Bussolengo, Italy). One 15-minute session per animal per day was performed (20 sessions per subject in total). The hand providing postural support and the hand involved in different behavioural actions were recorded. Data were collected using the focal animal sampling method. Frequencies of bouts were analysed and non-parametric tests were run to assess hand preference at individual and group-level. Results highlight that ring-tailed lemurs, Barbary macaques and chimpanzees showed hand preference at individual-level for postural support and unimanual actions. Furthermore Barbary macaques showed no hand preference at group-level, whereas ring-tailed lemurs showed a group-level hand preference for the left when starting locomotion. Moreover in chimpanzees a significant right-hand preference for all unimanual actions, particularly for manipulation, was found, whereas no group-level hand preference for simple-reaching movements was found. Our results seem to partially support the POT. As in chimpanzees hand preference emerged during manipulation, high level tasks could lead to the emergence of handedness, according to the “task complexity theory” (FAGOT and VAUCLAIR, 1991).

ANNETT M (1985): Left, right, hand, and brain: the right shift theory. London: Lawrence Erlbaum.

FAGOT J, VAUCLAIR J (1991): Manual laterality in nonhuman primates: a distinction between handedness and manual specialization. *Psych Bull* **109**, 76 - 89.

MACNEILAGE PF, STUDDERT-KENNEDY MG, LINDBLOM B (1987): Primate handedness reconsidered. *Behav Brain Sci* **10**, 247 - 303.

ROGERS LJ, ANDREW RJ (2002): Comparative Vertebrate Lateralization. Cambridge University Press: Cambridge.

SCHEUMANN M, JOLY-RADKO M, LELIVELD L, ZIMMERMANN E (2011): Does body posture influence hand preference in an ancestral primate model? *BMC Evol Biol* **11**, 52 - 61.

3D adrenal ultrasound – a new approach for the evaluation of stress in the critically endangered Iberian lynx *ex situ* population

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3D ultrasound is used routinely in human medicine for prenatal diagnostics and to assess the exact topography of organs and their function. We considered its scope to evaluate the ratio between adrenal cortical and medullary region in a reliable and repeatable way. During health check-ups of Iberian lynxes (*Lynx pardinus*) at the Iberian lynx conservation breeding program (ILCBP) in Spain and Portugal, we found remarkable individual changes in size and shape of adrenal glands.

In this study we included data from veterinary examinations performed on 14 captive Iberian lynxes in November 2012. All 2D and 3D ultra-sonographic datasets were reproducible and of high quality. We found significant negative correlations between ratio of adrenal cortex and adrenal medulla (C:M) and their ability to cope with stressful events ($p = 0.01$). This coping ability was categorised from 1 (very nervous) to 5 (very calm) and differentiated between daily routine work or unusual stressful events. Cortical measurements were on average 0.19 cm thick (range 0.11 – 0.33 cm), while medullary measurements were on average 0.22 cm thick (range 0.13 – 0.39 cm). 2D measurements on length, width and breadth were not at all in correlation to their real 3D volume ultrasound measurements. This indicates that size calculations based on 2D measurements do not give a true picture of the real size of adrenal glands. Furthermore, there was no significant correlation between the shape of the adrenal and the ability to cope with stress. The ratio of C:M assessed in 3D volume ultrasound and 2D images were comparable and was significantly negatively correlated with the ability to cope with stressful events in captive Iberian lynx. Animals coping less well with stress had a cortex relatively thicker than the medulla by a factor of two, whereas individuals coping better with stress showed ratios of C:M of almost 1:1. We conclude that adrenal ultrasound might be a valuable tool to evaluate chronic stress, adaptability to captivity and resilience towards stressful events in the Iberian lynx, although more data are needed to validate our preliminary results.

Factors influencing crop raiding behaviour of Indian elephants (*Elephas maximus indicus*) in Tamil Nadu, India - a case study

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Factors influencing crop raiding behaviour of wild Indian elephants were studied in Hosur Forest Division of the Tamil Nadu State, India. Factors such as crop pattern, water source, location of the affected place, sex, herd composition and season etc., were found to influence the incidence of crop-raiding. There was seasonal variation in crop raiding frequency. The raiding incidence was highest in December and January during the study periods. Incidences of crop raiding by lone bull elephants was almost equal to the incidences by family herd elephants. The more affected places were found to have good water sources nearby. The affected places were found to be located within the distance of five kilometres from the forest boundary. Among the various crops raided by the elephants, the highest affected crop was Finger millet (*Eleusine coracana*) and the least affected crop was Horse gram (*Macrotyloma uniflorum*). The relative impacts of the above factors on the crop raiding frequency are discussed.

Amur leopard cat litters pass through social changes associated with stress prior to dispersal

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Most cat species are solitary carnivores. Mother with kittens is the most long-term social aggregation of animals. There are only few data on mechanisms triggering dissolution of litters and the beginning of solitary life in young Felidae. The aim of our study was to assess changes in the social structure of litters and cortisol level fluctuations in Amur leopard cat (*Prionailurus bengalensis euptilura*) kittens during their ontogeny. The study was carried out at the research station “Tchernogolovka”, situated 60 km northeast from Moscow (Russia) from 2010 to 2012. Blood samples were taken from kittens at two-week intervals up to the age of 26 weeks, well after weaning. Serum samples were assayed for cortisol with an EIA. Detailed visual observations of kitten and mother behaviour were conducted in four litters (nine kittens) of four females every third day between the ages of 6 and 22 weeks. Frequency of kittens’ social play sharply increased from 6 to 8 weeks (Wilcoxon pair-matched test: $p = 0.03$) during the weaning period and kept being on a high level up to week 12. Different types of invitations to game were the main elements in kittens’ social play (52 %). Within this period cortisol level fluctuated insignificantly (range 100 - 191 ng/ml; Friedman test: $p = 0.1$), and hormone dynamics appeared to be related to the dynamics of kittens’ social play, probably reflecting energetic efforts of kittens for play activity. Frequency of kittens’ social play decreased significantly from week 12 to week 14 (Wilcoxon pair matched test: $p = 0.01$). Cortisol levels increased sharply by a factor of three ($p = 0.01$) to 16 weeks, and after that, from 18 to 26 weeks, cortisol concentrations were two times higher (range 266 - 313 ng/ml) than during the period from 2 to 14 weeks. Thus the period from 14 to 16 weeks may be considered as critical in social intra-litter relationships. Frequency of mothers’ social play also decreased after 12 weeks of age whilst the time she spent away from her kittens increased. Similarly, the frequency of friendly maternal vocalisations dropped whilst the frequency of aggressive vocalisations increased.

We conclude that the age of three to four months is critical for the dissolution of social relationships in the litter; keeping the kittens together after this period appears to be stressful for kittens. This information is useful for the captive management of rare cat species.

This study was supported by RFBR 12-04-32028.

On the track of diversifying selection: an adaptive genetic divergence in *Cheirogaleidae*?

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Identification of selective forces acting on adaptive traits maintaining genetic divergence among populations is essential for understanding the ecological origins of reproductive barriers that may ultimately lead to speciation in sympatric populations. The major driving forces in the process of diversification among populations are considered to be sexual selection, acting on divergence of mating traits, and adaptations to local ecological pressures. Traits that both respond to sexual selection and local ecological adaptations have been suggested as a possible mechanism facilitating selective divergence among populations. The potential for immune genes of the Major Histocompatibility Complex (MHC) to respond to both local ecological pressures (pathogen resistance) and sexual selection (mate choice) makes them ideal candidates to investigate a process of genetic diversification among closely related species.

Using 454-sequencing technology (Roche), we genotyped two highly polymorphic MHC genes (DQB, DRB) in a community of four nocturnal lemur species - *Microcebus berthae*, *Microcebus murinus*, *Cheirogaleus medius* and *Mirza coquereli* (*Cheirogaleidae*). These four sympatric species occupy four study sites ranging from continuous to isolated forest patches in Kirindy forest, Western Madagascar, and vary in population density. The MHC variability of endangered *M. berthae* and near threatened *M. coquereli*, was explored here for the first time.

We tested whether i) MHC variability is affected by population density, and ii) divergence in immunological repertoire (functional diversity) of MHC alleles reflects phylogenetic distances among species.

We predicted that MHC variability would be higher in species with higher population density (*M. murinus*, *Ch. medius*) than in two other species with lower population density (*M. berthae*, *M. coquereli*) and that divergence in immunological repertoire will not reflect phylogenetic distances among species, as it is likely to be determined rather by similar ecological pressure exerted upon them.

High-throughput 454-sequencing technology proved a competent and promising tool to address questions regarding the determinants of functional variation at a community level. We found a higher level of MHC variability in species with higher population density and considerable divergence in immunological repertoire of MHC alleles in both genes among all four species. Our results also indicate that the functional proximity of MHC alleles does not reflect phylogenetic distances among species. This study reports preliminary results on MHC differentiation between species, and investigated demographic effects on MHC variation within

species, and differentiation across species. In the next step, we will investigate whether richness of parasite communities predicts levels of MHC diversity and if overlaps in parasite communities predict proximities in MHC immunological repertoires.

The influence of environmental enrichment on social-sexual-behaviours and its correlations with faecal steroid hormone metabolites in captive black-tufted marmoset (*Callithrix penicillata*)

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The successful reproductive management and application of assisted reproductive techniques depend on previous knowledge of basic endocrine physiology and behavioural characteristics as well. The aim of this work was to describe the endocrine profile and their potential association with socio-sexual behaviour in captive black-tufted marmoset (*Callithrix penicillata*). It was also studied the influence of the introduction of environmental enrichment techniques on the behavioural and endocrine variables. The method of choice for the endocrine approach was the non-invasive monitoring of faecal metabolites of oestradiol (fEM), progesterone (fPM) and testosterone (fTM) by enzyme immunoassay (EIA) of six pairs of captive *C. penicillata* kept in a rehabilitation centre in São Paulo, Brazil. The sample collections were performed daily, always early in the morning, six days a week, for six months, being four months before and two months after the introduction of the enrichment techniques. The behavioural variables were recorded through a time interval focal sampling method. All the assays were previously validated for this species. The results of four females showed a cyclic pattern for the concentrations of fPM with clear peaks followed by sustained high concentrations indicating that ovulation has previously occurred. The cycle length was 24.3 ± 4.1 days. Two females did not show any cyclic pattern during a 130 days period but a sustained high concentration profiles instead. Both of them were suspected pregnant what was confirmed later on. The socio-sexual behavioural patterns were observed in both phases (follicular and luteal) showing no significant differences. When the peri-ovulatory period (one day before and one day after the estimated day of the ovulation) was considered as a third phase, there were evident higher prevalence of the behavioural variables compared with follicular and luteal phases. The introduction of environmental enrichment techniques such a variety of puzzle feeders with beetle larvae, branches with leaves and new hidden places did not show any influence on sexual behaviour or in endocrine profiles. These results are brand new data for this species.

This study is sponsored by a FAPESP Grant – 08/53562-8.

Non-invasive monitoring of adrenocortical activity in Iberian lynx (*Lynx pardinus*)

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The development of faecal glucocorticoid metabolite (fGM) enzyme immunoassays (EIAs) facilitates a non-invasive study design to monitor an animal's endocrine status and thus assess health and welfare without taking invasive samples. Despite the wide use of these techniques, EIAs need to be carefully validated for each species, sex and hormone. The goal of our study was to validate an appropriate EIA for monitoring adrenocortical activity in the world's most endangered felid species, the Iberian lynx, using Eurasian lynx (*Lynx lynx*) as a model. We compared six available EIAs in two captive Eurasian lynx (one female and one male) using ACTH challenges for detecting acute increases in fGM concentrations in response to ACTH. To characterise and identify faecal cortisol metabolites, a radiometabolism study was performed in a male Eurasian lynx applying ³H-cortisol. Using HPLC analyses radiolabeled metabolites were compared with immunoreactive metabolites, also including faecal extracts, of a male and a female Iberian lynx for species comparison. We then analysed faecal samples collected for nine months from six captive Iberian lynx (three females and three males) after a translocation to monitor changes in adrenocortical activity. Individual profiles were examined in relation to behaviour rated by the keepers. Our results demonstrated that the 11-hydroxyetiocholanolone assay is the most efficient for accurately reflecting adrenocortical activity after an ACTH challenge in both sexes. The administration of exogenous ACTH resulted in an increase in fGM concentrations within 32 h. HPLC immunograms show strong similarities across both lynx species, suggesting a conserved steroid metabolism among the sister taxa. The 11-hydroxyetiocholanolone assay measured amounts of immunoreactivity corresponding to the radiolabeled peaks. Furthermore, HPLC immunograms and GC-MS analyses identified the 11-hydroxyetiocholanolone metabolite in faeces of Eurasian and Iberian lynx. Longitudinal profiles of Iberian lynx revealed that captive male lynx have higher fGM levels than female lynx, which might be related to sex-specific variations in steroid metabolite excretion. Reproductive behaviour, manipulations in enclosures and veterinary examinations associated with chemical immobilisation were identified as strong biological stressors resulting in significant increases in fGM concentrations. In contrast, elevated fGM concentrations after translocation were only measured in a single male. Monitoring of fGM concentrations in the 11-hydroxyetiocholanolone assay constitutes a valuable and practical tool for assessing adrenocortical activity in

Iberian lynx. This non-invasive technique provides an opportunity to improve the husbandry conditions of captive lynx and thus contributes to advance the physiological and psychological health of this endangered species.

Population structures in two closely related seabirds – crested and whiskered auklets (*Aethia cristatella* and *A. pygmaea*)

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Crested auklets (CA) and whiskered auklets (WA) are small seabirds with bright plumage and complex social behaviour that breed in the North Pacific. Out of the breeding season, auklets spend time at sea, and it is still known nothing about the dispersion of young birds. Here we tested morphometric, acoustic and genetic variability in both species. We collected data for CA and WA at eight and three sites, respectively, around the Bering and the Okhotsk seas. We measured body weight and lengths of wing, tarsus, bill, crest and auricular plume (totally 309 CA from four sites and 108 WA from three sites). We also analysed two main call types, the Bark and the Trumpet call of CA (200 and 100 calls from four sites, respectively), and the Mew and the Beedoo call of WA (300 and 90 calls from three sites, respectively). Also for CA we analysed the control region's fragment (408 b.p.) of mitochondrial DNA (totally 128 samples from five sites) and four microsatellite loci (totally 183 samples from five sites). ANOVA post-hoc Tukey test shows a negligible effect of "site" on morphometric variables of CA ($p > 0.05$ for most of comparisons) and a highly significant effect on morphometric variables of WA ($p < 0.001$ for all comparisons). The differences between colonies of WA were large, so we did not find an overlap in two parameters from six. We also found a little effect of "site" on temporal-frequency variables of the Bark ($p < 0.001$) and no significant effect on those of the Trumpet call ($p > 0.05$) in CA, but in WA the effect of "site" on acoustic variables was again much more evident for both call types ($p < 0.001$ for all comparisons). Also, for CA no genetic differentiation between colonies was found. A high haplotypic ($H = 0.994 \pm 0.002$) and a relatively low nucleotide diversity (0.013 ± 0.007) were noted for all sites. We suppose that the gene flow is very intense between CA' colonies, but it is restricted between WA' colonies. This difference could reflect the ecology of the species: WA prefers to feed close to colonies during the whole year, whereas CA leaves them in winter and spends this time in the sea. So, we show that the relation to the colonies could be an important factor for the population structure formation in colonial seabirds. We suggest that gene flow in CA could be provided mostly by young birds' dispersion, because of the high level of adult nest fidelity.

How to live on 24 hours a day in a dining room: circadian rhythms of activity in common weasel and its potential prey

PUTILOV ARCADY

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ARNOLD BENNETT - an English writer – in his book “How to Live on 24 Hours a Day” (1910) offered practical advice on how one might “live” as opposed to just “existing” within the limits of 24 hours a day. But what if someone has to live in a dining room as common weasel (*Mustela nivalis*), the smallest carnivore in the world, does? Small size gives weasels a significant advantage over any larger predator in the exploitation of small rodents. They reside in the nests of their prey and are able to hunt them when they are resting in their burrows. However, due to their small size and elongate body shape, weasels have a more energy-intensive way of life in addition to more uncertainty in reproductive success and greater vulnerability to interference from other predators. Common weasels must consume, on average, about 40 % of their body weight in food each day and distribute their feeding among five to ten meals per day. The rapid processing of food means that they must either stay near cached food or forage every few hours. Therefore, they exhibit ultradian cycles of activity, a pattern that also characterises the activity of two other groups of small mammals, the voles and shrews, but not mice. Given that carnivores prefer to kill and eat the voles and reject the shrews (supposedly, they find them distasteful), one can hypothesise that common weasels might synchronise their activity with polyphasic patterns of activity of the former rather than the latter. Visual recordings of locomotor activity of captured small mammals were obtained under natural summer photoperiod with 1-min sampling interval. Data were averaged within each hour, across days, and across animals from the same population. The averaged 24-hour time course of activity of common weasel was compared with the time courses of 13 species of rodents (voles, mice, and birch mouse) and six species of shrews from 12 sympatric and 28 allopatric populations. The weasel’s time course most closely resembled the time courses of root voles (*Microtus oeconomus*) from the sympatric and two of three allopatric populations. Although this resemblance might be interpreted as providing evidence for synchronisation between ultradian cycles of activity of weasels and their most probable prey, some other explanations cannot be ruled out. For instance, this resemblance might reflect the independent attempts of both predator and prey to increase their nighttime episodes of activity in the presence of human observers.

