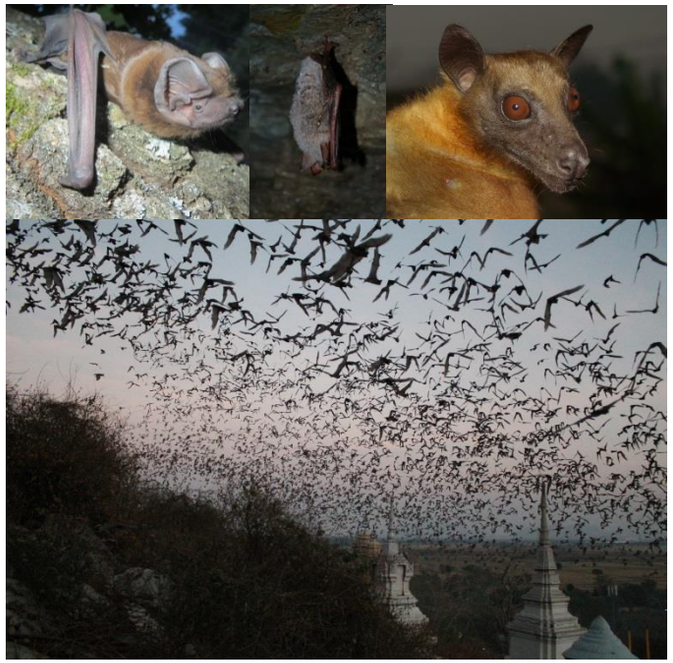
5th International Berlin Bat Meeting: Are bats special?



Berlin,
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5th International Berlin Bat Meeting: Are bats special?

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FOREWORD

Bats are outstanding among mammals in various ways. For example, they are the only mammalian taxon capable of powered flight. It has been shown that they are host of the highest number of pathogens within Mammalia most probably due to a qualitative and quantitative different immune responses compared to other mammals. Longevity of bats is exceptional and sensory abilities of bats, such as echolocation, have been the focus of decades of research. Yet, is there a unifying mechanisms underlying these traits? **Are bats special?** If yes, why are they special? What are the evolutionary drivers of key life-history traits of Chiroptera?

We have invited you to attend the **5th International Berlin Bat Meeting** (IBBM) to address and discuss all these questions. This conference is part of a series of topical meetings that is organized by the batlab of the Leibniz Institute for Zoo and Wildlife Research (www.batlab.de). Past conferences have focused on a variety of themes, such as bat migration (1st IBBM in 2009), bats and infectious diseases (2nd IBBM in 2010), bats in the Anthropocene (3rd IBBM in 2013) and movement ecology of bats (4th IBBM in 2015). We hope that you will find your visit to this conference and also to Berlin stimulating and pleasant.

This volume contains the contributions to the **5th IBBM**. The conference brings together more than 300 scientists and students from 33 countries with diverse and complementary backgrounds, such as researchers from universities and non-university research institutions, consultants, members of national and international non-governmental organizations and members of federal and governmental authorities. Oral and poster presentations cover a wide variety of topics related to traits which make bats unique among mammals. Ultimately, the meeting would like to foster an exchange of ideas, introduce new methods and concepts and aim at searching for unifying mechanisms underlying some of the outstanding traits for which bats are well known.

The first section of this volume contains the abstracts of invited plenary speakers, followed by the abstracts of the 8 sessions. Contributions were solicited for the following topics:

- Radiation and evolution
- Bat flight
- Longevity
- Heterothermy
- Vocalizations
- Vocal learning
- Immunity and pathogens
- Conservation

The abstracts in this volume are organized according to sessions. For each session abstracts of oral and poster presentations were listed separately, according to the sequence of the speakers (oral presentations) or chronologically (session, date of

receipt, poster presentations). All abstracts were printed as submitted. To help you find an abstract of interest we have included an index of authors.

We thank Stefanie Lenz, Karin Grassow and Sven Kühlmann for their significant contribution to the organization of this conference. We are grateful to the plenary speakers and chairpersons for their help in making the program highly attractive. We also thank Steffen Berthold, Dagmar Boras, Doris Fichte, Marcus Fritze, Lilith Johannsen, Olga Heim, Yvonne Klaar, Kseniia Kravchenko, Cecilia Kruszynski, Johanna Laß, Linn Lehnert, Oliver Lindecke, Anissa Otto, Katja Pohle, Manuel Roeleke, Julia Scholl, Steven Seet, Anne Seltmann, Sara Troxell, Wolfgang Tauche and Silke Voigt-Heucke for all their assistance in the preparation of the conference and its scientific program. We are very grateful to the session organizers in putting together the program of their sessions. Finally, we are very grateful to the *German Research Council* (Deutsche Forschungsgemeinschaft) for supporting the conference financially, to *Eurobats* for general support of the meeting and financial support of selected speakers from East European countries. We would also like to draw your attention to the companies that display their products in brochures or at their stands to the participants of the 5th IBBM. We thank the *Federal Institute for Risk Assessment* (Bundesinstitut für Risikobewertung), the *Museum of Natural History in Berlin* (Museum für Naturkunde Berlin) for kindly providing the facilities for our conference and the banquet, respectively, and to the *Leibniz Institute for Zoo and Wildlife Research* (www.leibniz-izw.de) for general support.

We hope that you will enjoy the scientific and social program of this meeting.

Berlin, February 2017

Christian C. Voigt and *Gábor Á. Czirják*

PLENARY TALKS

Plenary

Bats are special and we should care: the genomic bases of bat's extraordinary adaptations

TEELING EMMA[1]

[1] University College Dublin, Centre for Irish Bat Research, School of Biology and Environmental Science, Belfield, Dublin 4, IRELAND; emma.teeling@ucd.ie

Living mammals (~5,400 species) originated approximately 217-238 Million Years Ago, inhabit every biome on Earth, and are arguably one of the most phenotypically diverse group of vertebrates. From the largest, 170 ton blue whale, to the smallest, 2 g flying, echolocating bumblebee bat, the huge diversity and extraordinary adaptive radiations in mammalian form and function have fascinated evolutionary biologists for centuries. Increasingly, this environmental niche specialization is reflected in animal genomes and studying the molecular mechanisms that are responsible for this vast diversity has allowed some of the greatest insights into the functioning and evolution of our own genome. Exploration and harnessing of this vast diversity is now possible due to the development of state-of-the-art NGST which enable the 'parallel' sequencing of up to one billion base pairs per day at a comparably low cost. Bats represent one fifth of all mammalian diversity and arguably show some of the most spectacular of all mammalian adaptations (e.g. flight, echolocation). Phylogenomic studies have revolutionized our understanding of the evolutionary history of this order and bats' position within the mammal tree of life. The underlying genomic bases for bats' unique adaptations such as echolocation, flight, viral tolerance and extraordinary longevity are now being uncovered. The genomic revolution as provided great insight into the evolution of bats and the molecular bases of their unique adaptations, this will be discussed.

Plenary

Are bats birds with respect to flight?

HEDENSTRÖM ANDERS[1]

[1] Department of Biology, Evolutionary Ecology, Lund University, SWEDEN, anders.hedenstrom@biol.lu.se

Bats and birds are the two extant vertebrate groups capable of powered flight, but they evolved their ability to fly independently from each other. As a group birds are older than bats, but the age of bats and modern birds is similar at about 65 million years. Morphologically bats and birds differ in wing design and flight muscle arrangement, but are they more or less functionally equivalent? The largest birds are one magnitude larger than the largest bats, which has been attributed to physiological constraints. The number of bird species is also one magnitude more than bats. Considering that the same physical laws and properties of the atmosphere govern flight in bats and birds, a comparison of flight performance between bats and birds may shed light on the efficacy of evolution. Are bats occupying different adaptive peaks in the aero-ecological landscape than birds? It has been argued that birds are more energy efficient flyers than bats, being better suited for fast flight and even migration, while bats are better adapted for slow and maneuvering flight. Echolocation in bats often requires protruding ears to record echoes, which may compromise aerodynamic performance. Similarities and differences with respect to flight performance will be reviewed and evaluated.

Plenary

Causes and consequences of bat longevity

WILKINSON GERALD S. [1]

[1] Department of Biology, University of Maryland, College Park, MD 20742 USA

The evolutionary theory of aging predicts that life span should decrease in response to the amount of mortality caused by extrinsic sources. Bats live an average of four times longer than other placental mammals of similar body size. Some of their unusual longevity can be attributed to a relatively slow life history in which most species give birth to a single offspring each year. Nevertheless, considerable variation in lifespan is present among bats, which is not explained by reproductive rate. In this talk I will use comparative data to evaluate a number of potential extrinsic factors that could influence risk of mortality and explain some of the remaining variation in lifespan among bats, such as migration, hibernation, roosting site, diet, sexual conflict – as estimated by sexual dimorphism, and sociality. I will also consider the possibility that various intrinsic factors, such as reduced cancer risk or specialized cognitive and sensory ability, may have arisen as a consequence and then further contributed to the unusual longevity of some species.

Plenary

Is Bat Thermoregulation Special? Insights from Hibernating Bats in Central Canada

WILLIS CRAIG[1]

[1] Department of Biology, University of Winnipeg, 515 Portage Ave Winnipeg MB R3B 2E9 CANADA, c.willis@uwinnipeg.ca

Hibernation energetics can be considered in terms of three phases: a preparatory phase of positive energy balance before winter; a period of negative energy balance during hibernation proper throughout winter; and an emergence/recovery phase when positive energy balance is restored in spring. Most of what we know about all three phases is based on rodents (e.g., chipmunks, ground squirrels, marmots). Bats differ from rodent hibernators in important ways that could make bats special in terms of their winter energetics. In contrast to hibernating bats, rodent hibernators construct their own burrows, hibernate solitarily or in only small groups, use nesting material for insulation and often store food. In recent years, my group has been studying little brown bats (*Myotis lucifugus*) to test the broad hypothesis that similar selection pressures influence all three phases of hibernation for rodents and bats despite dramatic differences in their hibernation ecology and behavior. We have combined temperature telemetry, infrared video and passive transponders (PIT tags) to understand how individual or group characteristics (e.g., sex, personality, social structure), and environmental factors (e.g., weather, winter duration) affect hibernation energetics and phenology. In our study populations, sex differences in the timing of reproductive investment have a pronounced influence on winter energy expenditure and the timing of spring emergence, while individual behavioral traits (i.e., personality) appear to influence pre-hibernation fattening and hibernation energetics. Local weather and interactions among individuals within the hibernaculum influence the timing of arousals from torpor but only during late hibernation. In general, little brown bats from central Canada do appear special in terms of their capacity for extreme energy savings during hibernation relative to rodent hibernators. However, similar energetic and ecological tradeoffs appear to influence thermoregulation during hibernation, and the phenology of hibernation, for bats and rodents. Our findings are important for understanding the ecology of temperate-zone bats in general and have implications for understanding and potentially mitigating white-nose syndrome.