BENNETT A (1910): How to Live on 24 Hours a Day. Doran, New York, USA.

Conservation physiology of two sympatric lemur species - is the specialist more vulnerable to habitat degradation?

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Understanding how animals react to human-induced changes in their environment is pivotal to conservation biology. Conservation physiology, – i.e., the evaluation of physiological responses to such changes can help detecting, monitoring, and – in the best case – preventing conservation problems. According to their position along the specialist-generalist continuum, species are believed to react differently to environmental condition changes, with specialists usually being considered more vulnerable. In this ongoing project, we compare a set of physiological parameters in two lemur species across four habitats within Kirindy Forest which can be ordered along a gradient of human disturbance: an exclusive research area, a tourist area, a border savanna and an area used as a frequent connecting pathway between four small villages. The fat-tailed dwarf lemur (*Cheirogaleus medius*) is a specialist, and, at Kirindy Forest, Western Madagascar a rapid local population decline has been observed, while numbers of the more generalist, sympatric grey mouse lemur (*Microcebus murinus*) have increased. Hence, these two closely related species seem to be suitable candidates for a vulnerability assessment study with respect to habitat deterioration. Our specific project aims are to (i) relate habitat factors that are likely affected by human influence and known to be important for *C. medius* and *M. murinus* (food tree density and shelter quantity and quality) to several health indicators such as body condition, parasite load and stress level, and (ii) to investigate the potential effect of these health indicators on short term fitness components such as survival and recruitment. Preliminary results indicate a positive correlation between the parasite prevalence in *C. medius* and the degree of disturbance of the habitat, with a two-fold difference between the least and the most disturbed habitat. In contrast, *M. murinus* shows highest parasite prevalence in the least disturbed site, where it occurs in high densities.

Diet of puku antelope (*Kobus vardonii*) and dietary overlap among bovid species in Zambia

RDUCH VERA

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Resource partitioning of food enables sympatric occurrence of bovids in Africa. Aiming to evaluate the competition status, diets of puku (*Kobus vardonii*) and selected other bovid species were assessed in Kasanka and in and around Kafue National Park, Zambia.

Puku (*Kobus vardonii* Livingstone, 1857; Reduncini, Bovidae) are medium sized, gregarious antelopes of grassland areas along rivers or swamps in southern central Africa with Zambia being the centre of occurrence.

Microhistological analyses of 150 dung samples of bovids collected from 2009 to 2011 in different seasons and from different sexes of puku were performed. A hundred plant fragments found in each dung was differentiated into mono- and dicotyl plants, and furthermore into genera of grasses. Therefore, grasses (mainly Poaceae) were collected in the study regions. A reference collection of leave epidermises was compiled.

Diets were assessed based on the relative amount of the plant's fragment area in the samples. Furthermore, diets were checked for potential overlap via the Pianka-Index and principal component analyses.

Puku fed principally on monocotyl plants. Generally, their diet consisted of the grass genera *Panicum*, *Brachiaria*, *Sporobolus*, *Hyparrhenia* and *Eragrostis*. Differences in the respective amounts between sexes and seasons were observed. The puku's dietary niche was broadest in the cool dry season and narrowest in the late rainy season. In Kasanka National Park, dung from different sites revealed a high spatial variation concerning the proportion of different grass species in the diet, suggesting an opportunistic food choice of puku.

In Kasanka National Park, dietary overlap between puku and other grazing bovid species (sitatunga, *Tragelaphus spekii*; reedbuck, *Redunca arundium*; sable antelope, *Hippotragus niger*; Lichtensteins hartebeest, *Alcelaphus lichtensteinii*; buffalo, *Syncerus caffer*) was small in the dry season and unimportant in the progressing dry season. This might be one reason for the high numbers of puku in this park. In and around Kafue National Park, puku and impala (*Aepyceros melampus*) overlap in their diet in the late rainy season. However, dietary differences in the cool dry season might explain sympatric occurrence of both species at similar population densities (RDUCH, unpubl.).

Microhistological analyses of dung, thought time-consuming and depending on a good reference, but non-invasive and budgetary-friendly, provide a good tool to understand coexistence of both rare and abundant (grazing) antelope species. Awareness of food plants can explain antelope abundance and their distribution and thus point out potential threats. Hence they provide the background for purposeful conservation measures.

Ecology and distribution patterns of puku antelope (*Kobus vardonii* Livingstone, 1857) in Kasanka National Park, Zambia

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Explaining patterns of animal distribution and abundance is one major challenge of ecology. Further, habitats, food and predation determine evolution, adaptation and thus coexistence of bovid species. Knowledge of resource partitioning is of direct relevance to conservation and management of (protected) areas.

The aim of this research project is to explain abundance and distribution of puku (*Kobus vardonii*; Reduncini, Bovidae), a medium sized, relatively poorly studied antelope of southern central Africa. Data about autecological and synecological aspects of the puku's ecology in Zambia were collected during three field trips, from 2009 to 2011, during different seasons with a focus on Kasanka National Park (Central Province, Zambia).

Surveys along line transects focussed on antelopes lead through different areas and habitats of the park. Data were analysed with Distance 6.0 and reveal a patchy distribution of the puku, the most abundant (larger) antelope in Kasanka National Park. Furthermore, it occurs in different areas of the park than other antelopes. In combination with data about habitat choice, puku were shown to occur on grasslands near water, especially along Kasanka River in the middle of the park. Microhistological analyses of dung revealed that puku feed almost exclusively on grasses and choose grass species in an opportunistic way. This might enable the puku to cope well with the impacts of bushfires that happen every year at multiple locations within the park, especially on grasslands at the margin of floodplains. Puku can consume grasses that freshly sprout after bushfires and puku are able to feed on grass species of grasslands, floodplains and of miombo woodlands depending on availability. Moreover, the analyses highlight a low dietary overlap between puku and other grazers (sitatunga, *Tragelaphus spekii*; reedbuck, *Redunca arundium*; sable antelope, *Hippotragus niger*; Lichtensteins hartebeest, *Alcelaphus lichtensteinii*; buffalo, *Syncerus caffer*) in the cool and hot dry season, the time of presumed food shortage. Analyses of hairs in predator faeces reveal Nile crocodile (*Crocodylus niloticus*), white-tailed mongoose (*Ichneumia albicauda*) and African civet (*Civettictis civetta*) feeding on puku, presumably only the crocodile preys actively, in contrast to serval (*Leptailurus serval*) and caracal (*Caracal caracal*).

Predators and competitors might not influence numbers of puku. Instead, it seems that food plants, adequate habitats along Kasanka River and poaching, decreasing towards the centre of the park, affect the puku's numbers and distribution in Kasanka National Park.

Understanding mammal's motor lateralisation: paw preference in wolf

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Literature highlights asymmetrical behaviours in many vertebrate species, due to a functional lateralisation of the brain (VALLORTIGARA, 2000; ROGERS, 2002). Considering the preference for one limb or side is the ordinary way to investigate hemispheric specialisation. Although some authors investigated paw lateralisation in the domestic dog (*Canis familiaris*), no studies considered this asymmetry in the wolf (*Canis lupus*). Domestic dogs seem to lack a population level bias in paw preference; furthermore, dog pawedness seems to be task and sex-related (TAN, 1987; WELLS, 2003; BROWN *et al.*, 2007, REDDON and HURD, 2009). The aim of this study was to investigate the paw preference for manipulation and posture during an enrichment programme in seven wolves housed at Parco Natura Viva (VR) - Italy. First, no group level paw preference was found; however all subjects showed an individual paw preference for both posture and manipulation. Furthermore, a bias toward the use of one paw for manipulation and the other one for postural support was reported. Finally, no significant differences in paw use were found in the presence of different enrichment devices (feeding and olfactory). As no group level bias in paw use was found, our results report similarities in the use of paw between wolves and their domestic counterpart (TAN, 1987; WELLS, 2003). In addition, the fact that one paw rather than both is frequently involved in manipulation could indicate a practical advantage for each individual in being lateralised in paw use.

BROWN C, WESTERN J, BRAITHWAITE V (2007): The influence of early experience on, and inheritance of, cerebral lateralization. *Anim Behav* **74**, 231 - 238.

REDDON AR, HURD P (2009): Acting unilaterally: why do animals with strongly lateralized brains behave differently than those with weakly lateralized brains? *Bioscience Hyp* **2**, 383 - 387.

ROGERS LJ (2002): Advantages and disadvantages of lateralization. In: ROGERS LJ, ANDREW RJ (Eds.), *Comparative vertebrate lateralization*. Cambridge University Press; Cambridge, UK, 126 - 53.

TAN U (1987): Paw preferences in dogs. *Int J Neurosci* **32**, 825 - 829.

VALLORTIGARA G (2000): Comparative neuropsychology of the dual brain: a stroll through left and right animals' perceptual worlds. *Brain Lang* **73**, 189 - 219.

WELLS DL (2003): Lateralised behaviour in the domestic dog, *Canis familiaris*. *Behav Process* **61**, 27.

Hand preference in macaques: a multi-variable approach

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Right handedness seems to be the main indicator of hemispheric specialisation in humans, due to its diffusion, strength and consistency between tasks (PAPADEMETRIOU *et al.*, 2005). To understand the evolution and the adaptive value of human handedness, several non-human primate species have been studied. However, whether these species show a population level bias in hand use is still under intense scientific debate: indeed, non-human primate hand preference seems to be inconsistent, task-dependent and frequently determined by individual characteristics and experience (WARREN, 1977; FAGOT and VAUCLAIR, 1991; MCGREW and MARCHANT, 1997). The aim of this study was to investigate the hand use for different actions in 23 macaques (7 pig-tailed macaques and 16 Barbary macaques) hosted at Parco Natura Viva, Bussolengo (VR), Italy. Besides, the role of factors such as species, age and sex in explaining monkey's manual lateralisation was also assessed. Our findings suggest that no group level bias in hand use was present, whereas an individual level hand preference was found in 9 out of 23 subjects. However, a strong significant group level right limb preference for starting locomotion was found. Furthermore, the strength of manual lateralisation seems to be affected by the sex of the macaques. In conclusion, our findings add to the growing body of evidence that non-human primates show no group level bias in manual lateralisation (for review, FITCH and BRACCINI, 2013). However, the pattern of macaque hand use suggests important implications of handedness in postural support. Further studies are required to enlarge the sample size and examine the effect of social context and task complexity on non-human primate manual lateralisation.

FAGOT J, VAUCLAIR J (1991): Manual laterality in nonhuman primates: A distinction between handedness and manual specialization. *Psychol Bull* **109**(1), 76 - 89.

FITCH WT, BRACCINI SN (2013): Primate laterality and the biology and evolution of human handedness: a review and synthesis. *Annals of the New York Academy of Sciences* doi: 10.1111/nyas.12071.

MCGREW WC, MARCHANT LF (1997): On the other hand: current issues in and meta-analysis of the behavioral laterality of hand function in non-human primates. *Yearbook of Physical Anthropology* **40**, 201 - 232.

PAPADEMETRIOU E, SHEU CF, MICHEL GF (2005): A meta-analysis of primate hand preferences, particularly for reaching. *J Comp Psychol* **119**(1), 33 - 48.

WARREN JM (1977): Handedness and cerebral dominance in monkeys. In: HARNAD S, DOTY RW, GOLDSTEIN L, JAYNES J, KRAUTHAMER G (Eds.), *Lateralization in the Nervous System*, pp. 151 - 172.

How timing of birth in roe deer (*Capreolus capreolus*) depends on altitude and its changes over time in Switzerland

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Roe deer (*Capreolus capreolus*) is one of the most frequent wild ungulate species in Europe and widespread in Switzerland. It is a popular hunting bag for humans and a food resource for predators, e.g. threatened species like lynx (*Lynx lynx*). Over the last four decades 12,432 fawns were marked to better understand population dynamics of roe deer in Switzerland. The date of birth was estimated for each individual. We tested the correlation between timing of birth and altitude in general and how it changed over time. After analysing data for correlations between potential explanatory variables and normal distribution, we compared two models, with and without the altitude, with likelihood-ratio tests and year as repeated measures. As a result we found a significant influence of altitude which leads to later timing when birth location is at higher altitudes.

To analyse how the timing of birth changed over time, we used fawn data of first and last 5-years periods 1975 – 1980 ($n = 1051$) and 2006 – 2011 ($n = 2503$) from the same area at four altitude classes (< 1000 m, 1,001 – 1,500 m, 1,501 – 2,000 m, > 2,000 m a.s.l.) and found significant differences at altitude class 1,001 – 1,500 m a.s.l. and 1,501 – 2,000 m a.s.l. Our results showed that timing of birth was correlated with altitude (with increasing altitude birth up to three weeks later) and that the timing of birth in altitudes above 1,000 m is now up to seven days earlier than 30 years ago. We assumed that these patterns are explained by changing reproduction conditions (temperature, period of vegetation growth, etc.).

Winter tourism evokes a physiological stress response in mountain hares (*Lepus timidus*) and leads to changes in its behaviour

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Winter tourism is increasing in the European Alps and has a significant impact on wildlife. Wildlife is often disturbed by these activities as they mostly occur in an unpredictable manner, and animals may only have limited possibilities for adaptation. However, the physiological and behavioural reactions to tourism activities in mountain hares (*Lepus timidus*) are still unknown. In this study, we measured levels of faecal glucocorticoid metabolites (GCM) in mountain hare in areas that had zero, low, or high tourism activities during winter 2011. In predator challenge experiments, where terrestrial and avian predators were simulated, we compared changes in behaviour and food intake in six captive mountain hares between experimental stress and non-stress periods. Our results showed that GCM secretion was positively correlated with tourist intensities and simulated stress events lead to higher energy demands due to flushing and increased GCM levels, and disrupted energy intake that hares derive from faeces. In order to protect mountain hare populations, we recommend that managers keep forests inhabited by mountain hares free from tourism infrastructure and retain undisturbed forest patches within skiing areas.

Loss and preservation of genetic diversity in rapidly declining populations of the common hamster, *Cricetus cricetus*

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Once being an agricultural pest species the common hamster *Cricetus cricetus* is now considered one of the most endangered mammals in Western Europe. Massive population breakdowns have diminished populations across Europe, with particular strong effects in its western range margin. We used hair trapping, tissue samples, reanalyses of published genotype data, and sampling of museum specimens in order to reveal the effects of population declines and reconstruct the loss of genetic diversity in this species. Microsatellite genotypes from > 1000 hamsters confirmed that genetic diversity strongly decreased across the hamster's western range margin. However, genetic diversity has remained high in some relict populations, despite of massive range loss, indicating that range loss is not necessarily accompanied by high regional declines in effective population sizes in all hamster populations. In this presentation we summarise our findings regarding diversity declines in wild and captive hamster populations, population connectivity, and genetic monitoring of reintroduction success. Our results reinforce the need of a concise and well-directed genetic monitoring in the frame of hamster conservation management.

Thermobiology, energetics and activity patterns of an arid zone marsupial, the mulgara (*Dasyercus blythi*) in Central Australia

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The mulgara (*Dasyercus blythi*) is a medium-sized insectivorous, nocturnal marsupial inhabiting the Australian arid zone. Daily torpor, a controlled reduction of body temperature (T_b) and metabolic rate, is employed by some small arid zone marsupials to save energy. Therefore, we aimed to quantify torpor and activity patterns in free living mulgaras during the winter/spring reproductive season, when other mammals typically remain homeothermic. The study was conducted on a gibber plain at the western edge of the Simpson desert. Mulgaras were captured using box aluminium traps. Temperature-sensitive radio transmitters were implanted intraperitoneally into eight individuals (♀ = 3, ♂ = 5). After release implanted individuals were radio tracked daily shortly after sunrise for two months. Data loggers were then placed close to the burrows measuring absence/presence and T_b fluctuation. From a total of 224 days of data, 18,205 measurements of T_b were obtained. Capture body mass of mulgaras differed ($P < 0.05$) between sexes and averaged 83.8 ± 4.4 g (mean \pm sd, $n = 5$) for males and 62.0 ± 4.3 g ($n = 3$) for females. All animals were predominantly active during the night. Mulgaras used torpor even during the reproductive season, but males and females differed in torpor expression. In females torpor frequency was 93.4 % ($n = 3$, $N = 96$) during the entire study period, whereas in males a relatively sudden transition occurred from shallow or no torpor to regular daily torpor after the mating season. Torpor frequency in males before the transition was 23.4 % ($n = 3$, $N = 96$) compared to 96.1 % ($n = 3$, $N = 36$) after the transition, suggesting that male mulgaras can compensate energy expended during the mating season by entering torpor after the reproductive season. Minimum T_b ($T_{b \min}$) during torpor occurred at around midday and was on average $22.0 \pm 4.9^\circ\text{C}$ in males and $21.4 \pm 4.3^\circ\text{C}$ in females but on cold days could decrease in individuals to values as low as 11.2°C . Torpor bout duration (TBD) was on average significantly ($P < 0.05$) longer in females (7.4 ± 4.6 h) than in males (5.6 ± 3.9 h) and in both sexes $T_{b \min}$ was significantly ($P < 0.05$) influenced by TBD (females: $T_{b \min}(\text{C}) = 31.2 \cdot \text{TBD}(\text{h})^{-0.21}$, $R^2 = 0.62$; males: $T_{b \min}(\text{C}) = 29.7 \cdot \text{TBD}(\text{h})^{-0.21}$, $R^2 = 0.87$). Our results show that the use of torpor in male and female mulgaras differs substantially during the reproductive season and thus it seems that the use of daily torpor in species inhabiting arid zones, like the mulgara, cannot only balance daily energy expenditure but also energetic costs between seasons. Therefore, torpor in mulgaras is not only used for survival of adverse conditions, but also to permit reproduction on limited resources.

Effects of forest fragment size and human impact on glucocorticoid levels in two Neotropical primates

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Habitat loss, habitat fragmentation and anthropogenic disturbances are a major concern to the conservation of endangered species because they can have a negative impact on animal populations. These processes can inflict physiological stress (i.e., increased glucocorticoid output) on animals. Chronically elevated stress levels can have detrimental effects on the reproduction of animals and long-term population viability. Here, we investigated the effect of forest fragment size and level of human impact (logging and hunting pressure) on glucocorticoid levels of two sympatric Neotropical primate species, the brown spider monkey (*Ateles hybridus*) and the red howler monkey (*Alouatta seniculus*), two species that have been reported to contrast strongly in their ability to cope with anthropogenic disturbances. We collected faecal samples from eight groups of wild spider monkeys (from seven different fragments) and 31 groups of wild howler monkeys (from ten different forest fragments) in Colombia. We measured faecal glucocorticoid metabolite (FGCM) levels in both species while controlling for several potentially confounding factors (group size, time of sample collection, sex, age and female reproductive state). Surprisingly, fragment size did not influence FGCM levels in either species. Spider monkeys showed elevated FGCMs in forest fragments with the highest level of human impact, whereas we did not find an effect of human impact in howler monkeys. This suggests that the two species differ in their physiological responsiveness to anthropogenic changes, further emphasising why spider monkeys have a higher extinction risk than howler monkeys. We propose that FGCM levels could be used as a tool to monitor populations living in disturbed areas and to assess the success of conservation strategies such as corridors connecting forest fragments.

Factors influencing the stable nitrogen ratios in wing membrane samples of insectivorous bat species: a field study

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Stable isotope analysis became a useful tool in dietary studies enabling the analysis of dietary differences between species or individuals. Laboratory studies revealed several factors (e.g. habitat, the amount of ingested food, metabolic rate) that could influence the nitrogen isotope ratios in animal tissues. However, the influence of these factors was not validated for free-ranging bat species which is important for interpreting nitrogen isotopic data in dietary studies. We hypothesised that the diet, the age and the individual energy demand will influence the nitrogen isotope ratio in wing membranes of free-living bat species (*Myotis daubentonii*, *Nyctalus noctula* and *N. leisleri*). We took wing membrane and habitat samples and measured the nitrogen isotope ratio. To compare species foraging in different habitats (above waters and within forests) we corrected the $\delta^{15}\text{N}$ of wing membranes for the $\delta^{15}\text{N}$ of the foraging habitat. We found differences in the nitrogen isotope ratio of our study species. It was significantly influenced by the diet composition and reproductive status of individuals. No effect of the age of individuals could be detected. The inter-specific differences correspond to different prey spectra as described in the literature. Contrasting results were found for the influence of reproductive activity. While for one species reproductively active individuals had a lower nitrogen isotope ratio compared to non-reproductive ones the contrary effect was observed for the other species. We assume that this could be caused by their different feeding ecology. This study shows that several factors that influenced nitrogen isotope ratios in laboratory experiments are also important for field studies. Found differences in nitrogen isotope ratios need to be carefully interpreted with the species, reproductive state and feeding ecology in mind.

The population density of the European hedgehog (*Erinaceus europaeus*) in urban parks of Berlin and factors influencing it

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European hedgehog (*Erinaceus europaeus*) is not only found in rural landscapes but also in urban areas of large cities like Berlin with 3.3 million inhabitants. Within the research project “Hedgehogs in Berlin” we studied the population density of hedgehogs in 30 public parks of Berlin.

Investigated parks were characterised and clustered by their size, the portion of bush and shrubs, the mean insect biomass, the degree of human disturbances and the connectivity to neighbouring green areas. Furthermore, we also determined environmental factors like the content of heavy metal in the soil, the presence of natural water resources or of special dog playing grounds. Hedgehog density in all 30 parks was estimated by nightly area-wide transect surveys. Weight, sex and ecto-parasites load of all hedgehogs found were measured.

All parameters recorded were used in a model to find the most important factors that influence the population density of hedgehogs in urban parks of Berlin. The results may be used to develop conservation measures and strategies for this protected species and to provide guidelines for future concepts of structuring urban areas.

Exposure to low temperatures and cryopreservation of epididymal sperm cells from European bison (*Bison bonasus*)

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Gamete preservation can be applied post-mortem to salvage genetic potential in valuable species, but the development of specific cryopreservation protocols for epididymal sperm cells are necessary for the establishment of a genetic resource bank. This study aimed to evaluate the sensitivity of bison epididymal sperm cells to low temperatures and cryopreservation.

Epididymal sperm cells from a 10-years-old European bison housed at Barcelona Zoo were refrigerated for 72 h and cryopreserved following a conventional freezing-thawing procedure. Sperm cells were obtained by retrograde flushing of the tail of the epididymis and deferent duct with a skimmed milk-based medium. Sperm cell evaluation consisted on assessment of viability and acrosome integrity and motility parameters after eosin-nigrosin staining and a computer-assisted sperm analysis (Proiser, Valencia, Spain), respectively. The sample was split into two parts and diluted using the commercial extender Gent A or Gent B (Minitub, Tarragona, Spain) to reach a final concentration of 200×10^6 spermatozoa/ml. Samples in Gent A medium were kept at 5°C and the same parameters were re-evaluated at 24, 48 and 72 h. Samples in Gent B medium were packed into 0.5 ml straws and kept at 5°C for 2 h. The straws were then placed horizontally 5 cm above the surface of liquid nitrogen for 15 min, and then plunged into liquid nitrogen. After weeks of storage, straws were thawed in water bath at 37°C for 30 seconds. Data were analysed by ANOVA and Chi square test. Differences among groups were considered significant with $P < 0.05$.

At recovery, the percentages of viability, total and progressive motility and acrosome integrity were: 91.5 %, 89.8 %, 66.7 % and 90 %, respectively. No significant loss of viability was observed after 72 h of refrigeration (88.7 % and 83 % at 24 h and 72 h of refrigeration, respectively). Viability after freezing-thawing decreased significantly to 60.5 %. Significant loss of motility was detected after both refrigeration and freezing-thawing. Total and progressive motility were 70.7 % and 38.8 % at 24 h of refrigeration and 56.7 % and 27.2 % at 72 h of refrigeration, respectively. Cryopreservation in Gent B also showed a reduction in motility parameters (total: 26.6 % and progressive motility: 19.1 %).

In conclusion, the results indicate that post-mortem sperm cell recovery from European bison epididymis allows obtaining successful sperm long-term refrigeration and cryopreservation. Whereas viability was successfully maintained, motility was the mainly affected feature.

Species richness in the backyard

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Our environment is subjected to intensive development, urbanisation and thus loss of biodiversity. Therefore, it is crucial to search for sustainable solutions to maintain biodiversity. Moreover, expanding our knowledge about species richness under human pressure can contribute to conservation decisions.

The main goal of this project is to explore the richness of species in our urban backyard. We are interested in the potential of private yards in the urban environment as a retaining unit for habitats under ongoing human pressure.

The research area is a 0.25 acres yard located on the main road on the northern fringe of Binyamina, Israel (32°31' N, 34°56' E). The area receives ~600 mm rainfall annually. The dominant vegetation is semi-natural dwarf-shrubland. The yard is under minimal human intervention (e.g. minimal gardening and no pesticides).

Over a period of the last three years, we have performed series of species richness surveys: twice a month and two to three days at a time. We used light-traps and flashlights during night time. Individuals from each species were documented using macro photography. We also documented biological interactions, animal behaviour and reproduction. In order to identify the species, we used professional field guides and consulted with specialist taxonomists.

By now we have documented over 650 animals' species. Among our findings are: two species of amphibians out of seven species known in Israel; 10 reptilian species and 25 avian species. We found 495 insect species representing 15 different orders out of 30 known in the world, 16 species of butterflies representing 6 families out of 7 known in Israel and 79 spider species representing 24 different families out of ~50 known in Israel. In addition, we found a spider from the genus *Cyclosa* (Araneidae) which, to the best of our knowledge, was not reported in Israel before this survey.

We believe in applying this model of species richness survey as an educational tool that raises the awareness of the general public to the richness of organisms that surrounds them. "For in the end, we will conserve only what we love. We will love only what we understand. We will understand only what we are taught" (BABA DIOUM, 1968).

The differential behavioural and physiological responses of frugivores vs. granivores to secondary metabolites in ripe fruits

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Plant secondary metabolites in ripe fruits may discriminate between seed dispersers and seed predators. Indeed, there is some evidence that secondary metabolites deter seed predators but not seed dispersers. However, the differential behavioural and physiological responses of frugivores vs. granivores to secondary metabolites in ripe fruits are yet to be studied.

Ochradenus baccatus is a keystone species in the Israeli desert. It produces fleshy fruits which contain the 'mustard oil bomb'; the glucosinolates and the myrosinase enzyme found in the pulp and seeds, respectively. During whole fruit consumption the myrosinase from the seeds hydrolyses the harmless glucosinolates in the pulp, producing very active, toxic compounds. Here we present biochemical, physiological and behavioural data demonstrating the differential behavioural and physiological responses of frugivore birds vs. granivore rodents to fruits secondary metabolites.

The yellow-vented bulbul (*Pycnonotus xanthopygos*) is a frugivore, *Ochradenus* seed dispersing passerine. We found that although the bulbul consumes the whole fruits, it avoids the activation of the mustard oil bomb by eliminating 100 % of the pulp's glucosinolates in its droppings.

The spiny mice (*Acomys*) are granivorous murid rodents. We found that, in the wild as well as in the laboratory, the spiny mouse behaviourally avoids the activation of the mustard oil bomb by orally expelling vital seeds (e.g. *Acomys cahirinus*) or by making a whole in the pulp and consuming only the seeds (e.g. *Acomys minous*). In addition some *Acomys* (e.g. *Acomys russatus*) may have some physiological adaptations to deal with the mustard oil bomb.

According to our results, while frugivorous birds physiologically avoid fruits secondary metabolites, granivorous rodents avoid them behaviourally or physiologically confront them.

When social status threatens forest biodiversity: wild meat consumption in Vietnam

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The rich vertebrate biodiversity in natural forests of the Central Annamites in Vietnam is increasingly threatened by illegal exploitation. Although hunting is banned by Vietnamese law, game meat from protected areas is traded commercially to meet the demand for wild meat consumption in larger cities. We quantified whether the increasing urban wild meat consumption poses a major threat to faunal biodiversity. We analysed the scale of game species in trade, and developed consumer profiles amongst the male citizens of Hue City, inhabiting about 340,000 people and representing an important tourist hub in the center of Vietnam. Our survey comprised 329 interviews using semi-structured questionnaires. In addition, 20 game meat restaurants were visited to assess the species composition on the supply side as well as the nature of consumption patterns in restaurants. The likelihood of consumption was quantified against the explanatory variables education, occupation and personal disposable income using binary logistic regression. The most common species that were consumed in restaurants was wild pig (*Sus scrofa*), but also endangered ungulates (*Cervus eldii*, *Axis porcinus*) were probably consumed. The results showed that 85 % of all interviewees have eaten game at least on one occasion, and 58 % of all interviewed men consumed wild meat in the last 12 months. According to the results, a typical male consumer had completed secondary school education and ate wild meat three times a year. The most usual place of game meat consumption was in restaurants, accompanied by friends or with business partners or colleagues. Also students and unemployed people significantly contributed to wild meat consumption. However, regular consumers of game meat tended to have higher personal incomes than non-consumers and there was a statistically robust positive relationship between income and frequency of wild meat consumption. We conclude that, despite its ban, the commercial demand for wild meat in Vietnam is still growing amongst the emerging urban middle class as consumption of wildlife demonstrates high social status. In order to conserve the unique wildlife of the Central Annamites, it is of utmost importance to strengthen law enforcement and run awareness and communication campaigns, primarily targeting students and the corporate sector.

Chimpanzee face detection: an automated system for images captured from natural environments

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Non-invasive population monitoring of endangered species is possible using image data. Vast amounts of uncontrolled natural images can be generated using camera traps, which require detection of animal encounters before analysis. The feasibility of this approach is limited by the requirement to manually analyse the video for the presence of relevant specimens. Automation will greatly enhance the practicality of population monitoring using images. Here we present results for an automated image analysis system based on deformable part-based models (DPMs). Three detector configurations are trained and tested using 750 images containing wild and zoo specimen chimpanzees, with a manually annotated ground truth of faces for evaluation, (provided by the SAISBECO Project: www.saisbeco.com). All models have comparable average precisions and qualitatively capture different aspects of the data variation.

An existing chimp face detection system, building upon extensive human face detection work, has some robustness to illumination variance. Whilst capable of real-time detection, it has limited robustness to occlusion or pose variance, common in natural images. DPMs have already been applied to animal head detection with some success. They offer the potential to incorporate varied poses without extensive parameter tuning, whilst retaining illumination invariance and introducing partial occlusion robustness. Our three detector configurations use DPMs over the face region ('Face'); an expanded facial region ('Expanded'); and as the basis of a linear integration of multiple detectors, which we call 'detector fabric' ('Fabric'). Their cross-validated average precisions were measured as 70.12 %, 72.41 % and 70.84 % respectively.

The models' results differ qualitatively: favouring clear faces; distinct surroundings or a mixture of the two. The Face detector is capable of detection of well resolved faces, where the other two – more reliant on spatial context – fail. A reduced reliance on facial features alone, (Expanded and Fabric), has allowed detection where the face is less well resolved. Expanding the ground truth annotations to cover a greater image area has enabled detection in non-frontal poses and with some partial occlusion. Where only Fabric succeeds at detection, faces can be further fragmented by occlusion, and detection is possible where neither the face nor the surrounding regions are well resolved.

This is a promising prototype for applying DPMs to wild animal detection – capturing pose and occlusion variance, albeit at increased computational cost. The techniques are suitably generic to be applied to other species.

Is cryopreservation right for biobanking? Nature does it differently

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Biobanking throughout the world is done almost exclusively by cryopreservation followed by maintenance of the samples under liquid nitrogen. Cryopreservation, however, comes with a host of problems, including high costs, need for guaranteed continuous supply of liquid nitrogen, dedicated staff and storage facilities, complicated transportation and high carbon footprint, to name just a few. The process of cryopreservation is also highly species-specific and damaging to the cells. Because of these reasons, biobanking is largely restricted to the Western world and even there, only to relatively large centres. Like in many other walks of life, there is no reason why not search for better alternatives in Nature. Nature preserves by drying rather than freezing. Nature also created an assortment of materials that protect the organisms from damages during the drying and rehydration processes. Once dry, and in the absence of water, metabolism and chemical reactions within the cells are brought to a halt so that these cells can survive extended periods of time and be resistant to extreme conditions. Desiccation is routinely used in the pharmaceutical and food industries but only marginally studied with respect to biobanking. It is experiencing increased interest in recent years with some exciting developments. Still, the cells normally die in the process; so only by injecting their DNA into oocytes dry cells can be used to generate offspring. Work in our institute and elsewhere is trying to find solutions so that desiccation can be used routinely for long-term preservation.