Plenary

Auditory scene perception by echolocation in bats

MOSS CYNTHIA F. [1]

[1] Johns Hopkins University, Psychological and Brain Sciences, 3400 N. Charles Street, Baltimore, 21218, USA

Echolocating bats have evolved a spatial acoustic imaging system, which they exploit to forage, avoid obstacles and orient in the dark. Bats transmit brief, intense, ultrasound signals and process information contained in returning echoes to determine the position, size and shape of reflecting objects. Key features of bat echolocation enable 3D target localization and tracking: 1) high frequency, directional sonar signals, adapted to the bat's environment and behavioral task; 2) high frequency, directional hearing, with mobile ears; and 3) high temporal resolution to register the time of echo arrival, the bat's cue for target distance. Central to echolocation is adaptive feedback between action and perception. Specifically, the bat adjusts the feature of its sonar signal duration, repetition rate, spectral content and beam aim in response to spatial information extracted from echoes. The sensorimotor feedback system contributes directly to the bat's perception of objects in a natural sonar scene.

Plenary

Is the immunology of bats particularly potent?

BAKER MICHELLE L. [1]

[1] CSIRO, Australian Animal Health Laboratory, Geelong, Victoria, AUSTRALIA, Michelle.Baker@csiro.au

Bats are natural reservoir hosts to a number of emerging and re-emerging zoonotic viruses including rhabdoviruses, henipaviruses, coronaviruses and filoviruses. Although many of the viruses carried by bats are highly pathogenic to other mammals, they rarely result in clinical signs of disease in bats. To understand the nature of the immune response of bats to viral infections, we have developed the Australian pteropid bat, *Pteropus alecto*, the natural reservoir of Hendra virus as a model species for studying virus-host interactions. Genomic and transcriptomic analysis have provided evidence that bats have all of the major components of the immune system present in other species of mammals. However, the long co-evolutionary history of bats with viruses has likely played an important role in shaping their immune system with evidence from genomic data for differences in genes associated with the innate immune system of bats. To further examine the role of the innate immune system, we have focused on the interferon (IFN) response which represents the first line of defence following viral infection. Our results provide evidence for the constitutive activation of the innate immune response of pteropid bats with heightened activation of IFNA and downstream IFN stimulated genes in unstimulated bat tissues and cells. The constitutive activation of the IFN system has not been described in any other species and may allow bats to respond to viral infection more rapidly compared to other species. The ability of bats to maintain a constitutively active immune response in the absence of adverse side effects associated with chronic immune activation in other species is striking and provides evidence for unique differences in the functional activity of the immune system of bats.

Plenary

Are bats special as conservation targets?

RACEY PAUL A. [1]

[1] Centre for Ecology and Conservation, School of Biosciences, University of Exeter, Cornwall Campus, Penryn, Cornwall, TR10 9EZ, UK, p.a.racey@exeter.ac.uk

Those distinctive features of bats which may have particular relevance for their conservation are flight, echolocation, heterothermy, roosting ecology and synanthropy. Adaptability of flight and foraging behaviour is a key issue as the pace of landscape change accelerates. The fact that some bat species can fly in clutter has apparently resulted in forest-dependency and threats to these forests will have implications for bat conservation. Heterothermy has enabled the most extraordinary reproductive adaptations, unique among mammals, particularly a gestation length that depends on environmental factors instead of fetal genotype. Some species may take advantage of these adaptations in response to climate change – others may find them disadvantageous. Bats have the largest roosting aggregations among mammals and although these may confer advantages in confusing non-human predators, they may also facilitate disease transmission and attract hunters. Roosts are however the most tangible conservation targets – cave roosts by gating and for synanthropic species by maintaining access to roosts in buildings and where appropriate providing artificial roosts.

ORAL PRESENTATIONS

SESSION I: BAT EVOLUTION AND RADIATION, REVEALED BY NGS

Chairs: Stephen Rossiter, Emma Teeling

Conflicting evolutionary histories of the mitochondrial and nuclear genomes in New World *Myotis*

PLATT II ROY N. [1], FAIRCLOTH BRANT C.[2], SULLIVAN KEVIN A.M.[1], KERIAN TROY[3], GLENN TRAVIS C.[3], VANDEWEGE MIKE[1], LEE TOM[4], BAKER ROBERT[1], STEVENS RICHARD D.[5], RAY DAVID A.[1]

[1] Biological Sciences, Texas Tech University, Lubbock, USA
[2] Biological Sciences, Louisiana State University, Baton Rouge, USA
[3] Environmental Health Science, University of Georgia, Athens, USA
[4] Natural Resource Management, Texas Tech University, Lubbock, USA
[5] Department of Biology, Abilene Christian University, Abilene, USA

The diversification of *Myotis* into more than 100 species in just a few million years is one of the most extensive mammalian radiations available for study. Efforts to understand relationships within Myotis have primarily utilized mitochondrial gene markers and the few studies have used nuclear markers resulted in trees that lack resolution. As a result, our understanding of relationships within *Myotis* is biased towards a set of phylogenetic markers that may not reflect the true species tree. To resolve this issue we sequenced the full mitochondrial genomes of 37 representative *Myotis*, primarily from the New World, in conjunction with targeted sequencing of more than five thousand ultraconserved elements (UCEs). We explored various concatenation and summary phylogenetic methods as well as combinations of markers based on informativeness or levels of missing data. Of the 293 phylogenies generated from the nuclear UCE data, all are significantly different from phylogenies inferred from the mitochondrial genomes. Several factors can drive such conflic including, but not limited to, horizontal gene transfer, hybridization, and lineage sorting. Quartet frequencies indicate that around half of all UCE loci conflict with the estimated species tree. This suggests that *Myotis* genomes experienced massive amounts of incomplete lineage sorting, likely during the early stages of the radiation. Mitochondrial genomes, because they evolve as single loci, are likely to have been incompletely sorted along with nuclear loci, meaning that phylogenies inferred using this locus probably do not reflect the true species tree. Based on these results, we re-examine the evolutionary history of *Myotis* to better understand the phenomena driving the unique nuclear, mitochondrial, and biogeographic histories.

Selection, gene expression, and dietary divergence in Phyllostomidae

POTTER JOSHUA[1], DAVIES KALINA, TSAGKOGEORGA GEORGIA, WARREN KIM, YOHE LAUREL, LIM BURTON, DÁVALOS LILIANA, ROSSITER STEPHEN

[1] School of Biological and Chemical Sciences, Queen Mary University of London, London, UK; joshua.potter@qmul.ac.uk

Across all mammals, bats offer a candidate for the single family with the most-striking dietary diversification and accompanying radiation of adaptive phenotype: the Phyllostomidae (New World leaf-nosed bats). This large and varied family of Neotropical bats has members belonging to a number of specialist dietary ecotypes including insectivory, frugivory, nectarivory, vertebrate predation, sanguivory, as well as facultative generalism and omnivory. Molecular phylogenetics reveals a clear correlation between lineage diversification and dietary shifts, including what appears to be the dual origin of nectarivory within the family, with convergent morphology for flower feeding.

A number of candidate gene studies have linked nutritional adaptation in specific bat lineages to inferred signals of positive or relaxed selection on diet-associated genes. To determine the extent to which the radiation of phyllostomid bats has involved molecular adaptation in dietary genes at a genome-scale, we used high-throughput sequencing to generate transcriptomic data from 54 species, including 29 phyllostomids, and screens of selection in dietary orthologues across the group. We also hypothesised that adaptation to new diets might also be evident at the level of gene expression, and thus performed individual RNA-seq on tissue-specific samples from 15 species (primarily phyllostomids), including key dietary tissues such as stomach, gut, pancreas, kidney and gall bladder.

Selection tests performed on >1000 loci revealed, among other findings, positive selection on genes associated with facial morphology in the ancestral lineage of Phyllostomidae, and on carbohydrate metabolism genes in nectar feeding phyllostomids. Analyses to assess whether patterns of gene expression across tissues reflect dietary specialisation are ongoing, and will be discussed. In time, we hope to determine if patterns of codon selection and patterns of gene expression show similar correlation to lineage and diet, thus providing the framework for a synthesis between sequence evolution and regulation as joint mechanisms underpinning adaptive radiation.

Comparative 'auditory' and 'visual' transcriptomics in noctilionoid bats

DAVIES KALINA[1], YOHE LAUREL, DUMONT ELIZABETH, SEARS KAREN, DÁVALOS LILIANA, ROSSITER STEPHEN

[1] School of Biological and Chemical Sciences, Queen Mary University of London, London, UK; k.t.j.davies@qmul.ac.uk

Over the last 50 million years the Neotropical bat superfamily Noctilionoidea underwent an extreme adaptive radiation. During this rapid diversification, noctilionoids evolved highly divergent feeding ecologies; diets across the >200 extant species consist of nectar, fruit, insects, small vertebrates and blood. In concert with these dietary shifts, noctilionoids evolved divergent hunting strategies and sensory specializations. Hearing and vision are two key senses used by noctilionoids to locate prey. However, the utilization of the two associated sensory modalities varies widely across the superfamily. For example, some species locate prey with sophisticated high-duty cycle echolocation, and others use passive listening to detect prey-generated sound. Additionally, several species exhibit well-developed eyes that are sensitive to UV light.

Previous studies have suggested a sensory trade-off exists between echolocation and vision in bats. To further examine this assertion, we tested for molecular evidence of varying reliance on vision and hearing across noctilionoids. We assembled mRNA transcriptomes from the eyes and cochleas of ~30 bat species; representing 3 noctilionoid families and 6 outgroup species. We then estimated relative abundance of expressed genes by mapping tissue-specific short-read data against each assembly. Patterns of gene expression, estimated both across species and sensory organs, were visualized with clustering methods and heat-maps. We then constructed alignments for sensory genes (including ~100 and ~500 candidate 'hearing' and 'vision' genes, respectively), and used codon-based models to infer the presence of adaptive evolution at key branches in the noctilionoid species tree.

Our initial expression analyses suggested potential evidence of similar expression profiles in convergent sensory specialists. By combining our expression results with the presence of positive selection, we can begin to document the genetic changes that are associated with the specific sensory adaptations of the auditory and visual systems of these bats.

Olfactory receptor evolution shows association with phyllostomid dietary radiation

YOHE LAUREL R. [1], DÁVALOS LILIANA M.