Exploration behaviour of European bison after reintroduction into the wild

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On 11th of April 2013 a herd (1 bull, 2 cows, 2 subadults) of European bison (*Bison bonasus*) (Lowland-Caucasian line) was released into the wild in Germany for the first time. Before reintroduction the herd was kept in an 86 ha enclosure in this area for three years. The European bison was extinct in the wild since 1921 and survived only due to intensive conservation breeding in captivity.

This herd was reintroduced in an intensively used, working forest in a low mountain range with a medium human population density of 249 inhabitants / km² and 1.5 million tourists per year. The habitat mainly consists of beech- and spruce stands, interspersed with meadows and grasslands. We investigated the habitat utilisation (daily kernel home ranges h_{ref} , minimum covered distances and distance to the former enclosure) using GPS-telemetry and direct observation.

The animals left the enclosure for short explorations for the first time after five days. The first long-lasting exploration occurred from day 11 to 17. In a second phase from day 18 to 36 the daily core home ranges were more stationary and daily covered distances dropped to 52 % and covered a mean area of 26 ± 6 ha (50 % kernel \pm SE) with a daily minimum distance of 4.3 ± 0.4 km.

After the birth of a calf the home range area and the minimum covered distance decreased to 11 % respectively 80 % (compared to median of ten days previous) and remained at 37 % respectively 49 % afterwards for about one week.

The mean distance to the enclosure was 1.2 ± 0.15 km and never exceeded more than 3.2 km. These findings give insight into the ranging behaviour of European bison reintroduced to new areas and show the impact of calves on habitat exploration.

Oxidative stress increases during immune response in a free-ranging, long-living mammal

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Oxidative stress - the imbalance between reactive oxygen species (ROS) and neutralising antioxidants - is regarded as the main cause of ageing in aerobic organisms. The level of ROS should increase during infections as part of the activation of an immune response, leading to oxidative damage on proteins, lipids and DNA. Yet, it is unknown how long-lived organisms, especially mammals, cope with oxidative stress. Bats are known to carry a variety of zoonotic pathogens and at the same time are despite their high basal metabolic rate unusually long-lived, which may be partly caused by low oxidative damage of organs. Here, we study the effect of an immune challenge on the oxidative stress in free-ranging bats. We injected 20 short-tailed fruit bats (*Carollia perspicillata*) with bacterial derived lipopolysaccharides (LPS) and 20 individuals with phosphate-buffered saline solution (PBS) as a control. Individuals injected with LPS showed an immune reaction by increased white blood cell count after 24h, whereas there was no significant change in leukocyte counts in control animals. The biological antioxidant potential remained the same in both groups, but ROS increased after treatment with LPS, leading to a significant increase in oxidative stress in animals mounting an immune reaction toward the inflammatory challenge. Control individuals did not show a change in oxidative stress. We conclude that even in a long-lived mammal, the concentration of antioxidants can not immediately neutralise all ROS produced during a cellular immune response and thus, fighting a current infection may lead to oxidative stress in bats.

Oxidative stress of long-lived mammals varies with dietary niche

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Oxidative stress – an imbalance between reactive oxygen species (ROS) and antioxidants – is regarded as the main cause of ageing in animals. ROS are produced by every aerobic organism and damage proteins, lipids and DNA. The negative effect of ROS can be mitigated by neutralising antioxidants, which are partly synthesised by the organisms, but also partly ingested with food. Feeding on diets with high antioxidant content such as fruits should therefore reduce oxidative stress in animals.

Bats are despite their high mass-specific metabolic rate unusually long-lived and cover a variety of ecological niches. Here, we ask whether oxidative stress differs between dietary niche, measuring both ROS and antioxidants in the blood of 13 bat species. Furthermore, we compared parameters of oxidative stress of bats with those of similar sized, shorter living and terrestrial mammals from the literature. We found that bats have a significantly lower level of oxidative stress than mice and rats. Bat species feeding on fruits have the lowest oxidative stress level, followed by omnivorous bats and species feeding on insect and blood. Although the level of antioxidants measured in plasma did not differ between dietary niche, the level of ROS was lower in frugivores than in other species. Potentially, frugivores ingest more antioxidants with food and thus are able to neutralise more ROS, leading to lower oxidative stress levels than in species feeding on less or no fruits.

We conclude that the low levels of oxidative stress in bats may account for their long live span. Furthermore, we showed for the first time that oxidative stress in mammals varies according to dietary niche, shedding new light on the influence of the ecological niche on proximate mechanisms of ageing.

Recombinant expression of boar (*Sus scrofa domestica*) spermadhesins for potential use in assisted reproduction

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After their differentiation in the testis, spermatozoa are not yet able to perform the complex series of fertilisation related processes including the final fusion event with an oocyte. They acquire this competence during their passage through the changing environments of the male and female genital tract. Being transcriptionally inactive and unable to express new proteins after differentiation, the required modification of the cells has to be triggered by external molecules.

During ejaculation, spermatozoa come into contact and interact with the seminal fluid consisting of secretion products mainly from the accessory glands and, to a minor part, from the epididymis. A variety of proteins are important ingredients of this fluid amongst which the class of spermadhesins plays a major role in ungulates especially in pigs (*Suidae*). Proteins of this family bind to the sperm membrane and seem to play an important role in sperm-oocyte-binding, gamete recognition and capacitation (EKHLASI-HUNDREISER *et al.* 2008).

It has proven to be difficult to isolate single spermadhesins from seminal fluid to study their interaction with spermatozoa. Therefore, the aim of this study was to recombinantly express two porcine spermadhesins AWN and AQN-3 in *E.coli* and investigate interactions between these proteins and artificial phospholipid membranes as well as spermatozoa. Preliminary results show a phospholipid specific interaction between the recombinant proteins and artificial membranes.

While single steps of the isolation process have to be optimised, the recombinant expression is promising to provide sufficient amounts of AWN and AQN-3 for further studies and their potential application as additives for assisted reproduction techniques like artificial insemination or IVF in endangered porcine species, where predominately epididymal semen of dead or castrated animals are available.

EKHLASI-HUNDREISER M, MÜLLER P, TÖPFER-PETERSEN E (2008): Male secretory proteins - sperm tools for fertilisation. In: GLANDER HJ, GRUNDEWALD S, PAASCH U (Eds.), Biology of male germ cells. Shaker Publisher GmbH Aachen, Germany, 173 - 210.

Seasonal effects on litter size and birth weight in the wild guinea pig (*Cavia aperea*)

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In literature different information about the reproduction of wild cavies (*Cavia aperea*) can be found. TRILLMICH (2000) describes the reproduction of wild cavies as unaffected by photoperiod or low temperature (experimental influence). However, ROOD and WEIR (1970) characterise the reproduction of wild cavies as influenced by the annual cycle and even interrupted in a cold winter under natural conditions except that the animals got food supplementation. We investigated the reproductive activity and outcome throughout the annual cycle in 20 females. During four different breeding rounds (differentiated into seasons) the guinea pigs were exposed to natural photoperiod and temperature conditions (in a combined indoor-outdoor-housing).

Cavies breed all over the year but we found seasonal effects on litter size and birth weights. The lowest litter size was documented in winter (1.5 ± 0.5), increased over spring and had the highest values in summer (2.92 ± 1 ; $p < 0.001$). Besides the seasonal effects we found litter size correlating positively with weight of females shortly before pregnancy ($p < 0.001$) but negatively with pub birth weights ($p < 0.001$).

The sex ratio did not differ across seasons ($p = 0.54$) but there was a significant difference in birth weight between males and females in mixed sex litters with males weighing on average 6g more than females ($p < 0.001$). This difference was not apparent in unisexual litters ($p = 0.09$).

The reproduction of wild cavies can be classified as non-seasonal but the outcome is considerably influenced by season. Moreover, the offspring showed an intrauterine intersexual sibling conflict which caused differences in birth weight.

The project is funded by the Leibniz-Gemeinschaft (SAW-2011-IZW-2).

TRILLMICH F (2000): Effects of low temperature and photoperiod on reproduction in the female wild guinea pig (*Cavia aperea*). J Mammal **81**(2), 586 - 594.

ROOD JP, WEIR B (1970): Reproduction in female wild guinea-pigs. J Reprod Fert **23**, 393 - 409.

Assessing the re-introduction of a black rhino (*Diceros bicornis*) starter group in Namibia

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The black rhinoceros (*Diceros bicornis*) used to be the most widespread rhino species in the world throughout the first half of the 20th century. Its distribution range, once comprising most of the Sub-Saharan countries, was reduced to a small number of refuges during the early 21st century. Today, most of the remaining black rhino subpopulations are scattered across a few different and often isolated areas in Namibia and South Africa. The black rhino holds a particular important function for conservation strategies due to its unique status as an umbrella species.

In this study, we investigated a starter group of four re-introduced black rhinos (one male and three females). The animals were released into an 88.7 km² privately owned and fenced in reserve one year prior to the beginning of our investigation. The reserve is located at the southern border of the Etosha National Park in Namibia. We indirectly observed the rhinos by using camera traps attached to the seven waterholes of the study area. This set up was complemented by a) VHF radio telemetry in order to gain more detailed information on the spatial and temporal behaviour and to conduct direct observations and b) vegetation surveys to investigate the preferred habitat types. Our main objective was to assess the re-introduction process in this specific case by investigating the acclimatisation progress to the new environment. Four months of field work (March to June 2012) revealed the suitability of the area (size, number and distribution of waterholes, vegetation types, land use and the occurrence of other large mammals in this area), as well as the starter group's composition. All rhinos showed typical, species-specific behaviour (e. g. movements, home ranges, social and sexual behaviour) and no signs of fighting or distress. As expected, rhino image frequency at the waterholes increased during our study as the semi-arid environment became drier. Water uptake exclusively occurred during the night hours. The rhino group is characterised by a rather dynamic social structure: temporary dyadic (two- animal) associations between the male rhino and different females of the group could be observed over the course of the study. Furthermore, the data is revealing that all of the rhinos have a high affinity towards a certain habitat type at the study area. In conclusion, we can assume that this specific re-introduction was successful and that the rhinos already acclimatised one year post-release. We are confident that our study can serve as a suitable approach for future rhino re-introductions.

Dietary specialisation of Mednyi Island arctic fox (*Vulpes lagopus semenovi*)

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There is growing evidence for individual variation in diet and foraging behaviour across a wide range of species and ecosystems (reviewed in BOLNICK *et al.* 2003). In fact, it is important to distinguish individual variation caused by habitat heterogeneity, and true individual specialisation, caused by specific preferences. On Mednyi Island (Commander Islands, North Pacific), arctic fox population have been observed annually for almost twenty years, and most foxes are marked and individually recognised. We collected fresh scats from the reproductive dens with individually marked adult foxes and analysed diets of these families (1,756 scats from 19 families). We calculated the degree of similarity (the proportional similarity index, or PSI, FEINSINGER *et al.*, 1981):

a) between diets of different fox families, occupied the same dens in different years (variation between families, N = 11);

b) between diets of the same fox families, occupied the same dens in different years (variation within families, N = 3).

In 'same fox family' both adult foxes same in both compared years, and in different fox families both adult foxes are different.

The average PSI value was 0.615 (95 % CI = 0.562 – 0.669) between the families, and 0.740 (95 % CI = 0.588 – 0.892) within the families. Therefore the similarity in diet across different years within the same family of foxes occupying the same habitat was greater than across different families occupying the same habitat in different years.

This study was supported by grants from RFBR: 07-04-00745-a, 10-04-01788-a and 12-04-31013.

BOLNICK DI, SVANBACK R, FORDYCE JA, YANG LH, DAVIS JM, HULSEY CD, FORISTER ML (2003):

The ecology of individuals: incidence and implications of individual specialization. *Am Nat* **161**, 1 - 28.

FEINSINGER P, SPEARS EE, POOLE RW (1981): A simple measure of niche breadth. *Ecology* **62**(1), 27 - 32.

REM sleep as indicator for stress in giraffes (*Giraffa camelopardalis*)

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Well balanced sleep is important for animals' well-being. Thus, changes in the frequency or length of sleep could provide information about the ability of individuals to cope with changes in their environment (RUSHEN, 2000). Especially the REM sleep pattern seems to be important here, since it has been demonstrated that the REM sleep pattern changes for example at the beginning of infectious diseases or after traumatic events (MORISSON, 1989; FANG *et al.*, 1996). Because of their peculiar sleeping position during the REM sleep phases giraffes are very well suited to analyse REM sleep patterns in a non-invasive way via video observations. It was being analysed how the REM sleep pattern changes induced by stressful situations. Therefore, the sleeping behaviour of giraffes was observed before and after their transport to another zoo. In order to validate this new method, faeces samples were analysed with respect to the metabolite concentration of the stress hormone cortisol. This has been done by a well-established enzyme immunoassay (PALME and MÖSTL, 1997) that was applied to giraffes for the first time. In sum, the time spent in REM sleep was influenced by all observed stress events (et al. transport, nutrient deficiency in newborns, changes in herd structure). Hence, REM sleep is very well suited as a parameter to measure stress in giraffes. The continuous monitoring of REM sleep patterns allows detecting disturbances in the well-being of giraffes, such as malnutrition, injury or illness, at an early stage and, thus, allows for prompt intervention.

FANG I, TOOLEY D, GATEWOOD C, RENEGAR KB, MAJDE JA, KRUEGER JM (1996): Differential effects of total and upper airway influenza viral infection on sleep in mice. *Sleep* **19**(4), 337 - 342.

MORISSON AR (1989): Sleep disturbance as the hallmark of posttraumatic stress disorder. *Am J Psychiat* **146**, 697 - 707.

PALME R, MÖSTL E (1997): Measurement of cortisol metabolites in faeces of sheep as a parameter of cortisol concentration in blood. *Int J Mamm Biol* **62**(2), 192 - 197.

RUSHEN J (2000): Some issues in the interpretation of behavioural responses to stress. In: MOBERG GP, MENCH JA (Eds.), *The Biology of Animal Stress*. CAB International, New York, 23 - 42.

Non-invasive molecular procedures to identify domestic and wild endangered North African ungulate species

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Non-invasive sampling is becoming widely used in the study of elusive and rare wildlife species. Correct species identification is essential to provide reliable data to guide conservation action and molecular genetics is an important tool for identification. The vast majority of molecular tests used in the past served mostly to identify species that constitute well defined taxonomic units or require multiple laboratory steps to distinguish taxa to species. Hitherto powerful and simple technologies are available for species identification, even with very small samples of material, such as faeces or bones. Most of these protocols use mitochondrial DNA, a widely studied marker for barcoding that is especially prone to problems, including nuclear insert copies, high intraspecific diversity, namely in gazelles, or heteroplasmy. Although nuclear DNA is less abundant, is better protected by proteins, so it is less prone to degradation and damage over time, a key factor when working with non-invasive methods. In this work we have developed a molecular test based on polymorphisms in two small fractions of two genes: one mitochondrial [cytochrome b (cytb)] and one nuclear [kappa-casein (KCAS)]. These fragments showed polymorphic sites, including species-specific sites, which allowed individual identification of nine species of ungulates (wild and domestic) that cohabit in North Africa. The results were consistent in the identification of over 600 samples, including faeces and bones collected in the field. The method is an important tool in the management and conservation of wildlife, based on its simplicity, high reliability and low cost.

The occurrence of different call types in different behavioural contexts in captive cheetahs (*Acinonyx jubatus*)

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Vocalisations indicate intentions, social relationships, emotions and physiological states of animals, thus representing a tool for monitoring different aspects of animal life. This study investigates call types in behavioural contexts in captive cheetahs to reveal the functions of different vocalisations. Calls of three male and three female adult cheetahs were recorded between the 21st of May and the 1st of August 2012 in Volokolamsk Zoo Brooder (Russia, Moscow region). A total of 3,611 calls were subdivided according to three structural classes: tonal, pulsed and noisy. Tonal calls included meow, chirp and howl; pulsed calls included growl, chirr and purr; noisy calls included hiss. These seven call types were subdivided by eight behavioural contexts: aggression/attack, aggression/defence, friendly close-distant interactions with conspecifics, friendly far-distant interactions with conspecifics, friendly interactions with a human, soliciting from a human, anticipation of food and courting behaviour. We calculated the occurrence of each call type in each context. Then, we established the random distribution of the total call sample according to the eight contexts and compared the observed and random values of the occurrence of calls of each type with chi-square test. Certain call types were related to particular contexts. Growl, hiss and howl were specifically related to aggression: 74.09 % growls, 77.11 % hisses and 67.13 % howls were emitted during attack. Also, 20.95 % growls, 16.52 % hisses and 9.79 % howls were emitted during defence. Purr was specifically related to friendly interactions with a human (62.06 % of purrs occurred in this context). Chirp specifically attended friendly far-distant interactions with conspecifics (26.38 % of chirps occurred in this context). Meow attended soliciting and food anticipation contexts (41.71 % and 29.36 % of meows occurred in these two contexts respectively). The most tight relation occurred between chirr and the courting context (99.58 % of chirrs occurred in this context). In discomfort-related or in frustrating contexts (aggression, anticipation of food, or soliciting), the subjects were very vocal, whereas in comfort-related contexts they were mostly silent (as in friendly interactions with conspecifics) or produced only purrs (as in friendly interactions with humans). These results are in accordance with hypothesis that mammals vocalise mostly in response to discomfort. The frequent use of meows in soliciting context suggests that emission of this call type may be conditioned by operant stimuli from keepers, allowing the animals to use meows for manipulating the behaviour of their keepers.