[1] Department of Ecology and Evolution, Stony Brook University, Stony Brook, USA

New World Leaf-nosed bats (Phyllostomidae) occupy an enormous range of dietary niches and natural selection has shaped an array of morphological and sensory adaptations to exploit these dietary niches. However, the molecular mechanisms that allowed populations to depart from their ancestral insectivorous diet and detect novel resources, such as nectar or fruit, are unknown. Phyllostomids need to find these resources while flying in the dark, and behavioral evidence has shown the sense of smell is a critical supplement to echolocation for detecting food in a cluttered environment. Because of their reliance on olfaction, we hypothesized that the genetic machinery governing the detection of plant volatiles to also be shaped by natural selection. For example, a duplication event may have occurred prior to plant-visiting bats and undergone neofunctionalization to detect new ligands or significant duplicate retention. To test this, we sequenced the transcriptomes of the main olfactory epithelium and identified the olfactory receptor profiles in over 20 phyllostomids with divergent diets. While we predicted a large duplication event in plant-visiting bats, we identified many duplication events unique to particular bat subfamilies with unique diets. Some of these duplications occurred within groups with increased rates of speciation, and may be related to their diversification. For example, a unique cluster of olfactory receptors in subfamily OR2/13 is present only in fig-eating phyllostomids (Stenodermatinae). Stenodermatines have a significantly higher speciation rate compared to all other bats, attributed to their ability to exploit the novel dietary niche of consuming hard-fruits. This duplication of receptors that occurred prior to the divergence of stenodermatines may be connected to the diversity of olfactory receptor ligand profiles the ancestral stenodermatines explored. Our study illuminates how the evolution of olfactory receptors may have opened up novel dietary niches for bats.

SESSION II: BAT FLIGHT

Chairs: Anders Hedenström, Teague O'Mara

Metabolic rate and speed of migratory *Pipistrellus nathusii* during autumn migration

TROXELL SARA A. [1,2], HOLDERIED MARC W.[3], PETERSONS GUNARS[4], VOIGT CHRISTIAN C.[1,2]

[1] Leibniz Institute for Zoo and Wildlife Research, Department of Evolutionary Ecology, Alfred-Kowalke-Straße 17, 10315, Berlin, GERMANY; troxell@izw-berlin.de
[2] Freie Universität, Takustr. 6, 14195 Berlin, GERMANY
[3] School of Biological Sciences, University of Bristol, Woodland Road, Bristol BS8 1UG, UK
[4] Faculty of Veterinary Medicine, Latvia University of Agriculture, KI. Helamaņa 8, Jelgava 3004, LATVIA

Millions of bats migrate annually between their summer and wintering grounds, yet the speed at which bats migrate and what energetic costs they encounter are still largely unknown. Aerodynamic theory states that the relationship between metabolism and flight speed can be described as a U-shaped curve: more energy is required at slow and fast speeds than at intermediate speeds. To be efficient bats should migrate at the speed that allows them to move the greatest distance while expending the least amount of energy. This optimal speed is defined as maximum range speed (V_{mr}) and can be predicted using the theoretical models. However, these aerodynamic models were mainly constructed to predict avian flight and they are based on static models. Therefore, empirical evidence regarding the relationship between flight metabolism and flight speed in bats is absolutely necessary to verify theoretical calculations and to shed light on optimal flight speeds during bat migration.
We used the ^{13}C labeled Na-bicarbonate technique to measure flight metabolic rates of twelve *P. nathusii* in a wind tunnel at air speeds between 2 ms^{-1} and 11 ms^{-1}. Based on this relationship, we inferred V_{mr} exhibited by each individual. The theoretical expectation of a U-shaped power curve held true for 10 of the 12 individuals tested, however, our results indicated that the model-derived values for V_{mr} were overestimated when compared to values inferred from the wind tunnel measurements. We additionally measured flight speed in free-flying *P. nathusii* during autumn migration at a major migratory corridor in Latvia. Our results show an agreement between the flight speed of free-flying migrating bats and the inferred maximum range speed of bats flying in a wind tunnel, both of which are significantly lower than predicted by a theoretical model. Our results support the hypothesis that bats migrate at an energetically optimal speed.

Physiological counter-strategies of frugivorous bats to an energy-intensive lifestyle

O'MARA M. TEAGUE[1,2,3], WIKELSKI MARTIN[1,2], VOIGT CHRISTIAN C.[4],
TER MAAT ANDRIES[5], POLLOCK HENRY S.[3,6], BURNESS GARY[7],
DESANTIS LANNA M.[8], DECHMANN DINA K.N. [1,2,3]

[1] Department of Migration and Immuno-ecology, Max Planck Institute for Ornithology, tomara@orn.mpg.de
[2] Department of Biology, University of Konstanz
[3] Smithsonian Tropical Research Institute
[4] Leibniz Institute for Zoo and Wildlife Research
[5] Department of Behavioural Neurobiology, Max Planck Institute for Ornithology
[6] Program in Ecology, Evolution and Conservation Biology, University of Illinois at Urbana-Champaign
[7] Department of Biology, Trent University
[8] Environmental and Life Sciences Graduate Program, Trent University

The relationship between the energetic cost of life and how it is maintained within an ecological context is not well understood for most animals. Bats are the only mammals to actively fly and switch from a stationary resting posture to energetically expensive flapping flight in instants – a sudden burst of high energetic demands. We took a multi-pronged approach to estimate how fruit-eating bats (*Uroderma bilobatum*) manage their high-energy lifestyle fueled primarily by fig juice. We demonstrate that these bats use a novel strategy to maintain their energy-intensive lifestyle by employing miniaturized heart-rate telemetry; this method shows that heart rate is cyclically depressed from 400 bpm during typical periods of rest to less than 200 bpm, to help counteract rates as high as 900 bpm during flight. The heart rate depression we observe reduced total daily energetic expenditure by 10%. These low heart rates allow these bats to maintain a mean field metabolic rate of 46 kJ that is within predicted ranges for their body size, but with a large sustained metabolic scope of 5.4. Isotopic enrichment of exhaled carbon dioxide show that *U. bilobatum* use some of the fastest metabolic incorporation rates in flying vertebrates to support the explosive metabolic shift between rest and flight, and that they further support this high metabolic state by elevating circulating cortisol values from very low baselines to challenged values that are 10-15 times higher. This results in rapid fat turnover that exchanges 50% of their fat in 24 hours. Our data suggest that *U. bilobatum* suppress energetic expenditure at multiple physiological levels when at rest, but show enormous flexibility to fuel daily flight activity and facilitate their ecological specialization on a widely distributed, but temporally unpredictable fruit.

Foraging movements of grey-headed flying-foxes (*Pteropus poliocephalus*) roosting in Adelaide, South Australia

SÁNCHEZ CECILIA A. [1], REARDON TERRY B., BOARDMAN WAYNE S.J., ALTIZER SONIA

[1] University of Georgia, Odum School of Ecology, Athens, GA, USA, cecilia.sanchez@uga.edu

Flying-fox species occur across a large geographical area of eastern Australia, but their seasonal distribution is dictated by the variable and unpredictable availability of their preferred diet, especially eucalypt blossoms. Recently, human activities, including destruction of native habitat and planting of non-native vegetation that provides predictable foraging, have altered the distribution and foraging patterns of some flying-fox species. The consequences of this change are important for both bat and human health, given that bats harbor viruses that are transmissible to humans. In 2010, a group of grey-headed flying-foxes (*Pteropus poliocephalus)* established a permanent roost in Adelaide, South Australia, several hundred kilometers outside their previously established range. Despite facing significant juvenile mortality due to extreme heat events, the population has grown and now numbers approximately 4000. As part of a larger study to characterize the health and behavior of the Adelaide flying-fox population, we deployed lightweight GPS loggers on five *P. poliocephalus* to track their foraging movements. Loggers were programmed to record a bat's position every 30 seconds when flying and every 45 minutes when stationary, and also recorded data on acceleration, speed, and altitude. Deployments ranged from 7-12 days and resulted in 47 nights of movement data and 83000 GPS fixes. Two flying-foxes flew along a nearby river each night and fed at patches within 10 km of the roost. The other three flying-foxes foraged widely over the landscape, feeding at multiple, more distant sites. Factors that may affect foraging movement, such as weather and bat sex, age, and body condition, will be discussed. This work provides insight into a recently-established, understudied bat population and is useful both to local Adelaide stakeholders as well as other urban citizens seeking to manage the bats that share their space.

SESSION III: BAT LONGEVITY

Chairs: David Costantini, Joanna Kacprzyk

The role of proteostasis in bat's halted ageing: a comparative analysis of the efficiency of the autophagy machinery in young versus old bats

LOCATELLI ANDREA G. [1], KACPRZYK JOANNA[1], SACCHI CARLOTTA[1], STEWART GAVIN[1], TEELING EMMA C.[1]

[1] School of Biology and Environmental Science, University College Dublin, IRELAND; andreag.locatelli@gmail.com

Bats are unique mammals due to their ability to fly and extraordinary lifespans. Accumulation of damaged and misfolded proteins and organelles, leading to impaired cell function and disrupted tissue homeostasis, has been proposed to contribute to aging process. Autophagy is a mechanism mediating the clearance of dysfunctional cellular components. Decline in autophagy function occurs with ageing, whereas its stimulation has been correlated with anti-ageing effects. Flight induced high metabolic rate is linked with increased risk of oxidative stress and cellular damage. We hypothesize that to prevent these negative effects of flight, bats have evolved more efficient autophagy machinery to clear the cellular damage, consequently leading also to their extended lifespans. We tested this hypothesis using primary fibroblast cells from *Pipistrellus kuhlii.* We measured the induction of starvation induced autophagic flux in cells derived from individuals ranging from 0 years (juveniles) to aged (7+ year old). This approach allows to determine if the autophagy function is maintained as the animal age therefore contributing to the lifespan extension in bats, in contrast to age-induced autophagic flux decline observed for non-bat mammals. A non-lethal sampling method, 3mm wing membrane punches, was used to generate primary fibroblast cells from a number of individuals, imposing only minimum stress to the animal with no lasting adverse effects. The autophagic flux induction was studied by measuring the LC3II/I ratio (a well-established marker of autophagic flux) in total protein extract by Western blot. To elucidate bat specific adaptations to the proteostasis maintenance mechanisms, phylogenomic analyses of genes involved in autophagy and other proteostasis maintenance pathways were conducted.