Supported by RFBR grant 12-04-00260a.

Genotyping by sequencing to identify adaptation to environmental change in populations of two species of Australian rainbowfish

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Understanding the genetic basis of adaptation to environmental change is challenging but of central importance in biology. Although the theory on adaptation is well developed, the data needed to clarify the relative roles of plasticity and microevolution is lacking. Recent advances in acquisition and analysis of genomic data can be used to understand factors shaping the distribution of adaptive variation over the landscape and across environmental gradients. This enables the assessment of the nature of selection imposed by environmental changes, and also the assessment of the potential for populations to respond by evolutionary adaptation.

We present genomic data from populations of two rainbowfish species (Melanotaeniidae) sampled across a wide region in Australia. The Murray rainbowfish, *Melanotaenia fluviatilis*, is an inland species widely distributed in the Murray-Darling Basin in Australia, and the crimson-spotted rainbowfish, *Melanotaenia duboulayi*, is common in subtropical eastern QLD and northern NSW, Australia. *M. fluviatilis* is the most southerly ranging rainbowfish, the only species adapted to low winter (~10 - 15°C) as well as subtropical (~20 - 23°C) conditions. Although the species is found in many habitat types, it prefers relatively still, clear water and dense aquatic vegetation. *M. duboulayi* has a more narrow distribution, being common in warm and vegetated natural streams. These two species are closely related (they are sister to each other compared to all other rainbowfish) and likely diverged during the late Pleistocene.

For the genome-wide scan analysis we used samples from 37 sites (15 for *M. fluviatilis* and 22 for *M. duboulayi*) chosen to encompass all major habitat types of the region and the entire range of both species. We used a genotyping by sequencing approach on pooled samples (768 individuals) in 16 lanes of an Illumina HiSeq 2000 instrument. The run generated 20 088 SNP loci for *M. fluviatilis* and 17 118 loci for *M. duboulayi*. Initial analyses, using outlier loci detection and hierarchical analysis of molecular variance (AMOVA), indicate that the distribution of adaptive variation in these species is best explained by a model based on differences in temperature alone rather than one that also incorporates flow regime. Using our results it is possible to construct a catalog of genetic variation to determine whether populations of these species contain the adaptive potential to cope with habitat changes predicted by climate modelling over the next 100 years.

Semen cryopreservation protocol for Genetic Resource Banking and Artificial Insemination under field conditions in avian species using emu (*Dromaius novaehollandiae*) as a model

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Many avian species are either threatened or endangered due to loss of genetic diversity for various reasons. Cryopreservation of semen can be used as a means to establish Genome Resource Banking for artificial insemination in such species. Such methods of cryopreservation are now being used with increasing frequency in non-domestic mammals but are still uncommon for the non-domestic avian species. This perhaps is due to the costly equipment required for cryopreservation of semen. However, using emu sperm as a model, we worked on a cost effective protocol that can be used under field conditions and can be applied with some modifications in other birds [(Galliformes; Gruiformes and Columbiformes mainly tragopans (3 sp.), grouses (5 sp.), cranes (5 sp.), pigeon (1 sp.) *pers. observation*].

The existing emu semen cryopreservation protocol (MALECKI and MARTIN, 2000, 2005) was improved by conducting three experiments with an aim to: 1) minimise chilling injury during the cooling phase; 2) assess the effects of plunging at initial temperatures of -140°C and -35°C , with 6 or 9 % DMA; and 3) investigate the possibility of increasing DMA concentrations beyond 9 %. We measured in vitro sperm viability, motility and egg membrane penetration ability. Semen was collected at ambient temperature ranging between 5 and 20°C . In experiment 1, diluting semen 1:1 with diluent pre-cooled to 5°C prevented chilling injury. In experiment 2, the percentages of live and motile sperm were higher ($P < 0.001$) for semen plunged at -140°C with 9 % DMA (Path 2) than for all other combinations. In experiment 3, sperm viability was comparable and significantly higher ($P < 0.05$) with 18 and 24 % DMA than with other concentrations. The percentages of motile sperm and egg membrane penetration ability were higher with 18 % than with 24 % DMA, but comparable for 9, 12 and 18 % DMA. We conclude a) that loss of sperm function during the cooling phase can be avoided by using a diluent maintained at 5°C ; and b) that the current best practice for preserving post-thaw function in emu sperm is to use initial plunging temperatures of -140°C with 18 % DMA as a cryoprotectant.

MALECKI IA, MARTIN GB (2000): Emu Farming- Reproductive Technology. A report for the Rural Industries Research and Development Corporation **00/37**. 1 - 32.

MALECKI IA, MARTIN GB (2005): Reproductive Technologies for ratite farming. A report for the Rural Industries Research and Development Corporation **05/200**. 1 - 48.

Genotyping faecal samples of Amur leopards (*Panthera pardus orientalis*) for population estimation

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The modern range of Amur leopard includes only a limited mountain-forest region of about 10,000 – 15,000 km² at the border of three countries: the People's Republic of China, the People's Democratic Republic of Korea, and Russia. According to the most optimistic estimates, the entire world population of the Amur leopard does not exceed 40 – 52 individuals (YANG *et al.*, 1998). Permanent monitoring of the number of the last population of this unique predator, including noninvasive approaches to the analysis of the faecal DNA, is especially important. We performed a molecular-genetic analysis of the DNA extracted from the faeces (32 samples), hairs (1) and blood (6). To analyse nuclear DNA, 12 microsatellite loci and zinc-finger region were used (ROZHNOV *et al.*, 2013). Twenty-three different animals were found. There were 14 males and 9 females. The average value of the observed heterozygosity $H_o = 0.39 \pm 0.03$ and the mean number of alleles per locus ($N = 2.83 \pm 1.03$), are comparable with the data of previous research (UPHYRKINA *et al.*, 2002). A strong difference in the values of the expected and observed heterozygosity, as well as the presence of calculated linkage disequilibrium in a few loci, may indicate the absence of free mating and the existence of a kin structure within the group. Our data demonstrate that population of the Amur leopard consists to a great degree of close relatives: the coefficient of inbreeding (F) is 0.13. The developed method can be used effectively for monitoring and assessing the number of leopards on the territory of the entire range. The value of the probability of identity for sibling $P(ID)_{sib}$ for all loci constitutes 0.2 %. Genotyping error rates per locus ranged from 0 to 0.269. The average allelic dropout rate was 0.091 and false allele was 0.019.

This study was supported by grant of the President of the Russian Federation № MK-2553.2012.4.

YANG S, JIANG J, WU Z, LI T, YANG X, HAN X, MIQUELLE D, PIKUNOV D, DUNISHENKO Y, NIKOLAEV I (1998): A survey of tigers and leopards in eastern Jilin province, China, winter 1998: Final report to the UNDP and the Wildlife Conservation Society. 38.

ROZHNOV V, SOROKIN P, LUKAREVSKIY V, NAIDENKO S, HERNANDES-BLANCO J, LUKAREVSKIY S (2013): Individual identification of Amur leopards (*Panthera pardus orientalis*) using molecular-genetic methods and the population size estimation. *Biology Bull* **40** (no. 2), 124 - 29.

UPHYRKINA O, MIQUELLE D, QUIGLEY H, DRISCOLL C, O'BRIEN S (2002): Conservation genetics of the Far Eastern leopard (*Panthera pardus orientalis*). *J Hered* **93** (no. 5), 303 - 313.

Differences in bite size, bite rate and food intake rate between mammals and birds

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Food intake rate (FIR) (mg dry matter/min) is an important variable of foraging behaviour. In this respect, differences may exist between mammals with intensive food chewing (including considerable comminution) and birds that do not chew at all (but comminute food in their gizzard). Until now, FIR, bite size (BS) and bite rate (BR) have been estimated for a limited number of mammal species and for a small number of birds. In the present study initial FIR, BS and BR were quantified for three mammal (rabbit, goat, horse) and three bird (chicken, goose, ostrich) species using artificial microswards of fresh grass. For final analyses own data sets were combined with literature data for animals fed with fresh, uncut grass (artificial swards or pasture). In order to account for ancestry-based correlations in the data sets of the mammals and birds the data were controlled for phylogenetic influences using the “Phylogenetic Generalized Least-Squares” method.

No differences between mammals and birds were found for BS and BR (general linear model results: BS, $p = 0.94$; BR, $p = 0.10$). For FIR, birds showed significantly lower values than mammals ($p = 0.01$). Despite birds do not chew they had lower FIR. Accordingly non-chewing seems to be no advantage regarding this factor. One possible restriction should be the ‘spaghetti effect’ (VAN GILS *et al.* 2007) which describes the fact that birds also have to handle large bites before swallowing. VAN GILS *et al.* (2007) speculated that this effect is similar time consuming as the food handling and chewing of mammals. Comparing similar sized animals as the chicken and the rabbits used in this study, the chicken had a BS of only 39 % of rabbits. The FIR was also lower but reached 79 % of the rabbit value. Similar differences were found for ostriches which had BS and FIR of 35 % and 37 % of the goat values measured in this study. Studies showing that free ranging birds feed longer than mammals and additionally choose high quality forage point to a compensation of small BS (indications only in own data) and low FIR by behavioural adaptations in birds.

VAN GILS J A, GYIMESI A, VAN LITH B (2007): Avian herbivory: an experiment, a field test, and an allometric comparison with mammals. *Ecology* **88**, 2926 - 2935.

Insights from five years of large-scale genetic wildcat monitoring in Germany

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Until recently the status of the European wildcat (*Felis s. silvestris*) was virtually unknown among several regions in Germany. The development of an easy-to-use non-invasive method to obtain hair samples for subsequent genetic analysis, wildcat distribution and genetic status has been intensively assessed across its potential German distribution. During the past five years we analysed > 4000 hair samples which were obtained in the course of numerous lure stick trapping projects, involving extensive field work supported by hundreds of volunteers, including regional NGOs, school classes, and youth organisations. As a reference set > 300 tissue samples of wildcats based on morphology were used.

Mitochondrial haplotype sequences and microsatellite genotypes revealed a significantly larger distribution range than previously known. We show how lurestick samples can be used to estimate barrier effects of landscape elements such as highways and streams, indicating a considerable dispersal potential of this species. Our data further document that hybridisation rates between wild and domestic cats are low across Germany and that the observed recent range expansion is mostly due to natural dispersal.

Wild Boar Berlin – ecology of wild boar in urban environments

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The worldwide growth of urban areas replaces rural and natural habitats to the detriment of many wildlife populations. Even so, some wildlife species prosper in urban area, including the wild boar. Berlin is famous for wild boar (*Sus scrofa*) and there activities cause conflicts with the public. In response, authorities such as the forestry department conduct management strategies to reduce this conflict. However, more detailed knowledge of wild boar ecology would help develop more effective management strategies within Berlin. The city of Rostock has a similar wild boar problem.

We study the ecology of wild boars in Berlin and Rostock and our results can also serve as a model for wild boars in other cities. We hypothesise that cities are attractive areas which might serve as a source rather than an attractive sink. To test this we capture animals from different parts of Berlin and Rostock as well as from the periphery and the surrounding countryside and use telemetry to determine temporal and spatial movement patterns. Activity sensors allow us to monitor behaviours in different areas and are hence a useful tool for characterising habitats.

The projects will provide a comprehensive understanding of the flexibility of life-history strategies and adaptation of wild boar to urban areas. Our results will be provided to authorities to support the development of long term management plans and conflict solving strategies.

The impact of dry-season water resources on the spatial and temporal distribution of mammals in the Ruaha National Park, in Tanzania

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The Ruaha National Park (NP) in the Southern Highland of Tanzania is an area of outstanding biodiversity and species endemism. The Great Ruaha River is the main permanent source of water in the Ruaha NP throughout the long dry season, which typically lasts for a period of approximately five months between June and October. Since 1993 the flow of the Great Ruaha River has been significantly reduced and this has resulted in the river drying-up during some dry seasons. It is thought that this reduction in river flow results from increased human utilisation of water from the Great Ruaha River upstream of Ruaha NP. Little is known about the impact of dry season water availability in the Great Ruaha River on wildlife populations in the Ruaha NP. This study aims to assess the impact of water resources on the spatial and temporal distribution patterns of larger mammals in the Ruaha NP throughout the dry season. Wildlife distribution and abundance was assessed using line transects conducted in areas with and without water resources. Camera traps were employed to assess the use of key water resources by wildlife throughout the 24 hour cycle. Water quality was measured regularly at key water resources throughout the dry season until they dried up. Our initial results indicate that water resources have a significant impact on the distribution of large mammal species in the Ruaha NP. As the dry season progresses, the importance of permanent water in the Great Ruaha River to wildlife greatly increases as other non-permanent water sources dry up. The quality in non-flowing water significantly deteriorates during the dry season. Our results suggest that the increased concentration of large numbers of animals at the few remaining water sources towards the end of the dry season are likely to increase the transmission of wildlife pathogens both within and between species. Results of this study will provide essential baseline data necessary for (i) the long-term assessment of the importance of permanent water for larger mammals in the Ruaha ecosystem, (ii) predicting the effect of human utilisation of water resources from the Great Ruaha River up-stream of the Ruaha NP and (iii) predicting the likely effect of future climate change in the region on wildlife.

Insectivorous bats digest chitin in the stomach using acidic mammalian chitinase

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The gastrointestinal tract of animals is adapted to their primary source of food to optimise resource use and energy intake. Temperate bat species mainly feed on arthropods. These contain the energy-rich carbohydrate chitin, which is indigestible for the endogenous enzymes of a typical mammalian gastrointestinal tract. However, the gastrointestinal tract of bat species should be adapted to their diet and be able to digest chitin.

We hypothesised that (i) European vespertilionid bat species have the digestive enzyme chitinase and that (ii) the chitinolytic activity is located in the intestine, as has been found for North American bat species.

The gastrointestinal tracts of seven bat species (*Pipistrellus pipistrellus*, *Plecotus auritus*, *Myotis bechsteinii*, *Myotis nattereri*, *Myotis daubentonii*, *Myotis myotis*, and *Nyctalus leisleri*) were tested for chitinolytic activity by diffusion assay. Gastrointestinal tracts of *P. pipistrellus*, *P. auritus*, *M. nattereri*, *M. myotis*, and *N. leisleri* were examined for acidic mammalian chitinase by western blot analysis. Tissue sections of the gastrointestinal tract of *P. pipistrellus* were immuno-histochemically analysed to locate the acidic mammalian chitinase.

Chitinolytic activity was detected in the stomachs of all bat species and in the rectums of three individuals. Western blot analysis confirmed the acidic mammalian chitinase in stomach samples. Immunohistochemistry of the *P. pipistrellus* gastrointestinal tract indicated that acidic mammalian chitinase is located in the stomach chief cells at the base of the gastric glands.

In conclusion, European vespertilionid bat species have a chitinase (acidic mammalian chitinase) that is produced in the gastric glands of the stomach. Therefore, the gastrointestinal tracts of insectivorous bat species evolved an enzymatic adaptation to their diet.