The role of telomeres in the evolution of exceptional longevity in bats

FOLEY NICOLE M. [1], HUGHES GRAHAM M.[1], HUANG ZIXIA[1], CLARKE MICHAEL[1], PETIT ERIC[2], JEBB DAVID[1], WHELAN CONOR V.[1], JONES GARETH[3], RANSOME ROGER D.[3], KERTH GERALD[4], REBELO HUGO [3,5], RODRIGUES LUISA[6], PUECHMAILLE SÉBASTIEN J.[1,4], TEELING EMMA C.[1]

[1] School of Biology and Environmental Science, University College Dublin, IRELAND
[2] Ecologie et Santé des Ecosystèmes, INRA Rennes, FRANCE
[3] School of Biological Science, University of Bristol, ENGLAND
[4] Applied Zoology and Conservation, Zoological Institute and Museum, University of Greifswald, GERMANY
[5] CIBIO/InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos da Universidade do Porto, PORTUGAL
[6] Instituto da Conservação da Natureza e das Florestas, Lisboa, PORTUGAL

Telomere shortening with age has been reported in a variety of populations of phylogenetically diverse mammals from humans to sea lions, badgers, hyenas and chimps etc. Just nineteen species of mammals are longer lived than man given body size, eighteen of these species are bats. Bats are considered “Methusalehs” among mammals as, paradoxically given their small body size and high metabolic rate, they are exceptionally long lived. However, little is known about how telomere dynamics change with age in bats. Relative telomere length (rTL) was measured using a modified qPCR protocol originally designed for use in humans. For the first time, sampling from populations subject to long term monitoring programs, we investigate changes in rTL with age in four populations of long lived bat species: *Myotis myotis* (Maximum lifespan 37.1yrs), *Rhinolophus ferrumequinum* (MLS 30.5yrs), *Myotis bechsteinii* (21yrs) and *Miniopterus schreibersii* (22yrs). Our results show telomeres shorten significantly with age in *Rhinolophus ferrumequinum* and *Miniopterus schreibersii* but there is no significant relationship between rTL and age in either *Myotis* species. A comparative phylogenetic approach was used to determine if bat telomere maintenance genes show signs of adaptation compared to all other mammals. Data was mined from 51 mammalian genomes, including 12 bat species, using a custom mining method to maximise data from poorly annotated genomes. Codeml was used to investigate the selective pressures acting on telomere maintenance genes in bats. The Codeml analyses were automated and throughput increased through the use of a custom Snakemake pipeline. Our analysis shows that genes with functions in DNA repair are evolving differently in *Myotis* bats compared to other mammals which suggests that perhaps these bats have evolved a way to better protect and repair their telomeres.

SESSION IV: BAT HETEROTHERMY

Chairs: Yi-Hsuan Pan, Craig Willis

Blood fatty acid composition and its influence on bat resting metabolism

FASEL NICOLAS[1], GENOUD MICHEL, CLÉMENT LAURA,
MÈNE-SAFFRANÉ LAURENT, CHRISTE PHILIPPE

[1] Department of Ecology and Evolution, University of Lausanne, 1015 Lausanne, SWITZERLAND, fasel.nicolas@gmail.com

Fatty acids differ in length and unsaturation levels, which confer them varying biochemical and physiological properties. Polyunsaturated fatty acids (PUFAs) increase the fluidity of cellular membranes, affect trans-membrane proteins and/or improve fat mobilization. The relation between the basal metabolic rate and PUFA concentration in cellular membranes is still debated. However, it was repeatedly shown that PUFAs are crucial for heterotherms. Higher ω-6 PUFA concentrations were related to lower minimum resting metabolic rates and body temperatures, and to longer torpor bouts. These adaptions further lead to lower body mass losses. The role of ω-3 PUFAs on torpor is less clear, however, with recent studies also showing negative effects. To fulfill their needs for PUFAs, insectivorous bat species rely on their prey, whose lipid compositions generally depend on the larval habitat. In contrast to other terrestrial mammals, bats can hunt flying insects with aquatic larval stages. These insects offer more ω-3 PUFAs than terrestrial ones, richer in ω-6 PUFAs. Insectivorous bats also show extreme physiological fluctuations, shifting from flight to torpor metabolism. Surprisingly, the link between the fatty acid composition and the metabolism has rarely been investigated in bats. In this study, we measured the spring resting metabolic rate of *Myotis daubentonii* and *Nyctalus noctula* at and below their thermal neutral zone. We related these measures to the proportion of PUFAs and to the ratio of ω-6 to ω-3 PUFAs in the red blood cells and blood plasma. The ω-6 to ω-3 PUFA ratios of both plasma and red blood cells were higher in *N. noctula*, as expected due to the diet of *M. daubentonii*, mostly composed of aquatic insects. Our results did not, however, support a negative role of ω-6 to ω-3 PUFA ratios on torpor resting metabolic rates. The varying but important proportion of aquatic insects in the bats' diet may have counter-selected the negative effects of ω-3 PUFAs on torpor, observed in other species.

Using Multidisciplinary Approaches to Explore Molecular Mechanism and Evolution of Bat Hibernation

PAN YI-HSUAN[1]

[1] Laboratory of Molecular Ecology and Evolution, School of Life Science, East China Normal University, Shanghai, CHINA

Some bat species hibernate to survive cold weather. Mammalian hibernation is the repeated cycles of torpor and arousal, in which fat is consumed as the main energy source. Understanding the mechanisms by which hibernators control their metabolism during hibernation to overcome stress conditions would aid in the prevention or treatment of human diseases. To learn the molecular mechanism and evolution of bat hibernation, we compared liver and brain tissues of bats of different hibernation sates using systematic and evolutionary analyses. Our previous findings suggested that phenylalanine and tyrosine catabolism is activated by torpid bats for metabolic detoxification and that mitochondria play critical roles in brain activities of torpid *Myotis ricketti* bats. We also found that the gnomes of mammalian hibernators is more accessible to the regulation of some transcription factors, such as peroxisome proliferator-activated receptor alpha (PPARα). PPARα regulates the expression of many genes involved in lipid metabolism. Although additional mechanisms and macromolecules in co-regulation of bat hibernation remain to be uncovered, our studies shed the light on multiple protection strategies adopted by small mammals against cold environments.

Deeply torpid bats can change position without elevation of body temperature

BARTONIČKA TOMÁŠ[1], BANDOUCHOVA HANA[2], BERKOVÁ HANA[4], BLAŽEK JÁN[1], LUČAN RADEK[3], HORÁČEK IVAN[3], MARTÍNKOVÁ NATÁLIA[4,5], PIKULA JIRI[2], ŘEHÁK ZDENĚK[1,6], ZUKAL JAN[4]

[1] Department of Botany and Zoology, Masaryk University, Brno, CZECH REPUBLIC
[2] Department of Ecology and Diseases of Game, Fish and Bees; University of Veterinary and Pharmaceutical Sciences, Brno, CZECH REPUBLIC
[3] Faculty of Science, Charles University in Prague, Prague, CZECH REPUBLIC
[4] Institute of Vertebrate Biology, Academy of Sciences of the Czech Republic, Brno, CZECH REPUBLIC
[5] Institute of Biostatistics and Analyses, Masaryk University, Brno, CZECH REPUBLIC
[6] Faculty of Education, Masaryk University, Brno, CZECH REPUBLIC

Because body temperature is tightly coupled to physiological function, hibernating animals entering deep torpor are typically immobile. We analysed thermal behaviour and locomotory activity of hibernating greater mouse-eared bats *Myotis myotis* and found two types of movement behaviour related to body temperature, i.e. movement at normal body temperature and at low body temperatures (Tblow; < 5 °C). First Tblow movements appeared at the beginning of March and often occurred during long torpor bouts. In most cases, Tblow events represented slow displacements between clusters of bats. In several cases, however, departure or arrivals from and into clusters was also recorded without any elevation in body temperature. Distance travelled, flight duration and speed of locomotion during Tblow events was lower than in normothermic events. Such behaviour could allow bats to save energy long-term and prolong torpor bouts. Tblow movement in torpid bats significantly changes our understanding of basic hibernation principles and we strongly recommend further studies on the subject.

SESSION V: BAT VOCALIZATIONS

Chairs: Holger Goerlitz

A new on-board recording tag for studying echolocation behavior in free-flying bats in the wild

STIDSHOLT LAURA[1], JOHNSON MARK, BEEDHOLM KRISTIAN, JAKOBSEN LASSE, BRINKLØV SIGNE, TEGLBERG MADSEN PETER

[1] Zoophysiology, Department of Bioscience, Aarhus University, Laura.Stidsholt@Bios.Au.Dk

To quantify the sensory information that echolocating bats extract from their surroundings to guide their navigation and foraging behavior, it is necessary to record the echoic scene from the perspective of the bat. However, due to technological constraints on what can be attached to a small and flying bat, most knowledge on echolocation has been based on recording the outgoing calls, and analyzing how these calls are adapted to different behaviors. To meet this challenge, we have developed a 2.6 gram archival tag that can be attached to the back of a bat. It features an ultrasonic microphone with a sampling rate of 250 kHz enabling full bandwidth recordings of the outgoing calls and the incoming echoes, while triaxial accelerometers permit recordings of the movement in three dimensions. In this study, we have tested the tag on a European Noctula (*Nyctalus Noctula*) during a landing exercise in a flight room. As the bat weighed between 26 to 30 grams during the experiments, the tag did not exceed 10 % of the body weight, and the bat was able to fly with no visual effects on its flight maneuvers. Our results showed that the outgoing calls recorded off-axis from the back of the bat could be reconstructed to represent on-axis calls by compensating with a back-to-front transfer function. In addition, echoes reflected off the walls up to a distance of ten meters and off a landing platform (TS = -10 dB @ 10 cm) up to four meters were recorded. The accelerometer data provided a categorization of behavioral events as flying, scratching and eating, but only flights could be reliably distinguished without video or audio confirmation. The flights were identified based on accelerations above $20 m/s^2$ caused by the up and down strokes, while the wing-beats were determined from the frequency of the accelerations. For the first time, we have developed an on-board tag that can record the echoic scene of the bat concomitant with the movement in three dimensions. This tag can be attached to the back of free-flying bats echolocating in the wild and may therefore substantially aid our understanding of just how special echolocation in bats is.

The bat-moth arms race goes on: Barbastelle bats lead through the combination of low-intensity echolocation and intensity compensation

LEWANZIK DANIEL[1], GOERLITZ HOLGER R.

[1] Acoustic and Functional Ecology Research Group, Max Planck Institute for Ornithology, Eberhard- Gwinner-Str. 11, 82319 Seewiesen, GERMANY

The predation pressure of insectivorous bats on their insect prey led to the evolution of ears in several insect taxa. Eared moths perform evasive flight manoeuvres when they hear bat echolocation calls, thereby decreasing their risk of predation. Yet, barbastelle bats, *Barbastella barbastellus*, are able to capture eared moths in large quantities. We hypothesized that barbastelles lower the intensity of their anyway low-intensity search calls while closing in on their prey, such that the intensity at the moth's ear remains below the moth's hearing threshold until capture and the moth fails to elicit its life-saving evasive manoeuvre. Yet, in many vertebrate taxa, background noise causes an increase in vocalisation amplitude. Thus, we further hypothesised that background noise alters the predator-prey interaction between barbastelles and moths.

We tested these hypotheses in both the wild and captivity by offering tethered moths to barbastelles under silence and noise conditions. We reconstructed the bats' three-dimensional flight paths based on time-of-arrival differences of the echolocation calls at four microphones, measured the received sound levels at the moth's position with an additional miniature microphone, and calculated call source levels.

We show that barbastelles continuously reduced call intensity upon detecting a moth, thereby remaining below the moth's hearing threshold and rendering the bat's approach undetected by its prey until shortly before capture. Background noise caused an increase in call intensity.

Barbastelles have combined intensity compensation with low-intensity echolocation to counter moth hearing during an attack. This novel strategy might have given them exclusive access to a formerly unavailable food source, thereby probably altering competition between sympatric bat species tremendously. In turn, selection pressure for eared moths might have increased, potentially fostering new anti-bat traits to evolve. Yet, increased source levels in noisy environments could foil the bat's stealth strategy if the moth's hearing threshold remains the same.

Directionality of nose-emitted echolocation calls from bats without a nose-leaf (*Plecotus auritus*)

JAKOBSEN LASSE[1], HALLAM JOHN[2], HEDENSTRÖM ANDERS[3]

[1] Centre for BioRobotics, Dept. Biology, University of Southern Denmark, lasse@biology.sdu.dk
[2] Centre for BioRobotics, Maersk Mc-Kinney Moller Institute, University of Southern Denmark
[3] Centre for animal movement, Dept. Biology, Lund University

Most bats use echolocation to hunt and navigate: they emit high frequency sound pulses and localize objects in their surroundings from the returning echoes. All bats investigated to date emit sound directionally, that is, sound pressure is highest in front of the bat and the pressure attenuates progressively at increasing off-axis angles. The directional emission presumably carries a number of advantages for the bats; it acts as a spatial filter, adds inherent directional information and increases the source-level of the calls. Most bats emit sound through their open mouth and the size of the mouth, to a large extent, dictates the directionality of the emitted call (Jakobsen et al., 2013). However, around 30% of echolocating bats emit calls through the nose (e.g. Phyllostomidae, Rhinolophidae, Hipposideridae) and most of these have very prominent nasal structures thought closely associated with sound emission. For these nose-emitting bats, the overall directionality is likely generated by the interference pattern from the two nostrils (horizontal directionality) and the nose-leaf (vertical directionality) (Hartley & Suthers, 1987). Given the apparent benefits of emitting a directional sound beam, it is intriguing that multiple nose-emitting bats do not have prominent nose structures (e.g. Rhinopomatidae, *Craseonycteris thonglongyai* and vespertilionid bats of the genus *Barbastella* and *Plecotus* (Pye, 1960)). In this study we sought to determine if nose-emitting bats without prominent nose structures emit directional sound in the vertical plane despite the lack of external structures.
We measured directionality from three free flying brown long-eared bats (*Plecotus auritus*) as they captured mealworms in the lab at Lund University in Sweden. The results show that *P. auritus* do emit directional calls and, surprisingly, that vertical directionality is higher than horizontal directionality (-6dB angle = 22° vertically and 35° horizontally). The exact mechanism for generating the vertical directionality is still unknown but we believe that the placement and fine-structure of each nostril plays an important role in shaping the beam. The emission of directional sound from the nose without closely associated nasal structures underlines the importance of sound beam directionality for navigation through echolocation, and speaks to the possibility of directional emissions from animals that at first glance may not appear directional.

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Forebrain networks for controlling vocal sequences in bats

SMOTHERMAN MICHAEL[1]

[1] Texas A&M University, College Station, TX USA 77843-3258

Understanding how the bat's brain differentially controls sonar pulses versus social calls is a critical step towards uncovering the evolutionary origins of echolocation. In bats social calls and sonar pulses are generated and modulated by different but overlapping brainstem circuits, but very little is known about the upstream forebrain networks that selectively activate these circuits to produce behaviorally relevant pulse or call sequences and patterns. The free-tailed bat, *Tadarida brasiliensis* offers an opportunity to fill the gap between the production of simple syllables and the coordination of complex vocal sequences because this species sings complex courtship songs displaying a flexible phonological syntax that varies with social context. Here we report that both sonar pulses, strobe groups, social calls and singing can all be elicited by pharmacological activation of a discreet area of anterior cingulate cortex (ACg) in a time and dose-dependent manner. A combination of neuronal tracing and immunohistochemistry revealed that drug-evoked vocalizations correlated with activation of key components of the medial forebrain and hypothalamus, mediodorsal thalamic nucleus, globus pallidus, striatum and substantia nigra, which connect to form a limbic forebrain motor loop. These results suggest that both syllable selection and the temporal patterns of stereotyped vocal sequences in bats may be defined by the patterns of neural activity emerging within this limbic motor loop. It is hypothesized that this circuit plays a central role in the integration and translation of sensory, motor and motivational influences into a series of discreet activation states that differentially drive the vocal pattern generators to produce different sonar and social communication sequences.

SESSION VI: BAT VOCAL LEARNING

Chairs: Mirjam Knörnschild, Lutz Wiegrebe

Vocal production learning in *Saccopteryx bilineata* - social modification and imitation

KNÖRNSCHILD MIRJAM[1]

[1] Freie Universität Berlin, Takustr. 6, 14129 Berlin, GERMANY; mirjam.knoernschild@fu-berlin.de

Bats comprise one of the few mammalian taxa capable of vocal production learning, with current behavioral evidence for four species belonging to three families. The taxon's speciose nature makes bats well suited for phylogenetically controlled, comparative studies on proximate and ultimate mechanisms of mammalian vocal production learning. I will highlight findings on two different forms of vocal production learning in the greater sac-winged bat *Saccopteryx bilineata*, namely social modification and vocal imitation. *Saccopteryx -bilineata* pups modify innate isolation calls based on auditory input from fellow pups in their social group and thus develop a group signature in isolation calls as they mature. Moreover, pups imitate male territorial song during ontogeny based on they auditory input they receive from singing males in their vicinity. Vocal imitation of pups commences during a conspicuous vocal behavior in which pups combine various elements from the adult vocal repertoire, including precursors of male territorial song, into long vocal sequences which can last for up to 30 minutes. These vocal sequences are reminiscent of the canonical babbling of human infants and the plastic song of young songbirds. Corresponding to our findings in *S. bilineata*, babbling is considered to be crucial for mastering the phonological challenges of speech acquisition in humans and song in songbirds. Apart from humans, *S. bilineata* is the only mammal known to date that is both a babbler and a vocal imitator, which makes this species highly interesting for comparative biolinguistic studies.

Insights into the Evolution of Vocal Complexity From Molossids

BOHN KIRSTEN[1]

[1] Johns Hopkins University, Dunning Hall Suite 434, 3400 N Charles St, Baltimore MD 21218. kbohn1@jhu.edu

Birds are well known for songs while bats are well known for their developed sonar system. However, recent research has revealed that in addition to echolocation, bats produce highly sophisticated "songs" whose complexity is only rivaled by birds, humans and cetaceans. Here, I present comparative research on territorial calls/courtship songs of five species of molossids. There is considerable variation in vocal sequence generation, vocal complexity and the potential for vocal learning across species. In addition, I discuss co-evolution of echolocation and social calls since molossids embed "echolocation" calls into complex song phrases and produce calls in flight. These findings indicate that complex social calls may be an exaptation of highly specialized echolocation systems rather than innate precursors to echolocation. Finally I discuss where bats fit into our current models – birds, anurans, cetaceans and rodents – and how using a comparative approach can greatly expand our understanding of acoustic communication.

Induced culture in the lab: formation of dialects through social vocal learning in bats

PRAT YOSEF[1], AOULAY LINDSAY, YOVEL YOSSI

[1] Department of zoology, Tel-Aviv University, Tel-Aviv, ISRAEL

The Egyptian fruit bat (*Rousettus aegyptiacus*) is an extremely social and vocal mammal, living in colonies of dozens to thousands of individuals. In the wild, these bats are exposed to extensive vocal communication throughout their entire lives. A typical vocalization is composed of a sequence of multi-harmonic syllables where the fundamental frequency (F0) of the vocalizations is high (ca. 8-15 kHz) in newborn pup isolation-calls, and gradually decreases to ca. 0.2-1.2 kHz in adults, in a process which we have previously shown to involve vocal learning. In this study, we housed pregnant female fruit bats in three identical acoustic chambers. The females gave birth in these chambers, and were released after the pups were weaned. In each of the three chambers a different playback was constantly played. The playbacks, which were sampled from a set of thousands of vocalizations previously recorded in this setup, were assigned to each group according to their fundamental frequency content: the *High-F0* group (n=4) was exposed to playbacks with an average high fundamental frequency, the *Low-F0* group (n=5) was exposed to playbacks with an average low fundamental frequency, and the control group (n=5) was exposed to playbacks randomly sampled from the adult repertoire (reflecting the common auditory exposure of young bats in wild roosts). In order to quantify the effect of the playbacks on the vocalizations of the pups, we calculated a set of acoustic features, including the (log-) fundamental frequency, for each recorded syllable and for each of the playback syllables. While at very young age large variability was observable with no clear distinction between the three groups, when the pups matured the groups became acoustically separable. These findings present the formation of three vocal dialects in the lab, and show a connection between the established dialects and the auditory experience of the pups. Interestingly, and in line with our previous studies, the pups do not imitate the playback as is, but are rather influenced by it, and incorporate its characteristics into their adult repertoire. Some of this repertoire is innate, while some of it was probably acquired from the adult females, which were present in the chamber at young age.

Studying the neurogenetic bases of vocal learning in bats

VERNES SONJA C. [1]

[1] Max Planck Institute for Psycholinguistics, Neurogenetics of Vocal Communication Group, Wundtlaan 1, Nijmegen, NETHERLANDS

Vocal learning is a crucial feature of human spoken language, making it a trait of intense interest for understanding how humans develop the capacity for language. However vocal learning is rare and bats are one of the few mammals that display this ability. This capacity, together with a long history of studying the neuroethological traits of bats, makes them an excellent system to model vocal learning. We are part of a working group studying the behavioural, neurobiological and genetic mechanisms of vocal learning in bats. I will present work investigating neurogenetic mechanisms, including the role of individual genes and gene networks in vocal learning. These studies encompass single gene studies and genetic knockdowns, transcriptomics and network building, and de novo genome sequencing. These approaches will ultimately show how genetic mechanisms can drive a complex behaviour like vocal learning and may shed new light on the biological encoding of human speech.