Comparison of continuous behaviour assessment and thermal imaging of large felids with focus on thermoregulatory behaviour

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Felids ranging from a variety of habitats and climates are kept in zoos in climates that may drastically differ from that of their typical home range. To date no comparative studies of behaviour repertoire or thermoregulation have been conducted with species from the *Panthera* genus. Thermoregulatory behaviour inherent to all homeotherms could be used to investigate differences among these species in captivity which may be transferable to their wild counterparts. Species from differing habitats should exhibit different thermoregulatory behaviour strategies and thermoneutral zones. A case study approach will be used to investigate daily maintenance and thermoregulatory behaviours via continuous behaviour observation, along with infrared thermography images for every animal, and measurements of ambient air temperature, relative humidity, wind speed and solar radiation recorded every 15 minutes throughout the observation period. Work has been done at Lowry Park Zoo, Tampa, Florida where Malayan tigers (*Panthera tigris jacksoni*) and cougars, a subpopulation of *Puma concolor* isolated to southern Florida, are housed. In addition, work has been done at Toronto Zoo in Ontario, Canada where lions (*Panthera leo*), jaguars (*P. onca*), tigers (*P. tigris*, *P. tigris sumatrae* and *P. tigris altaica*), cougars (*Puma concolor*) and snow leopards (*P. uncia*) have been studied. There are indications that some behavioural and thermoregulatory needs differences exist across species related to natural habitat of origin. Time budget assessments have yielded insight into potential gender differences in addition to a potential influence of dominance hierarchy within groups on the performance of some thermoregulatory behaviours which place an individual in a vulnerable position, for example loin exposure. The case study approach is welcomed by the zoo community who realises the limitation of low animal numbers housed at these institutions as a common limitation of zoo animal research (HUTCHINS *et al.*, 2003). This work should have an immediate impact on the animals involved in the study and has the potential to provide a new diagnostic health tool for zoo veterinarians. There is an immediate need for work in this area and for the development of a non-invasive method of core body temperature assessment for routine health examinations not yet available for dangerous carnivorous species.

HUTCHINS M, DRESSER B, WEMMER C (2003): Ethical Considerations in Zoo and Aquarium Research. In: ARMSTRONG SJ, BOLTZLER RG (Eds.): The Animal Ethics Reader. New York (NY): Routledge, 459 - 470.

Factors modulating multi-scale responses of vertebrate species to human disturbance

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Human outdoor activities are growing in intensity and space. Areas and habitats that previously were inaccessible to most people, for economic or logistic reasons, are now being disturbed more and more. Human-fauna encounters are therefore increasing throughout areas and taxa, which raises the concern among researchers and conservations about the fate of some populations and species. Even in non-aggressive encounters, animals are likely to perceive humans as predators, and thus mount a physiological and behavioural stress response, which in turn may have important negative consequences for them. However, despite the large amount of research performed on this topic in recent years, sometimes it is difficult to find clear or generalisable patterns. Results appear to vary or be contradictory among studies, which is in part a consequence of the degree of unawareness of factors modulating the relationship between human presence and final human-induced response. Thus, our aim was to perform a comprehensive literature review about these factors.

Many factors affect vertebrate responses to humans. They can be divided into three groups: 1) Factors related to the source of disturbance, that is, quality (type of activity, presence of pets), intensity (number of people visiting an area and frequency) and distribution (e.g. on-trail vs. off-trail, clustered according to countries or cities). 2) Related to the internal properties of the focus of the disturbance, such as, intraspecific (i.e. differences in age, sex, body condition, stress phenotype, previous exposure to humans, population density dependence) and species-specific characteristics (e.g. sensory abilities, antipredatory or breeding strategy, and cognitive level). 3) Finally, the spatio-temporal context in which the disturbance occurs may also modulate the response observed. For example, these may include the phase of the ultradian, circadian or annual cycles, and variability in habitat quality and climate. We present an overview of the different scales at which factors modify expected responses (from immediate physiological responses to demographic or evolutionary changes in species) in order to provide a clearer vision of the variables that should be considered when designing or interpreting specific disturbance studies.

Preliminary results on hair cortisol detection as a tool to evaluate chronic stress in Sahrawi dorcas gazelle (*Gazella dorcas neglecta*)

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Detrimental effects of chronic stress on animal health can have a significant impact on captive or free-ranging animals in conservation programmes. However, reliable evaluation of stress is complex and poses a major challenge in wild animals. High levels of glucocorticoids, especially cortisol, are considered to be a stress indicator as they reflect the increased activity of the hypothalamic-pituitary-adrenocortical axis. Cortisol levels have been measured using different matrices such as plasma, saliva, urine, faeces or, in recent years, hair. Hair cortisol detection is likely to be useful to detect chronic stress because circulating cortisol is deposited in the hair during folliculogenesis and makes this method a potential key tool in welfare studies.

The aim of this study was to assess the technique of detection of hair cortisol in Sahrawi dorcas gazelle (*Gazella dorcas neglecta*) as a way to measure stress in this species. We tested the technique in all-male groups from Barcelona Zoo (Spain, n = 5) and Guembeul Special Fauna Reserve (Senegal, n = 9). Hair samples were harvested by shaving the rump and stored at room temperature until steroid extraction. In order to assess variability due to sampling site, a second hair sample was obtained from the lateral femoral region in the animals from Barcelona Zoo. Cortisol extraction was performed on 250 mg of hair after washing with isopropanol, drying, mincing and mixing with methanol. After 18 h of moderate shaking, samples were centrifuged and supernatant evaporated at 38 °C. Dried extracts were reconstituted with EIA buffer provided with a competitive immunoassay ELISA for cortisol (Neogen Europe, Ayr, UK) and analysed following the manufacturer instructions. The assay was validated by determination of assay specificity, accuracy from spike recovery, precision from intra- and inter-assay variabilities and sensitivity. Plasma and faecal samples were obtained from animals at Barcelona. No significant differences were detected between body regions in cortisol levels. Hair cortisol concentrations were not correlated ($P > 0.10$) with cortisol levels in plasma or cortisol metabolites in faeces. Mean hair cortisol concentration from males from Barcelona and Guembeul of 1.99 and 2.80 pg/mg of hair significantly differed (Mann-Whitney U-test, $P = 0.03$). Studies are in progress to detect possible effects of environment, age, social status and group composition on hair cortisol levels. In conclusion, hair cortisol analysis seems to be promising to study stress and welfare in wildlife.

Individual identification and genetic variation of lions (*Panthera leo*) from two protected areas in Nigeria

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This survey was conducted in two protected areas in Nigeria to genetically identify individual lions and to determine the genetic variation within and between the two populations. We used faecal sample DNA, a non-invasive alternative to the risky and laborious task of taking samples directly from the animals, often preceded by catching and immobilisation. Data collection in Yankari Game Reserve spanned through the period of five years (2008 - 2012), whereas data in Kainji Lake National Park was gathered for a period of three years (2009, 2010 and 2012). Eight individuals (2 males, 3 females, 3 unknown) were identified from Yankari Game Reserve while ten individuals (7 males, 3 females) were identified from Kainji-Lake National Park. The two populations were found to be genetically distinct as shown by the high fixation index ($F_{st} = 0.17$, $p = 0.05$) bootstrapping over loci $\pm 95\%$ CI (0.10 - 0.23) with each population exhibiting significant signs of inbreeding (YGR $F_{is} = 0.49$, KLNP $F_{is} = 0.38$, $p = 0.001$) respectively. The significant genetic differentiation between the Yankari and Kainji lions is assumed to result from the large spatial geographic distance and the physical barriers reducing gene flow between these two remaining wild lion populations in Nigeria.

The effect of diel activity pattern on immune system and stress in wild rodents: a meta-analytical approach

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In mammals, the circulating immune cells in blood fluctuate along rest-to-activity rhythms. Rodents are the most diverse mammalian group and have evolved different diel activity patterns (diurnal, nocturnal, and a-rhythmic). It has been shown that the diel activity patterns of rodents are constrained by their phylogeny. Using a meta-analytical approach, we hypothesised there are differences in basal immune investment (estimated by total WBC counts) and stress (estimated by neutrophil/lymphocyte ratio) among diel activity patterns in wild rodents. We compiled a database based on a systematic literature search. To compensate for potential lack of independence, we analysed the data sets with the phylogenetic generalised least squares models. We logarithmically transformed the data sets to fulfil the assumption of normality, and reconstructed the phylogenetic tree using data from published literature. We found that 1) both the total WBC counts and neutrophil/lymphocyte ratio were significantly associated with body mass, 2) nocturnal species showed higher total WBC counts than diurnal rodents, and 3) the neutrophil/lymphocyte ratio of diurnal species tended to be higher than that of nocturnal rodents. These findings suggest differences in basal immune investment between diurnal and nocturnal rodents, which could be explained by two non-mutually exclusive scenarios. Firstly, diurnal rodents tend to be more social and accordingly have less ectoparasite richness, compared with the nocturnal species, which could explain the lower investment in immune cells. Secondly, under the melatonin-linked immunoenhancement hypothesis, the secretion of melatonin in diurnal rodents is suppressed during daytime, which might lead to the differences. Further studies are required to test the validity of these hypotheses.

Large-scale genetic census of wildcats (*Felis silvestris*) using standardised sampling grids

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The endangered European wildcat (*Felis silvestris*) serves as an umbrella species for natural forest communities in Germany. While the species has gained increased public attention due to extensive conservation and monitoring action, there is still uncertainty concerning important population parameters such as genetic differentiation and both effective and census sizes of local populations. In the frame of a large-scale project, named *Wildcat Leap* (“*Wildkatzensprung*”), 17 standardised grid cells are equipped with valerian lure sticks as hair traps (STEYER *et al.*, 2013) and sampled over three consecutive years. The grids are spread across the wildcat's distribution in Germany and cover both high and low density wildcat habitats. Here we present data of the first sampling season in 2011/2012. Microsatellite analysis of 780 hair samples obtained from lure sticks resulted in the detection of 183 individual wildcats. We provide estimates of genetic diversity, population density and gene flow among the sampled grids. Ultimately, our aim is to provide basic data on wildcat population structure which will serve as baseline for optimised conservation plans. Moreover, combining our genetic data with habitat models will help to provide a well-founded census estimate for the wildcat in Germany.

STEYER K, SIMON O, KRAUS RHS, HAASE P, NOWAK C (2013): Hair trapping with valerian-treated lure sticks as a tool for genetic wildcat monitoring in low-density habitats. *Eur J Wildlife Res* **59**, 39 - 46.

Classifying wild boar (*Sus scrofa*) behaviour with a tri-axial acceleration sensor using linear discriminant analysis

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Technology in biotelemetry studies is advancing quickly and new three-dimensional acceleration sensors (ACC) allow for a detailed description of animal movement behaviour. We used e-obs ACC-tags to classify the movement of a wild boar and a domestic hog. Eleven behavioural categories were considered: resting/recumbent, standing, walking, trotting, galloping, scratching, shaking, searching/standing, feeding/standing, digging/standing and searching/walking. Sensor data was processed using autocorrelation and Fast Fourier Transform to calculate the weighted mean of each time series. Arithmetic mean, standard deviation and the inverse coefficient of variance (mean/standard deviation) were used alongside the weighted mean as predictor variables for automatic behaviour classification with linear discriminant analysis (LDA). The LDA identified group-memberships with a correctness of 84.8 % for the wild boar and 80.9 % for the domestic hog. Joining the four foraging (searching/standing, feeding/standing, digging/standing, searching/walking) behaviours to only one group called “foraging”, improved the behaviour assignments significantly. Therein, wild boar movement classification scored 97.3 % correctly and the domestic hog 96.0 %. A model data set of at least 450 processed time series (950 for the domestic hog) and all applied predictor variables were necessary for high correctness scores. The combination of time series functions and linear discriminant analysis proved to be a powerful tool for behaviour classification. The next step will be to analyse movements, involving various behaviours within one time series.

Male reproduction is affected by short term intrauterine exposure to glucocorticoids in common marmoset monkeys

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It is commonly known that stress during pregnancy does affect the foetus in different ways. The kind of alteration depends on the time point and duration of the irritation. There is rising evidence that foetal programming plays a role which implicates that following generations may be affected, too.

Therefore, the aim of the study was to investigate effects of short-term dexamethasone (DEX) application, representing a stress stimulus, during pregnancy on reproduction of the male filial generations (F1-F3) in common marmoset monkeys (*Callithrix jacchus*).

Male common marmoset monkeys of different filial generations (F1: n = 6, F2: n = 6, F3: n = 5) were analysed due to their endocrine and lipid metabolic status as well as the expression pattern of markers for male fertility in the testes.

Peripheral sex steroid levels were similar in the intrauterine DEX treated male offspring in F1 (7.3 ± 3.6 ng/ml) versus control at adult stage (7.2 ± 4.5 ng/ml). In the adult F3 generation, lower plasma levels of testosterone than in control animals of similar age were detected. Analysing the blood parameters of lipid metabolism, the F1 generation showed no significant differences, whereas interestingly in the F2 and F3 generation significantly higher levels of plasma cholesterol (F2: M = 3.95 mM, F3: M = 4.40 mM) than control (M = 3.23 mM) and lower triglyceride levels (F2: M = 0.89 mM, F3: M = 1.26 mM) than control (M = 1.41 mM) were observed.

Furthermore, enhanced testicular gene and protein expression in the DEX group compared to control were detected for the following parameters: androgen receptor, aromatase, oestrogen receptor 1, 17β -hydroxysteroid dehydrogenase type 7, relaxin receptor 2, Ki 67 and ras. Semen, collected by penile vibrostimulation, was not affected in terms of sperm morphology and vitality. However, concentration and total quantity of spermatozoa was slightly reduced in the F3.

In summary, the prenatal environment has profound effects on adult life as well as on following generations as shown by our glucocorticoid application. It needs further analysis whether the enhanced testicular factors in combination with increased cholesterol levels are signs of a highly effective steroid biosynthesis although peripheral testosterone levels were lower along with poor sperm quality. Or one could ask whether the higher expression of proliferation markers (ras, Ki67 and oestrogen receptor 1) would support the development of tumours in the testis.

Brown hyaenas on farmland in Namibia

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We evaluate biodiversity on various farmland types (livestock and game farms with different stocking rates; guest and hunting farms) in relation to resource dispersion, resource availability, habitat fragmentation and human wildlife conflicts for selected species. Here we present results on number and distribution of brown hyaena (*Parahyaena brunnea*) on five farms encompassing 520 km² in the Otjimbingwe in west-central Namibia. Brown hyaenas are officially harvested as trophies. Hunting quotas are based on (sometimes unrealistic) population estimates of farm owners/managers.

Baited camera traps were used to identify individual brown hyaena and their distribution. Scat samples were collected and analysed to determine their diet. Game was counted on line transects with distance sampling. We use software PRESENCE 5.8, CAPTURE2 and DENSITY 6 to estimate occupancy, abundance and densities of brown hyaena and leopard. Game count data are analysed with DISTANCE v 6.0. We visualise results in ArcGIS vs 9.2. to 10. Scat analyses revealed 11 mammal and two bird species as diet of brown hyaenas in the study area. More than half of the samples contained hair of mountain zebra (*Equus zebra*, 54.14 %), followed by kudu (*Tragelaphus strepsiceros*, 8.6 %), birds (7.74 %), small mammals like rodents (6.88 %), and rock hyrax (*Procapra capensis*) at 3.44 %. Two samples contained domestic animals (goat hair). Zebra and kudu bones were also the most frequent remains found at the den. Hair of horse (the species used for baiting) was detected in 6.03 % of scat samples.

We identified 33 brown hyaenas within the study area. We calculated a tentative estimate of average population density following the method given by MILLS (1990). Our estimate is 1.84 – 2.81 individuals per 100 km² and thus within the range of already published data. Brown hyaena numbers varied between farms and farmland types. For example, at Okomitundu (180 km²), the open and unused eastern part of 80 km² held seven individuals and an active den, whereas the game fenced western hunting area of 100 km² hosted four individuals and a deserted den. Because game counts revealed a higher abundance of game in the hunting area than in the open farmland (+15 %) and a larger number of species (17 versus 7), abundance of potential prey does not seem to affect spatial distribution of brown hyaenas.

MILLS MGL (1990): Kalahari hyenas: Comparative behavioral ecology of two species. 304 pg, Blackburn Press, Caldwell, USA.

Impact of the invasive common myna on endemic Seychelles warblers: evidence for adult predation?

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The global increase in the number of introductions of non-native species has raised widespread concern about the impact on endemic species and as such has been implicated as a threat to native biodiversity. Despite this concern there is poor knowledge of the impact of invasive birds on biodiversity and evidence is often based on anecdotal observations. The same is true for the impact of the common myna (*Acridotheres tristis*), which was declared by the IUCN as one of the world's most invasive species. The highly aggressive common myna impact native fauna through competition for nest sites and nest predation, however the magnitude of its impact has been rarely quantified. Despite its aggressive behaviour the common myna has not yet been regarded as a threat to adult individuals. Here we present the first empirical study quantifying the impact of the common myna on adult mortality rates of the Seychelles warbler (*Acrocephalus sechellensis*). The Seychelles warbler is a small insectivorous species endemic to the Seychelles islands. The worldwide population of the once critically endangered Seychelles warbler has grown to over 2.500 individuals due to habitat restoration and successful translocations. Although high initial population growth rates indicated the successful establishment of a fourth island population, skewed population sex ratios (0.62 since 2004) caused by low female survival rates (0.61 vs. 0.83 in the source population) hampered population growth rates. Here we investigate whether the common myna attacks incubating females on the nest resulting in observed severe injuries or death. To quantify the effect of the island's common myna population on the Seychelles warblers we measured adult and juvenile survival rates and annual population growth rates before, during and after the reduction of the common myna population by over 90 %. Survival and population growth rates were compared with predator free warbler populations. With this study we determine whether a new factor has to be considered in the way common myna impact endemic bird populations. This study highlights the need for quantitative measurements on the effects of invasive species and their implications for conservation projects.