SESSION VII: BAT IMMUNITY AND PATHOGENS

Chairs: Gábor Á. Czirják, Marcel Müller

Has the bat innate immune response evolved to suppress inflammation-mediated viral pathology?

BANERJEE ARINJAY[1], RAPIN NOREEN[1], BOLLINGER TRENT[2], MISRA VIKRAM[1]

Departments of [1]Microbiology and [2]Pathology Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, Saskatchewan, CANADA, Vikram.misra@usask.ca

In recent years, viruses similar to those that appear to cause no overt disease in bats are thought to have spilled over to humans and other species causing serious and often fatal disease. These include coronaviruses that cause Severe Acute Respiratory Syndrome, Middle-East Respiratory Syndrome and Porcine Epidemic Diarrhea. Since pathology in these diseases is largely attributed to an over-active inflammatory response, we tested the hypothesis that *bat cells respond to stimulation of their receptors for viral pathogen ligands with a strong antiviral response, but unlike in human cells, the inflammatory response is not overtly activated*. We compared the response of human and *Eptesicus fuscus* (North American big brown bat) cells to poly(I:C), a viral RNA surrogate and known agonist for the viral RNA toll-like receptor (TLR) 3. We measured the transcripts for several inflammatory, interferon and interferon response genes using quantitative real-time PCR. We found that stimulated human and bat cells both contained significantly higher levels of transcripts for interferon beta than unstimulated cells. In contrast, only human cells responded to poly(I:C) stimulation by producing robust amounts of RNA for tumour necrosis factor alpha (TNFα), a transcription factor that enhances the expression of several pro-inflammatory genes. To determine if this lack of TNFα responsiveness to poly(I:C) could be attributed to features of the bat TNFα promoter, we examined promoters for both *E. fuscus* and human TNFα genes. We found that the bat TNFα coding sequences are preceded by a motif that resembles the binding site for homodimers of cRel, a protein known to regulate the expression of pro-inflammatory genes. Deletion of this motif in the promoter enhanced activation by poly(I:C) and suppression of cRel RNA in bat cells by specific siRNA increased basal levels of TNFα transcripts. In addition, and in contrast to most human cells not involved in the immune response, we detected cRel transcripts in most bat tissues and in a bat cell line. Poly(I:C) stimulation of cells expressing cloned bat cRel caused increased translocation of the protein to the cell nucleus. Our results suggest that as a survival strategy bats may have evolved to uniquely suppress the expression of pro-inflammatory cytokines in response to viral infection thereby preventing inflammatory pathology.

Does habitat disturbance result in chronic stress and increased viral shedding in forest-dwelling paleotropical bats?

SELTMANN ANNE[1,2], CZIRJÁK GÁBOR Á.[3], CORMAN VICTOR[4,5], RASCHE ANDREA[4,5], DROSTEN CHRISTIAN[4,5], BERNARD HENRY[6], STRUEBIG MATTHEW[7], VOIGT CHRISTIAN C. [1,2]

[1] Department of Evolutionary Ecology, Leibniz Institute for Zoo and Wildlife Research, Alfred-Kowalke-Str. 17, 10315 Berlin, GERMANY, seltmann@izw-berlin.de, voigt@izw-berlin.de
[2] Institute of Biology, Freie Universität Berlin, Takustr. 3, 14195 Berlin, GERMANY
[3] Department of Wildlife Diseases, Leibniz Institute for Zoo and Wildlife Research, Alfred-Kowalke-Str. 17, 10315 Berlin, GERMANY
[4] Institute of Virology, University of Bonn Medical Centre, Sigmund-Freud-Str. 25, 53127 Bonn, GERMANY
[5] German Centre for Infection Research, partner site Bonn-Cologne, GERMANY
[6] Institute for Tropical Biology and Conservation, Universiti Malaysia Sabah, Jalan UMS, 88400 Kota Kinabalu, Sabah, MALAYSIA
[7] Durrell Institute of Conservation and Ecology (DICE), School of Anthropology and Conservation, University of Kent, Canterbury, Kent, CT2 7NR, UK

Emerging infectious diseases (EIDs) are considered as a major threat to human health worldwide. Most of the EIDs seem to result from an increased contact between wildlife and humans, especially when humans encroach into formerly pristine habitats. Yet, habitat deterioration may negatively affect the physiology and health of wildlife species, for example by stress-related immune suppression, which may eventually lead to a higher susceptibility to infectious agents and/or increased shedding of the pathogens causing EIDs. Here, we tested in a paleotropical forest with ongoing logging and fragmentation whether habitat disturbance influences the body mass, immunity and occurrence of astro- and coronaviruses in eight species of bats, a taxon implicated as a major reservoir for highly virulent viruses. We measured and compared body mass, chronic stress (indicated by neutrophil to lymphocyte ratios) and the number of circulating immune cells between bats with different roost types living in recovering areas, actively logged forests, and fragmented forests in Sabah, Malaysia. In a cave-roosting species, chronic stress levels were higher in individuals from fragmented forests compared with conspecific from actively logged areas. Foliage-roosting species showed a reduced body mass and decrease in total white blood cell counts in actively logged and fragmented forests compared with conspecifics living in recovering areas. In contrast to our hypothesis, anthropogenic habitat disturbance was not associated with higher corona- and astroviral detection rates in fecal samples. However, we found a higher detection rate of astroviruses at the beginning of the rainy compared to the dry season and a trend that individuals with a poor body condition had a higher probability of shedding astroviruses in their feces. By identifying the beginning of the rainy season as a risk factor for increased viral shedding that may potentially result in increased interspecies transmission, we

contribute to means of preventing viral spillovers from bats and other wildlife reservoirs to humans.

Moving beyond borders: understanding the past to better predict the future for a bat fungal pathogen

PUECHMAILLE SEBASTIEN J. [1], STECKER RUTH-MARIE[1] FISCHER NICOLA M.[1], DOOL SERENA[1], ALTEWISCHER ANDREA[1], FRITZE MARCUS[1], TOSHKOVA NIJA[1], ZHELYAZKOVA VIOLETA[1], SANTOS HELENA[2] REBELO HUGO[2]

[1] Greifswald University, Zoology Institute & Museum, Soldmann-Str. 14, D - 17489, Greifswald, GERMANY; s.puechmaille@gmail.com
[2] CIBIO/InBio, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto. Campus Agrário de Vairão, PORTUGAL

Fungi make up a remarkably diverse kingdom, with an estimated 1.5 million species, and interact with a broad array of other organisms. Their longstanding utility to all life on earth has often been matched by their ability to cause devastating diseases in humans, animals and plants. In animals, an unprecedented number of fungal diseases have caused some of the most severe die-offs and extinctions ever recorded in wild species, with chytridiomycosis in amphibians and White-Nose Disease in bats. Given that emerging fungal infectious diseases pose serious threats to wildlife health, food security and ecosystem stability, understanding the factors leading to their emergence has never been more urgent. Also, besides just understanding past emergences, we need to learn from them and develop predictive tools to tell us when and how new pathogens will emerge. North American bat species are now faced with extinction from a devastating disease caused by a fungus, *Pseudogymnoascus destructans* recently introduced in North America from Europe. To prevent such an event from happening again, elucidating the precise source in Europe and knowing when the introduction happened would provide us with critical information to infer the mode of introduction. Hence the first objective of the project is to elucidate the location of the source population in Europe and the timing of introduction. The second objective is to characterise population structure of the fungus across Europe and evaluate whether intra-European movements of the fungus are of concern (e.g. if different geographically separated lineages exist). The third objective is to use reciprocal modelling techniques based on a large database of known sites (North America, n=324; Europe, n=284) to predict the suitable areas that are yet to be colonised in North America. We used an unprecedented number of samples (n>1,300) collected from 20 countries in Europe and genotyped for a set of 18 variable microsatellites, to build a genetic reference collection that is critical for identifying the source population of the North American introduction. Based on this reference dataset, we developed a novel method that allows precise identification of the origin of any sample based on its genetic fingerprint. This large genetic dataset also revealed a surprisingly strong population structure of the fungus across Europe. Finally, the results from the reciprocal modelling indicated that the fungus is currently occupying only half of its potential distribution in North America, suggesting that the disease will soon threaten many more bat populations and species.

Specificities of bat life cycle drive the need for an environmental reservoir for the pathogen *Pseudogymnoascus destructans*, the causative agent of White-Nose Disease

FISCHER NICOLA M. [1], ALTEWISCHER ANDREA[1], PUECHMAILLE SEBASTIEN J.[1]

[1] Greifswald University, Zoology Institute & Museum, Soldmann-Str. 14, D - 17489, Greifswald, GERMANY; s.puechmaille@gmail.com

Unlike most mammals and birds, numerous bat species use hibernation as a strategy to avoid starvation during long periods of low food abundance (typically winter). However, the decrease in metabolic rate and body temperature result in the severe reduction of the thermal barrier for protection against infection with a large number of fungi. Among them, *Pseudogymnoascus* (*Geomyces*) *destructans*, the causative agent of White-Nose Disease, is unable to grow at temperatures above 20°C and therefore only grows on bats during the hibernation period. Hence the particular life cycle of temperate bats in which 5-6 months is spent in hibernation followed by a 6-7 month active period allows them to clear infection. As the bats are infected every winter, it remains unclear how they get infected by the fungus each year and whether the transmission rate is exacerbated during hibernation by inter-individual contacts. To answer these questions, we isolated >500 isolates of *P. destructans* from bats during hibernation as well as from the environment at different times of the year (before and after hibernation) during four years and investigated patterns of *P. destructans* genetic diversity and distribution. The fungus was genotyped at 18 variable microsatellite loci making it possible to genetically identify (via multi-locus genotypes) and follow each individual of *P. destructans* as it infects bats in different parts of the hibernaculum and over the years. The spatio-temporal distribution of *P. destructans* individuals from the environment and bats shows a very clear pattern of infection from the hibernaculum with bat-to-bat infections only playing a minor role in the transmission of the pathogen. The frequency of the different *P. destructans* individuals on the hibernating bats was strongly correlated to the individuals' frequency in the environment prior to the hibernation period. We also demonstrated the survival of spores from April to October on the walls of the hibernacula even in the absence of bats. These results clearly show for the first time that the environment operates as a passive reservoir for this pathogen allowing yearly autumnal re-infection of bats as they enter their hibernacula. The critical role of the environment needs to be considered when planning the management of White-Nose Disease in North America. Once the fungus has been found at a site it will not be eradicated by the absence of bats alone, but needs to be actively removed from the environment to prevent re-infection of bats the next year.

An integrated study of Nipah virus eco-epidemiology at the flying-fox/human interface in Cambodia

CAPPELLE JULIEN[1,2], THAVRY HOEM[1], FUREY NEIL M.[3], VIBOL HUL [4], PRIGENT STEVEN[5], EPSTEIN JONATHAN H. [6], NGAMPRASERTWONG THONGCHAI[7], VISAL HOK[8], VEASNA DUONG[4], SOWATH LY[1], DUBOZ RAPHAËL[1,2], TRAN ANNELISE[2,9], DUSSART PHILIPPE[4], TARANTOLA ARNAUD[1], BINOT AURÉLIE[2,10]

[1] Epidemiology and Public Health Unit, Institut Pasteur du Cambodge, 5 Bd Monivong, BP983, Phnom Penh, CAMBODIA
[2] Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD), UR Animal et Gestion Intégrée des Risques (AGIRs), F-34398, Montpellier, FRANCE, Julien.cappelle@cirad.fr
[3] Fauna & Flora International (Cambodia Programme), PO Box 1380, No. 19, Street 360, Boeng Keng Kong 1, Phnom Penh, CAMBODIA, 12000.
[4] Virology Unit, Institut Pasteur du Cambodge, 5 Bd Monivong, BP983, Phnom Penh, CAMBODIA
[5] Associate member IrAsia (CNRS UMR 7306), Marseille, FRANCE
[6] EcoHealth Alliance, New York, NY, USA
[7] Department of Biology, Faculty of science, Chulalongkorn University, THAILAND
[8] Centre for Biodiversity Conservation, Room 415, Department of Biology, Faculty of Science, Royal University of Phnom Penh, Confederation of Russia Boulevard, Phnom Penh, CAMBODIA
[9] Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD), UMR Territoires, Environnement, Télédétection et Information Spatiale (TETIS), Sainte-Clotilde, Reunion Island, FRANCE
[10] Kasetsart University, Faculty of Veterinary Medicine, Bangkok, THAILAND

Nipah virus (NiV) was first reported in Malaysia in 1998 after the virus emerged in pigs, causing 265 human, with 105 deaths. Flying foxes are considered to be the main reservoir of the virus which re-emerged in Bangladesh and India where over 200 human cases have been identified since 2001. Evidence of NiV circulation in flying fox populations has been reported in Thailand and Cambodia but little is known in South East Asia about the risk of transmission of NiV to domestic animals and Humans.

In order to better assess the risk of emergence of Nipah virus in Cambodia, we implemented a multidisciplinary study involving researchers (in ecology, epidemiology, virology, genetics, anthropology and modelling), conservationists and local and national authorities. We monitored the population dynamics and the diet of a colony of Lyle's flying fox (*Pteropus lylei*) as well as the circulation of Nipah virus in the urine of these bats. We investigated the perception of the bats by local communities and their practices relating them to the bats (such as hunting, collecting guano, harvesting fruits, harvesting and drinking palm juice). We studied the bat / human interface by deploying GPS collars on 14 bats.

Our results show seasonal patterns in both population dynamics and virus circulation, allowing us to identify a period when local communities' practices may put them at a higher risk of contamination. The GPS locations of the bats during this period reveal potential routes of transmission of the virus from the bats to the humans and areas with increased potential contacts. A serological survey of people living in these areas was subsequently implemented.
The development of an integrative model and participatory approaches are being used to help transfer this knowledge and to advocate the use of prevention measures, despite the absence of a perceived risk by local communities.

SESSION VIII: BATS AS CONSERVATION TARGETS

Chairs: Dina Dechmann, Tigga Kingston

Still special: cracks in island keystones as threat synergies and feedback loops push island flying foxes (*Pteropus* spp.) to the brink

KINGSTON TIGGA[1], VINCENOT CHRISTIAN, FLORENS VINCENT

[1] Texas Tech University, Lubbock, Texas 79409, USA, tigga.kingston@ttu.edu

The Mauritian Fruit Bat, *Pteropus niger*, is special in the worst way possible; it is one of the few, if not only, species on the IUCN Red List to be subject to a government-implemented cull. Following pressure from litchi and mango growers, in late 2015 the Government of Mauritius deployed its Special Mobile Force to shoot > 30,000 individuals of this island endemic, a population reduction of about a third. *Pteropus niger* was special even before the cull, being the last of three *Pteropus* species to survive on Mauritius, and likely the only remaining effective long-distance pollinator and seed disperser. The Mauritian Fruit Bat is just one of 49 island *Pteropus* species, or flying foxes. Although the ecological importance and vulnerability of island flying foxes was clearly elucidated in a series of publications arising from the Pacific Island Flying Fox Conference over 25 years ago, collectively island flying foxes remain the most vulnerable bats in the world. Fifty-three percent of species are threatened (assessed as Critically Endangered, Endangered, Vulnerable), with a further 7% Near Threatened. Moreover, conservation status of threatened species, as measured by the Red List Index, continues to decline at a far more rapid rate than other bats and most vertebrate groups, and four of the five bat species lost to extinction globally were island *Pteropus*. Here we assemble evidence from the last 25 years in support of the special role that flying foxes play in island ecosystems, and describe the threat synergies and feedback loops driving many species to the brink of extinction. As dispersers and pollinators on islands, flying foxes are distinguished by fast, long-distance flight, rapid digestion and in-flight defecation, ability to move large seeds, and benign or positive effect of food selection, handling and digestion on germination rates. In some cases, they are the only long-distance dispersers to have reached isolated islands and in others, megafaunal downsizing and anthropogenic extinctions have left them as the sole effective agents. Stochastic threats like tropical storms and cyclones, are of growing concern as populations decline from anthropogenic pressures, many of which are intensified on islands. Notably, extensive and rapid habitat destruction, and invasion by alien species, reduce natural food resources and precipitate human-bat conflict over fruit crops. A growing hostility against island *Pteropus* compound these threats leading to increased persecution, poaching and culling, alarmingly met with silent indifference when not explicit complicity by authorities in many countries.

Using Key Biodiversity Areas for Global Bat Conservation: Opportunities and Challenges

FRICK WINIFRED F. [1], WALDIEN DAVID L., KINGSTON TIGGA

[1] Bat Conservation International, PO Box 162603, Austin, Texas USA, wfrick@batcon.org

Effective biodiversity conservation requires identifying and mitigating threats to populations as well as protecting critical habitats. The IUCN recently launched global standards for criteria and thresholds for identifying and demarcating 'Key Biodiversity Areas' (KBA) to acknowledge the importance of habitat conservation for biodiversity preservation. The global standards for KBAs provide a set of quantitative criteria and thresholds for identifying critical habitats that species depend on for viability. We explore the applicability of global KBA standards to bat conservation with focused attention on how the special ecology of bats may challenge the KBA process. There are 5 main criteria for KBAs, but only a few of these will relate to bat conservation. Areas with breeding populations of bat species listed as critically endangered or endangered by the IUCN Red List or have geographically restricted ranges will qualify as KBAs. Bat species that roost in large colonies will also be good targets for KBA designation as one of the criteria focuses specifically on demographic aggregations. However, determining the size of a KBA to achieve a conservation impact for highly mobile bat species may prove challenging and requires credible information on how bats use landscapes. These challenges may not be unique to bats and approaches used on other mobile and communally roosting species (e.g. seabirds) could be informative. In general, data deficiency on global population sizes and adequate data on occurrences are likely significant challenges to applying the KBA process for bat conservation. We present approaches to KBA designation using case studies and discuss the merits and challenges in applying this concept for global bat conservation efforts. A global initiative for designating KBAs for bat conservation will require collaborative efforts among researchers, conservation groups, and local communities.

Effect of shade management and distance from forest on insectivorous bat communities in coffee plantations of the Western Ghats, India

ONGOLE SHASANK[1], SANKARAN MAHESH[2], KARANTH KRITHI K.[3,4]

[1] Post-graduate Program in Wildlife Biology and Conservation, Wildlife Conservation Society-India, National Centre for Biological Sciences, Tata Institute of Fundamental Research, GKVK, Bellary Road, Bangalore 560065, INDIA, ongoleshasank@gmail.com
[2] National Centre for Biological Sciences, Tata Institute of Fundamental Research, GKVK, Bellary Road, Bangalore 560065, INDIA
[3] Centre for Wildlife Studies, 403 Seebo Apartments, 26/2, Aga Abbas Ali Road, Bangalore 560042, INDIA
[4] Wildlife Conservation Society, Bronx, NY, USA

As production landscapes occupy far larger areas than formal protected areas, their potential for supporting biodiversity has been widely studied. Agroforestry systems such as shade coffee plantations have shown considerable promise in this aspect. However, insectivorous bats have been understudied in such systems, especially in the Paleotropics, even though they are known to provide important pest control benefits. We investigated the influence of local features of coffee plantations such as shade management and distance to contiguous forests on insectivorous bat communities in Chikmagalur district in the Western Ghats biodiversity hotspot, India. In this area, shade coffee is grown in proximity to contiguous forests under a range of shade management varying from one dominated by native tree species to a monoculture of an exotic tree, silver oak (*Grevillea robusta*). We monitored bats using ultrasound detectors in 20 plantations, visiting each location three times during the study period. We used regression modelling and a model selection approach to quantify the response of bat species richness and activity at a plantation level to tree density, tree cover, proportion of silver oak and distance to contiguous forest. To account for missing species and heterogeneous species detectability, we also performed this analysis with species richness estimates obtained using a capture-recapture framework. We detected 9 phonic types/species in the study area. Tree cover and distance to forest together explained up to 36% of the variation in species richness, which declined with increase in tree cover. These patterns were qualitatively similar when estimated species richness was used. Tree density, tree cover and distance to forest explained up to 32% of the variation in bat activity. Data showed a possible negative association of activity with tree density and tree cover. Proportion of silver oak had no effect on either species richness or activity. We suggest that in this landscape, local features of coffee plantations are likely to affect how bats use the plantations to a greater degree than surrounding forests. Increase in proportion of silver oak does not appear to affect the movement of bats at the scale of the plantation but effects of large scale conversion to monoculture still need to be investigated. No decline in species richness or activity with increasing distance from the forest suggests that shade coffee offers low contrast with forest areas in this landscape, which is in broad concurrence with Neotropical bat studies in agroforests.