Improving the golden-headed lion tamarin (*Leontopithecus chrysomelas*) breeding schemes by establishing founder relatedness through combined microsatellite marker and pedigree analysis

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To conserve a self-sustaining captive population, the population must be genetically managed to minimise loss of genetic diversity, inbreeding and adaptation to captivity. Accurate genetic management of a captive population relies mostly on pedigree analysis. However, the majority of the pedigrees in captive breeding programmes are far from perfect for various reasons. Most importantly, founders are assumed to be unrelated, often resulting in an overestimation of the genetic diversity present in a population.

The captive population of the golden-headed lion tamarin (*Leontopithecus chrysomelas*), which is endemic to the Atlantic forest of South-Bahia and threatened with extinction, has grown in the last decades from 46 founders to a size of approximately 220 animals in the European Endangered Species Programme. The pedigree is known for about 98 % and the genetic diversity retained is estimated on a good 97 % of the source population. However, the golden-headed lion tamarins (GHLT) were imported from Brazil in small groups for which mutual relatedness was unknown. The main objectives of this study were to estimate the genetic relationship between the GHLT founders and to resolve gaps in the pedigree of the captive GHLT population. Tissue samples were collected post-mortem and for live animals non-invasive hair samples were used for DNA extraction. We used 21 microsatellite marker loci to infer genetic relatedness among 95 captive individuals in the first generations. Pedigree and molecular data were combined into a single estimator of relatedness through a weighing method developed by BÖMCKE *et al.* (2011). Integration of the relatedness estimates was completed through the use of the program PMx. The changes in mean inbreeding (F), mean kinship (MK), founder genome equivalents, and genetic diversity were assessed. Using these values we aimed to improve the breeding schemes and to make a more accurate evaluation of the current genetic status of the population.

BÖMCKE E, SOYEURT H, SZYDLOWSKI M, GENGLER N (2011): New method to combine molecular and pedigree relationships. *J Anim Sci* **89**, 972 - 978.

Quantitative genetics in the captive Congo peafowl (*Afropavo congensis*, Chapin 1936)

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Being the only pheasant species in Africa, the Congo peafowl (*Afropavo congensis*) holds a unique position within bird taxonomy. Apart from some knowledge regarding its breeding biology (the bird is monogamous and both parents and their offspring take part in raising the chicks) little is known about the general biology of this vulnerable bird species (IUCN Birdlife International, 2012) in the wild.

In the early 1960's, a captive breeding programme (Europäisches Erhaltungszuchtprogramm, EEP) was set up by the Royal Zoological Society of Antwerp by importing several peafowl of which six became founders of the current captive population. Regardless of careful management, inbreeding is suspected to have increased over time. The main reasons for increased inbreeding are the small population size and the lack of additional founders. Inbreeding depression is expected to cause breeding problems: low reproductive rates and high infant mortality. Here we analysed historical studbook data and clutch data to test the effects of inbreeding depression and to evaluate the genetic constitution of reproductive (quantitative) traits with statistical variance analysis and studbook software R (Core Team, 2013) and PMx (BALLOU *et al.*, 2010).

At the moment the average generation time of the living zoo specimens is seven years, currently one out of two of the mitochondrial haplotypes is lost, since these are maternally inherited and one female founder has no female offspring. If the complete captive population is split into four groups of equal size based on levels of inbreeding (lowest, low, high, highest), the most inbred group ($F > 0.2^*$) of the population has severely lowered survival compared to the remaining groups. No significant difference was found between remaining groups. The total lifespan of animals is to some extent heritable ($h^2 = 0.25$).

* = provisional data

BALLOU JD, LACY RC, POLLAK JP (2010): PMx: software for demographic and genetic analysis and management of pedigreed populations. Chicago Zoological Society, Brookfield, Illinois, USA.

R CORE TEAM (2013): R: A Language and Environment for Statistical Computing, R Foundation for Statistical Computing, Vienna, Austria. <http://www.R-project.org>

Bat fatalities at wind turbines: Germany's central role in the conservation of migratory bats

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Following the traumatic event of the Fukushima blast, Germany decided against the continuation of nuclear power production and the large-scale promotion of renewable energy, including wind power. As a consequence, wind turbines have been established throughout many parts of Germany. Yet, the consequences for wildlife populations, particularly bats, are poorly understood. Similar to North America, thousands of bats are killed annually at wind turbines in Europe. For Germany, estimated numbers of yearly bat fatalities at wind turbines range between 50,000 and 250,000 individuals when no mitigation measures are practiced. These numbers may be largely underestimated because bats with mild barotraumas, one of the major causes of death for bats at wind turbines, may not die immediately and may thus remain unnoticed by surveys. Since mostly migratory bats are affected, bat fatalities at wind turbines threaten the connectivity between Northeastern breeding areas and Southwestern wintering ranges of migratory bats. Indeed, the current installation of more and larger wind turbines in Germany may entail severe costs to the biodiversity of Northern and Northeastern European countries. Mitigation measures (i.e. implementation of cut-in speeds) are at hand, yet seem to be poorly practiced because of potential monetary losses for companies (usually < 1 % of net power production per wind turbine) and because the political goal of increasing the proportion of wind energy by 50 % until 2020 may be at risk. Here, I will review the status quo and development of the conflict between wildlife and German politics using bats as an example.

Same roost as every year? Settling dynamics and male advertisement behaviour in an urban population of noctule bats (*Nyctalus noctula*)

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Few temperate bat species have managed to adapt to urban life. Among these, noctule bats (*Nyctalus noctula*) have conquered cities as suitable habitats, not only for foraging but also for mating. To date however, little is known about the social life of city bats in general and of noctule bats in particular. Here, we monitored individual settling dynamics and advertisement behaviour of a population of noctule bats during the mating seasons 2009 to 2012 in a municipal park in Berlin, Germany. We hypothesised that flexible settling decisions are a pre-requisite in rapidly changing urban environments, and thus expected individuals to show high flexibility in their roost choices. We also investigated if and how spatial distribution of noctule males might be related to their advertisement activity. Male noctule bats establish mating roosts in autumn that they acoustically defend against other males and/or display to females with song. During the mating season, all noctule bats were weighed, sexed, aged and individually banded, and we recorded the settling dynamics of territorial males and monitored individual courtship activities in standardised activity rounds each night. Mating roosts were predominantly established by males being at least two yrs ($n + 1$) old. Some males returned to the study area in successive years. Males did not follow an even spacing strategy when choosing mating roosts, but clustered in mating hot spots in the park. Furthermore, noctules differed considerably in their singing activity, with males within clusters singing more, and more complex songs, than males without close roosting neighbours. We conclude that the advantage of advertising in a cluster might be more important than the return to the same roost every year.

Effects of garden LED lights on small rodent behaviour and physiology

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It has been noticed that in the last two decades an increasing amount of research projects have been focusing on the extent and intensity of artificial night lighting. Lighting-at-Night does not only lead to disorientation of wildlife and loss of the night sky in industrial countries, but has also direct effects on activity phases of organisms and their metabolic processes. That would consequently affect individuals' fitness as well as alter interspecific interactions such as predation and competition. We investigated the effects of lighted nights on bank voles (*Myodes glareolus*), which are a common prey for owls and are known to reduce their activity during moonlit nights. Even the dim light of LED garden lamps may enhance visibility for owls and possibly the predation risk for voles. Voles are generally polyphasic, nevertheless their main activity is during the time of dawn. We examined illumination effects in two different seasons (summer and winter). Voles' activities and home ranges were tracked using automated radiotracking, which is based on a recording system unit, eight fixed antennas and small – size radiotransmitter (Holohill 100BPM). In summer during New Moon, 12 voles in four enclosures, where each enclosure displays an area of 50x50 meters, were exposed to three lighted nights using halogen spotlights (500 W). In total, activities and home ranges were recorded for six days and nights without interruptions. All senders were read ten times in a row by eight antennas, meaning every four minutes the activity of one vole was recorded. Moreover solar powered lights run for short time during winter and the entire night during summer, thus enhance seasonality of light. From November 2012 until May 2013, 89 voles in total were observed in eight semi-natural enclosures. In four enclosures 85 LED garden lamps were installed, whereas for the other fields mockups were used. During the winter period (December - March), the voles were counted once per month, afterwards every ten days. Within this experiment the activity of 33 voles was recorded two times 24 h by means of radio-telemetry. Individuals' locations were calculated through angular relationship between each pairs of antennas. Stress response was monitored measuring non-invasive faecal glucocorticoid titers. Voles' onset of breeding was compared to illuminated populations and populations with natural light. During summers, voles shifted and increased their daily activities and reduced their home ranges at night when nights were illuminated. Results from winter and spring will be discussed.

Identification of activity patterns of white-tailed sea eagles (*Haliaeetus albicilla*) using bi-axial accelerometry

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GNSS-telemetry devices attached to animals is a widely used method to study wildlife space-use. Additional sensor (acceleration, temperature, etc.) enable researchers to study the behaviour of the animals as well.

We collected activity-data of 14 white-tailed sea eagles (*Haliaeetus albicilla*) of different ages, sexes and from different regions of northern Germany. The data reveal changes in the activity of the sea eagles over the year as well as in daily activity patterns. The strong correlation with the diurnality depends on the available light which is sufficient on average one hour before sunrise and last until one hour after sunset. Since diseases such as intoxications and injuries, but also habitat quality and disturbances affect the behaviour of the eagles, activity analysis enable researchers to better understand and interpret the eagle's behaviour.

Citizen Science as valuable tool to include public knowledge in science

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In the last few years, it has increasingly been recognised that biodiversity research is particularly suitable for the involvement of volunteers in the design of research projects and in data collection. Lay contributors can provide their views on questions of societal relevance and contribute data on the observation of many animals and plants. Although this concept is not suitable for all research questions, it can be highly valuable in many cases: more extensive datasets can be collated with the help of trained volunteers than by scientists alone, and the involvement of citizens may also increase the public acceptance of scientific results. Conversely, interested citizens gain knowledge about biodiversity and contribute to solving interesting scientific problems.

Within the Berlin-Brandenburg Institute of Advanced Biodiversity Research (www.bbib.org), an online platform “*Portal Bee*” - *Biodiversität erkennen, erforschen, erhalten*” (“Discover, explore and preserve biodiversity”; www.portal-bee.de) was recently established to foster Citizen Science as a practical approach to biodiversity research in the Berlin-Brandenburg region. The first two projects of the pilot phase investigate the behaviour, ecology and health status of wild boar and hedgehogs in Berlin. Citizens of Berlin are invited to report their sightings and observations of both species in *Portal Bee*. Tapping into the knowledge of the citizenship of Berlin opens a new resource for scientists, who would otherwise be restricted in the amount of data they can collect by their own limited time and the limited personnel available to them. By combining our own data with observations by citizens, we expect to collect information which allows us to identify areas of high encounter rates between people and wildlife as an index of areas of high wildlife population densities. This information will be used as background for genetic population analyses in the case of the hedgehog and to record activity patterns in the case of the wild boar. During the course of the two projects, we will develop and test novel statistical methods in order to increase the validity of datasets which include contributions by laymen. Currently, the project is in the first phase, in which we concentrate our efforts on the recruitment of participants.

Genetic monitoring of reintroduced Eurasian lynx (*Lynx lynx*) in the Harz Mountains, Germany

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The Eurasian lynx (*Lynx lynx*) became extinct across central Europe westwards the Slovakian Carpathians until the end of the 19th century. Following successful reintroduction in several European regions, such as Slovenia and Switzerland, 24 lynx (9 males, 15 females) were reintroduced in the Harz Mountains, Germany between 2000 and 2006. Here we present the first results of a genetic monitoring project which aims to reveal evidence for individual survival and reproduction success as well as monitor genetic diversity over time. In total 131 tissue, blood, hair, scat and urine samples from released animals and field-collected samples were analysed by means of mitochondrial haplotype sequencing and microsatellite analysis. The Harz example shows the usefulness of noninvasive genetic analyses for monitoring lynx, particularly in snow-rich areas, where snow tracking allows the collection of urine and scat samples. Genetic diversity in the Harz population was found to be moderate (expected heterozygosity $H_e = 0.68$, observed heterozygosity $H_o = 0.59$), due to the fact that lynx were reintroduced from different captive lineages. While the use of 15 autosomal microsatellite markers is clearly not sufficient to fully resolve kinship relations among lynx in the Harz regions, several samples from the field could be assigned to parental lineages of reintroduced individuals. We discuss our findings with regard to the genetic status and the long-term viability of the lynx population in the Harz Mountains.

Epigenetic effects in the wild guinea pig

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Animals need to adapt to environmental changes such as global warming. Epigenetic factors are heritable regulators of gene expression. Their pattern may change as a direct response to environmental factors, thus allowing short and long-term adaptation processes. The best-studied epigenetic factor is DNA methylation. It is important in cell differentiation, and misregulation leads to diseases, such as cancer and mental diseases, as shown in studies on human cell lines and model organisms such as mouse and rat. To address epigenetic adaptation in the wild, we are investigating DNA methylation patterns in the male wild guinea pig (*Cavia aperea*) and whether they change after heat exposure. Therefore we exposed five male wild guinea pigs for the duration of two months (time period for one spermatogenesis cycle) to 30 °C temperature using heat plates. This “heat stress” is accompanied with reduction of living space. After mating which was allowed before and after treatment (each male with two females), we sampled all fathers and their respective sons. We are expecting paternal transmission and therefore differences in methylation patterns between the sons sired before and after treatment. Applying restriction-reduced-bisulfite-sequencing (RRBS) on liver samples of 34 sons, we were able to cover 75 to– 88 % of the methylome, representing 4 to 6 % of the whole *C. aperea* genome. So far we have shown that heat treatment has behavioural as well as physiological consequences. During exposure, animals were irritated, more tense and jumpy. Their fur got shaggy and less shiny. Physiological effects were reflected by an increase in dry matter intake (DMI) of 9.1 % /kg body weight until day 24 after heat exposure. This compensation was followed by a steady decrease, which we recorded in six sampling points during the exposure. After day 24 DMI sank below basic value and in the final exposure phase animals ate < 80 % DMI. These changes may display direct adaptational processes which we expect be based on DNA methylation changes.

The project is funded by the Leibniz-Gemeinschaft (SAW-2011-IZW-2).

**Paternal kin bias in free-ranging rhesus macaques (*Macaca mulatta*):
development, mechanisms and cues**

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In female philopatric species, there is extensive evidence that the most pronounced bonds are formed among maternally related females. However, recent studies suggested that individuals of several species of mammals also recognise their paternal kin as they socially prefer paternal kin over non-kin. How these kin bonds develop through ontogeny, what mechanisms and cues are involved in paternal kin recognition is addressed in a long-term study on the free-ranging rhesus macaque population at Cayo Santiago (Puerto Rico) using different methodological approaches. First, combining behavioural observations from birth to maturation (> 3500 hrs) with paternity data, results of a GLMM revealed a significant social preference of paternal kin over unrelated group member by male subjects at the age of four (prior to natal dispersal) when compared to female subjects of the same age (prior to first breeding). Considering focal subjects and adult group males only, paternity in interdependence with other factors was a significant predictor of male-infant affiliation, peaking at two years of age and being independent of mother's presence. Second, the most likely mechanisms (familiarity and phenotype matching) of paternal kin discrimination have been investigated via acoustic and visual cues using field experiments (playbacks and looking-time tasks, respectively). Results of a GLMM suggested that both mechanisms and multimodal cues are involved. Overall, the data strengthen the evidence that paternal relatedness influenced the evolution of social behaviour in primates.

Conservation priorities for Bornean mammals

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Southeast Asia hosts ~13 % of all known mammal species on only ~1 % of the world's land mass. Borneo – the largest island in the Southeast Asian biodiversity hotspot – is shared by Malaysia, Indonesia and Brunei and hosts ~ 300 mammal species of which ~25 % are endemic. Echoing the biodiversity crisis elsewhere in the region, the island faces unprecedented levels of habitat loss. Coupled with climate change forecasts, the future of Borneo's biodiversity is therefore of high conservation concern. How well biodiversity is represented in Borneo's protected areas under range-shifting forecasts of environmental change is central to conservation planning on Borneo. Using hierarchical modelling we evaluated the role of protected areas in conserving three mammal groups (81 species of primate, carnivore and bat) across the island under present-day and future (2020, 2050, 2080) climate and land-cover changes scenarios. We show how an integration of species distribution modelling, expert knowledge, and future climate and land-cover scenarios into a systematic conservation assessment can support important decisions concerning the future of tropical biodiversity. Our results highlight that for Bornean mammals, the sustainable management of forests under commercial timber management will be increasingly important under forecasts of environmental change.

Wild cyclic voles maintain high neutral and MHC diversity independently of parasitism

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Understanding the selective forces that maintain genetic diversity is a major focus of evolutionary biology. In particular, the high variability of genes of the Major Histocompatibility Complex (MHC), which plays a prominent role in vertebrate immunity, is thought to arise from a combination of parasite-mediated and sexual selection. An outstanding question involves the degree to which balancing selection on the MHC can oppose genetic drift and maintain genetic variation in the face of severe population bottlenecks. To address this question we examined genetic diversity and population structure at neutral and MHC genes, and measures of parasitism in a fluctuating population of montane voles (*Microtus montanus*). We found high measures of neutral and MHC allelic variability, indicating genetic drift has had little impact on this vole population, despite regular population cycles. Next, we tested whether individuals with greater diversity at the MHC experienced lower measures of infection by several gastrointestinal parasites. MHC diversity did not predict overall parasite richness or the presence/absence of two common endoparasites. Two specific MHC alleles predicted *Eimeria* and cestode intensity, but no other associations between specific alleles and infection measures were detected. Measures of neutral genetic diversity based on microsatellites were positively associated with host body condition, total parasite richness and cestode intensity. One explanation for greater parasite loads among hosts with greater genome-wide diversity is that these individuals might better tolerate heavy infections than more inbred hosts. Overall, these results suggest that the parasites examined here do not have a strong role maintaining the high observed MHC variation in cyclic wild voles, and other potential mechanisms of selection such as mate choice should be considered.

Carrying out non-invasive monitoring of faecal glucocorticoid metabolites (FGM) levels in Asian elephants (*Elephas maximus*) in Peninsular Malaysia

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Habitat loss, forest fragmentation and human-elephant conflicts are the biggest threats to Asian elephants (*Elephas maximus*). Peninsular Malaysia has an estimated population of 1223 to 1677 wild Asian elephants. From 1974 to 2010, over 600 wild elephants were captured in conflict areas and translocated to large patches of continuous forest by the wildlife authority. Not much is known about the fate of these elephants. Our study aims to use faecal glucocorticoid metabolites (FGM) to assess the impact of translocation on wild elephants in Peninsular Malaysia. The tropical rainforest however is a tough environment to study wild elephants, and it presents a different set of challenges for non-invasive hormone monitoring. Due to dense vegetation and difficult accessibility, researchers face difficulties in locating elephants, conducting direct observations to identify individuals, observing defaecation and collecting fresh dung. The lack of direct sightings also leads to a poor understanding of elephant social structure and physical health, factors that are known to influence FGM levels in elephants. There is also a need for a method to store hormone samples that is suitable for field conditions (i.e., high humidity, high rainfall, no electricity and minimum equipment to be carried into the jungle). This FGM monitoring is carried out under a broader research programme called “The management and ecology of Malaysian elephants (MEME)”. MEME includes: (i) deployment of satellite GPS collars to track wild elephants and obtain faecal samples, (ii) usage of non-invasive DNA testing to identify individuals and their sex, (iii) camera-video trapping to study wild elephant social structures and (iv) drone technology to map elephant habitat. The initial experiments carried out under this study include validation of an enzymeimmunoassay to monitor Asian elephant’s FGM, identifying the effect of environment and exposure time on FGM level and enhancing hormone metabolite storage method using solid-phase extraction cartridges. In addition, faecal parasitology will be explored as possible indicators for environment and animal’s health. The interpretation of FGM levels will be thus

supported with data from GPS tracking, habitat, DNA and parasitology. MEME is a joint project between university researchers and the Malaysian wildlife authorities and the results of this study will be used to influence management policies for the conservation of Malaysian elephants.

A next-generation sequencing approach to genotyping the Tasmanian devil

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The Tasmanian devil (*Sarcophilus harrisi*) has suffered recent drastic population declines due to a rare form of transmissible cancer, devil facial tumour disease (DFTD). In less than 20 years DFTD has wiped out 85 % of the devil population, threatening its survival in the wild (MCCALLUM *et al.*, 2007). An insurance population has now been established to prevent extinction of the species with the goal of maintaining 95 % of wild genetic diversity in captivity for 30 years (JONES *et al.*, 2007). After this time extinction in the wild is predicted to occur or a vaccine may be developed, allowing reintroduction to the wild of captive bred animals. For reintroduction to be successful it is essential that genetic diversity in the captive population is maximised and wild behaviours are maintained. With genetic diversity being low in the devil, traditional markers have often lacked the discrimination required to conclusively determine pedigrees, vital for appropriate captive management. We have used a next-generation sequencing approach to develop a new genotyping assay to assess the captive population of Tasmanian devils. We have whole genome sequences from nine Tasmanian devils and have compared these with the Tasmanian devil reference genome (WTSI version 7.0) to identify regions of high polymorphism. We have designed amplicons targeting single nucleotide polymorphisms (SNPs) in regions expected to be involved in neutral as well as adaptive variation. In total, we currently have sequences covering around 100 Kb of the devil genome and aim to include more genomic regions to complete the assay. Targeted regions include genes involved with immune response, reproduction and behaviour. We aim to incorporate this genetic data into captive breeding programmes to ensure the survival of the species and enhance the success of future reintroductions to the wild.

MCCALLUM H, TOMPKINS D, JONES M, LACHISH S, MARVANEK S, LAZENBY B, HOCKING G, WIERSMA J, HAWKINS C (2007): Distribution and impacts of Tasmanian devil facial tumor disease, *EcoHealth* **4**, 318 - 325.

JONES M, JARMAN P, LEES C, HESTERMAN H, HAMEDE R, MOONEY N, MANN D, PUKK C, BERGFELD J, MCCALLUM H (2007): Conservation management of Tasmanian devils in the context of an emerging, extinction-threatening disease: devil facial tumor disease. *EcoHealth* **4**(3), 326 - 337.

Back from the brink: translocations, bottlenecks and functional genetic diversity in the Seychelles warbler

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The maintenance of genetic diversity is a global conservation priority (MCNEELY *et al.*, 1990). Populations at risk of extinction are often small in size and suffer genetic consequences such as loss of functional diversity and inbreeding depression which can further increase this risk (CHARLESWORTH and CHARLESWORTH, 1987). Diversity at functional loci such as the major histocompatibility complex (MHC) is critical for both current survival and long-term evolutionary potential. However, little is known about how population-level processes such as bottlenecks or conservation-driven translocations affect functional genetic diversity. We study the Seychelles warbler (*Acrocephalus sechellensis*), an endemic island passerine with a model conservation history, to investigate the effects population-level processes have on genetic diversity in the wild. We use a combination of longitudinal population sampling, museum specimens, neutral molecular markers and MHC data to reconstruct the population history (SPURGIN *et al.*, 2013) and investigate potential loss of genetic diversity during translocations. These data will help us better understand the impact of historic and contemporary fluctuations in population size and subsequently enable us to improve future conservation management decisions for such species.

CHARLESWORTH D, CHARLESWORTH B (1987): Inbreeding depression and its evolutionary consequences. *Annu Rev Ecol Sys* **18**, 237 - 268.

MCNEELY JA, MILLER KR, REID WV, MITTERMEIER RA, WERNER TB (1990): Conserving the world's biological diversity. International Union for Conservation of Nature and Natural Resources.

SPURGIN LG, WRIGHT DJ, VAN DER VELDE M, COLLAR NJ, KOMDEUR J, BURKE TA, RICHARDSON DS (2013): Museum DNA reveals a drastic and recent bottleneck in the Seychelles warbler. Submitted manuscript.

The impact of artificial selection on the genetic variation during horse domestication

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Although modern domestic horses (*Equus ferus caballus*) show a huge diversity in their maternally inherited mitochondrial DNA they have nearly no variation at their paternally inherited Y chromosome. In contrast, pre-domestic stallions displayed a formidable number of paternal lineages. The decline and disappearance of these lineages is addressed by screening a recently discovered set of SNPs located at the Y chromosome in a broad set of samples ranging from pre-domesticated via early domesticated up to medieval stallions from different Eurasian regions. Using the same sample set, I also investigate a set of coat colour-associated genes considering the fact that the occurrence and the number of coat colour phenotypes are valuable indicators for domestication and breed formation.

This interesting desert shrew: pups call like adults, and adults vibrate

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In most mammals, an ontogenetic growth of sound-producing structures results in lower- frequency calls of adults compared to juveniles. From June to August 2011, we examined 39 piebald shrews (*Diplomesodon pulchellum*) from 11 litters, kept in Moscow Zoo, for ontogeny of body and acoustic variables from birth to maturity at 24 days, i.e. the age of separation from their mothers. Body mass, body measures and acoustic recordings (Fostex FR-2LE with Sennheiser K6-ME64, frequency range up to 24 kHz and ultrasonic Pettersson D 1000X, frequency range up to 350 kHz) were taken every two days. With Avisoft SasLab Pro we analysed spectrographically 3,689 calls, taken uniformly for litters and ages. In addition, we analysed 640 calls from 25 adults, recorded during male-male, male-female and female-female interactions. From the 1st to the 24th day, body mass increased from 0.94 ± 0.27 to 7.51 ± 1.29 g, body length from 25.4 ± 2.3 to 62.43 ± 3.17 mm. Vocal repertoire comprised the same nine call types in young and seven in adults. Audible location clicks, not exceeding 15 kHz, were usual in young and very rare in adults. All calls were audible; no ultrasonic click was found. But we documented body vibration of adults (5 males, 6 females), placed on a drum membrane. The airborne waves of the vibratory drumming were digitally recorded and then analysed spectrographically. The mean frequency of vibration was 160.5 Hz. The frequency and period of vibration were similar to parameters of shrews loud screech calls (159.4 Hz). The body vibration was not related to thermoregulation, hunger-related depletion of energy resources or fear, as we tested well-fed, calm animals at warm ambient temperatures. We hypothesise, that in the solitary, nocturnal, digging desert piebald shrew, body vibrations may serve for seismic exploration of substrate density, to avoid energy-costly digging of packed sand for burrowing and foraging.

Contrary to expectances, the fundamental frequency of tonal squeaks was not reduced across ages of young and in adults. Moreover, the fundamental frequency and pulse rate of pulsed screeches even increased with age. Therefore, piebald shrews represent another mammalian species (in addition to ground squirrels, sea otters and bats), with lack of the ontogenetic decrease of frequency from pups to adults.

Supported by RFBR grant 12-04-00260.

Complete mitochondrial genome of wild aurochs (*Bos primigenius*) reconstructed from ancient DNA

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Extinct aurochs (*Bos primigenius*), accepted as the ancestor of domestic cattle, was one of the largest wild animals inhabiting Europe, Asia and North Africa. The gradual process of aurochs extinction finished in Poland in 1627, were the last recorded aurochs, a female, died. Some aspects of cattle domestication history and the distribution of aurochs genetic material among modern cattle breeds still remain unclear. Analyses of ancient DNA (aDNA) from bone sample deliver new genetic information about extinct wild aurochs as well as modern cattle phylogeny. DNA was extracted from a fragment of aurochs named PWA (Polish Wild Aurochs) fossil bone found in the Pisz Forest, Poland. The sample was radiocarbon-dated to about 1500 yBP. The aDNA was used for Whole Genome Amplification in order to form a DNA bank. Aurochs mitochondrial DNA sequences were amplified using sets of 41 primers overlapping the whole mtDNA, cloned and sequenced. The sequence of the whole mitochondrial genome was reconstructed and deposited in GenBank [Acc.no. JQ437479]. Based on the phylogenetic analysis that involved 62 nucleotide sequences of mtDNA: three sequences of haplotype P (including the sequence of the analysed PWA individual), seven sequences of each haplotype Q, seven sequences of each haplotype R, six sequences of I, 37 sequences of five haplotypes and suphaplotypes of macro-haplogroup T and one mtDNA sequence of wisent, a phylogenetic tree was created. The tree clearly shows that the mtDNA sequence of the analysed PWA individual belongs to haplogroup P. In the course of the comparative mtDNA analysis we identified 30 nucleotide positions for haplogroup P and nine unique PWA differences compared to the two remaining haplotype P representatives. Our analysis provides the next step to the reconstruction of the demographic history of this extinct but exciting species.

Habituation to anthropogenic nuisance of European rabbits along a rural-urban gradient

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Once common in Germany and representing a popular game species, population densities of the European rabbit (*Oryctolagus cuniculus*) in rural areas are declining at an alarming pace. At the same time, the species reaches surprisingly high population densities in urban and suburban areas. Here, rabbits often cause wildlife-human conflicts, resulting in population management (i.e., hunting). Detailed knowledge about potential differences in population dynamics and habitat use between urban and rural populations is necessary to successfully manage rabbit populations in the long-term. We asked whether the degree of urbanity is indeed a predictor of rabbit and burrow densities in Frankfurt am Main in Germany and its hinterland. We further radio-tracked rabbits in downtown Frankfurt and at a park site situated in the suburban periphery. Additionally, we determined flight initiation distances of rabbits along the rural-to-urban gradient to uncover potential habituation to human disturbances.

We found a positive correlation between rabbit (or burrow) density and the degree of urbanity, while flight initiation distances became significantly shorter with increasing urbanity. Moreover, we found the smallest home range sizes ever reported for European rabbits in our urban and suburban study populations. We argue that altered habitat conditions are the major reason for why rabbits became more abundant along the rural to urban gradient and exhibit smaller home ranges. Heterogeneous habitat structures arising from the diverse mosaic of buildings, parks and gardens in cities meet the habitat requirements of the European rabbit by providing sufficient food and shelter in close proximity. In contrast, rural areas in Germany are increasingly characterised by homogenous land-use patterns, leading to consolidated, open landscapes. Also, a more constant food supply, milder microclimate as well as lower predation and hunting pressures are known to positively affect population densities of wild animals in urban and suburban environments.

Our data suggest that urban habitats will play an important role in the future conservation of the European rabbit in Germany. Ongoing studies into population genetics, population dynamics and health status of the examined rural, urban and suburban rabbit populations aim to provide additional insights into the adaptability of this mammal to urbanisation.

Expression of steroidogenic enzymes in different *corpora lutea* stages of pregnant and pseudopregnant Iberian lynx (*Lynx pardinus*)

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Since the Iberian lynx (*Lynx pardinus*) is specified as critically endangered by the IUCN, a captive breeding programme was initiated in 2002 with the final goal of reintroduction. For two female lynxes from captive breeding centres in Spain and Portugal, Saliega (11yr) and Azahar (9yr), a permanent gonadectomy was medically recommended. Seven days after natural mating an ovariohysterectomy was performed. Oviducts were flushed to obtain embryos. In one female, early morulae indicated for pregnancy (PR), whereas in the other animal unfertilised oocytes were found (pseudopregnancy – PP). On each ovary, two groups of *corpora lutea* (CL) were characterised: fresh (recent ovulation) and old (persistent CL of previous years). In this study, we measured mRNA expression of steroidogenic acute regulatory protein (StAR), cytochrome P450 oxidases and hydroxy steroid dehydrogenases in each obtained CL by Real Time PCR.

Comparing enzyme expression in fresh CL of PP and PR, no differences were detected, what is not surprising for the preimplantation stage of pregnancy. For StAR and CYP11A1, expression was significantly higher in old compared to fresh CLs, revealing that CL of previous cycles are still capable for *de novo* steroidbiogenesis even in a much higher extent than in the freshly formed CLs. CYP19A1 showed also significantly higher expression in old CLs. Unexpectedly, the expression in old PP CLs was higher than in old PR CLs. The expression of CYP19A1 was not in line with intraluteal oestradiol (E2) levels, with concentrations 20 fold higher in fresh compared to old CLs. This may be due to residual E2 of follicle cells still detectable in freshly ovulated CLs. CYP19A1 expression was also not related to serum E2 levels, pointing to a local intraluteal action of E2. Noteworthy, only HSD3B1 expression was significantly higher (up to 40 fold) in fresh CLs compared to old CLs. However, these differences in expression were also not reflected by intraluteal progesterone (P4) concentrations, being identical within the four groups, but were supported by increasing P4 levels in serum. We suppose an immediate secretion of synthesised P4 into the blood flow. Concluding, our analysis revealed that expression of steroidogenic enzymes significantly differs between freshly ovulated and physiologically persistent (old) CLs in the Iberian lynx. The regulation of steroidbiogenesis seems to occur mainly via HSD3B1 expression.

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