Novel lighting technologies, bats and insects

JONES GARETH[1], ZEALE MATT, WAKEFIELD ANDY, BROYLES MOTH, STONE EMMA, HARRIS STEPHEN

[1] School of Biological Sciences, University of Bristol, 24 Tyndall Avenue, Bristol BS8 1TQ, UK: gareth.jones@bristol.ac.uk

Our recent experimental studies confirmed that lamps that emit short wavelengths of light, especially UV, attract more insects. Insect attraction in turn determines attraction of bats, with species that fly in open spaces often exploiting insects attracted to lamps. Some bats are averse to all light types studied however, and these are often species of conservation concern. We tested how bat species responded to emerging lighting technologies, including LEDs, lamps that attract fewer migratory birds, and lamps that minimise impacts on species sensitive to short wavelengths. We radio-tracked lesser horseshoe bats whose commuting routes were exposed to these novel lighting types, and measured potential fitness proxies such as foraging time and distance travelled to foraging sites. We evaluate whether novel lighting technologies have the potential to reduce impacts on light-averse bat species.

Non-invasive genetics: guano, a neglected but highly promising fertilizer for bat research and conservation

LEHNEN LISA[1], JAN PIERRE-LOUP[2], ZARZOSO-LACOSTE DIANE[2], KERTH GERALD[1], PETIT ERIC[2], PUECHMAILLE SÉBASTIEN J.[1]

[1] Institute of Zoology & Museum, Greifswald University, Soldmannstr. 14, 17489 Greifswald, GERMANY, lisa.lehnen@uni-greifswald.de
[2] Ecology and Ecosystem Health, INRA, Agrocampus Ouest, F-35042 Rennes cedex, FRANCE

To date, the majority of prediction and conservation efforts do not account well for species biology, thus failing to provide effective conservation measures. Although field study methods are many and varied, their utility in providing critical information for conservation is limited in species that are rare, elusive, endangered or cryptic, which represents a large majority of bat species across the world. Our project aims to harness the power of non-invasive genetic methods to follow individuals through time (across the year and over multiple years) and space (between colonies), allowing the estimation of life history parameters. These can be used to create, amongst other things, a sound basis for model parameterization or estimating survival and reproduction success in relation to biotic and abiotic factors. We developed a high-throughput approach to assess population demographic parameters for 34 colonies of *Rhinolophus hipposideros* in France and Germany. Faeces were collected in three successive years, with distinct sampling sessions before and after parturition within each year. DNA isolated from faeces was genotyped at 8 microsatellite loci and one sex-specific locus. We have successfully obtained high quality genotypes for an extensive data set of more than 10,000 samples. Individuals and their re-capture rates within and between sampling sessions/years were identified. Contrasting these data with established methods of determining population sizes revealed that genetics-based estimates enhance encounter probability and perform better at capturing roost use heterogeneity in relation to sex and reproductive status (both estimated from the collected data). The possibility to control for presence of males in maternity roosts via a sex-specific marker provides a more accurate evaluation of reproductive rates. The genetic data can be used to infer mother-offspring pairs within each year and hence provide data on reproductive status and success but also on social structure. This individual-based approach was further used to directly identify dispersal events and the sex and age cohort of the dispersing animals. Indirect genetic methods complement this approach and suggest isolation by distance and inhibition of gene flow by fragmentation. Non-invasive genetics provide reliable estimates of life history parameters without having to catch the individuals and can be sustainably applied to a wide range of organisms including threatened species. Accounting for species biology enhances the accuracy of population status estimates and will increase the predictive power of modelling approaches. The collected data also contains information that can be used by ecologists, geneticists, epidemiologists, physiologists and virologists amongst others.

POSTER PRESENTATIONS

SESSION I: BAT EVOLUTION AND RADIATION, REVEALED BY NGS

Poster 1: The first appearances of extant European bat species: are bats exceptional?

HORACEK IVAN[1], TRAVNICKOVA EVA, HULVA PAVEL

[1] Department of Zoology, Charles University, Vinicna 7, CZ 128 44 Praha, CZECH REPUBLIC

Bats are often given as example of extreme bradytely. Several extant genera are reported first from the Late Eocene, obviously much earlier than it is the case with the other mammalian clades. At species level the situation is much less apparent, of course.

We briefly surveyed the Late Cenozoic history of European bat communities as revealed by current fossil record. Particular attention was paid to turning points in their taxonomic structure, appearances of the clades contributing the extant fauna and their role in bat communities of particular horizons. With aid of a detailed morphometric analyses we compared a degree of correspondence between the extant populations and the fossil forms (mostly represented by population samples). We focused particularly on genera *Myotis*, *Plecotus* and *Eptesicus* for which a relevant fossil record is available. The respective genera grew core elements of bat communities since the late Miocene, showing even clear phenotype resemblance to extant species since the Early Pliocene. Yet, the detailed morphometric data based on mass population samples from several Pliocene sites (Javoricko, Urwista, Gundersheim, Podlesice) show significant differences from extant species in pattern of phenotype variation, except for *Plecotus auritus* and *Eptesicus serotinus*. This suggests that the phenotype patterns characterizing the extant species became established as late as during the Early Pleistocene at least in those clades which form the core of the extant communities. Thus, against expectancy, it suggests that, at least as FAD of extant species is concerned, the bats are *not* exceptional.

This conclusion is confronted with the signal of speciation dynamics as revealed of the genotypic data. The phylogenetic relevance of phenotype analyses in bats is discussed.

Poster 2: Species composition and genetic structure of *Pipistrellus pipistrellus/ pygmaeus* complex in Belarus

SHPAK ALIAKSEI[1]., LARCHENKO ALIAKSANDRA

[1] Laboratory of Molecular Zoology, State Scientific and Production Amalgamation «Scientific and Practical Center for Bioresources» of the National Academy of Sciences of Belarus; Akademicheskaya str., 27, Minsk 220072, BELARUS
shpak.dvergr@gmail.com

The results of mitochondrial gene *cyt b* analysys, which reflects the species composition and genetic structure of the complex *Pipistrellus pipistrellus /pygmaeus* in Belarus are presented in the poster.

Poster 3: Analysis of *Myotis peninsularis* (Chiroptera: Vespertilionidae) blending morphometrics and phylogenetic datasets

NÁJERA-CORTAZAR LAURA ALEJANDRA[1, 2],
ÁLVAREZ-CASTAÑEDA SERGIO TICUL[2], DE LUNA EFRAÍN[3]

[1] University of Leeds, Leeds, LS2 9JT, England, UNITED KINGDOM, bslanc@leeds.ac.uk
[2] Centro de Investigaciones Biológicas del Noroeste, S.C., Instituto Politécnico Nacional 195, Playa Palo de Santa Rita Sur, La Paz, Baja California Sur 23096, MÉXICO
[3] Instituto de Ecología, A.C., Carretera antigua a Coatepec 351, El Haya, Xalapa 91070, Veracruz, MÉXICO

Myotis peninsularis is an endemic bat from the Cape Region in Baja California Sur, Mexico. Its taxonomic status is unclear, either as a valid species or as a subspecies of *M. velifer*, which is wide distributed in the North American continent. Both species share a cryptic morphology, but the lack of studies for *M. peninsularis* populations have not allowed a proper distinction. In order to assess its taxonomic status, the phylogenetic relationship of *M. peninsularis* was performed, using molecular and geometric morphometric data. Cytochrome oxidase subunit I and cytochrome *b* genes were analyzed. Phylogenetic analysis showed that *M. peninsularis* and *M. velifer* are sister groups, collectively forming a monophyletic assemblage. We observed less than 2% of genetic distance with both mitochondrial genes, which is considered an interval at the subspecies level. The geometric morphometric analysis showed differences in skull shape. We obtained three morphotypes: *M. peninsularis* (Cape Region), *M. velifer incautus* (northern population) and *M. v. velifer* (southern population). The most important differences were located in the braincase, the sagittal crest area and in the rostral slope. Morphologically, the three lineages tend to possess the same normal variation between Mexican population of *M. velifer*; but with a specific morphotypes associated to its distribution. In a combined molecular and landmark configurations phylogenetic analysis, the monophyletic assemblage was confirmed. The ancestral shape corresponded to an intermediate shape between *M. peninsularis* and *M. velifer*, presenting similar variation to the intra-specific level in *M. velifer*. With this results, *M. peninsularis* is proposed to be considered as a population from *M. velifer*, highlighting the need for more population level studies within this bats.

Poster 4: Illuminating the single shift in diversification rates across Chiroptera

DÁVALOS LILIANA M. [1], DUMONT ELIZABETH R., ROJAS DANNY, SEARS KAREN E., YOHE LAUREL R.

[1] Department of Ecology & Evolution, Stony Brook University, Stony Brook, NY, USA; lmdavalos@gmail.com

The great taxonomic richness and ecological diversity of bats suggests they are a classic adaptive radiation of the kind first outlined by G.G. Simpson. But analyses of diversification rates for both New World noctilionoids and all bats have identified only one large change in rates, corresponding to the first emergence of the phyllostomid subfamily Stenodermatinae. Hence one critical condition for adaptive radiation, the rapid emergence of many independent lineages, applies only to stenodermatines and to no other clade in the bat phylogeny. Here we compare traditional explanations for the evolution of so many species, focused on abiotic drivers of speciation, with biotic explanations. We find no association between Pleistocene glacial cycles and important changes in speciation rates among stenodermatines, or any other New World noctilionoids. Instead, the invasion of a trophic niche including figs inaccessible to other bats seems to be the critical factor leading to higher diversification rates through higher speciation rates or, less likely, lower extinction rates. At least two sets of stenodermatine genomic adaptations — in olfactory receptor genes and blue-light opsins— appear to be associated with this new trophic niche. Although the genomic basis of the novel skull architecture conferring the high bite force of stenodermatines is unknown, both phylogenetic and ontogenetic analyses suggest changes in skull elongation likely account for this trait. More genomic changes linked to the stenodermatine adaptive zone remain to be uncovered, and can be guided by comparative and ecological analyses.

SESSION II: BAT FLIGHT

Poster: Interspecific Variation in Aerial Rotations During Bat Landing in Relation to Landing Impact Forces

SWARTZ SHARON [1], BOERMA DAVID, RUMMEL ANDREA, SCHUNK COSIMA, BREUER KENNETH

[1] Brown University, Department of Ecology and Evolutionary Biology and School of Engineering, Box G-B206, Providence, RI USA 02912, sharon_swartz@brown.edu

Bats are the only extant flying animals that roost head-under heels, requiring them to perform acrobatic maneuvers to reposition the limbs for landing. These maneuvers differ among bat species, and have diversified into at least three distinct landing styles, which can be described as two-point, three-point, or four-point landings based on the number of limbs used to grasp the landing surface. However, the distribution of landing styles across extant bats is unknown, and the correlation between rotational complexity and peak impact force is poorly understood. In this study, we aim to explore the functional consequences of this variation in patterns of landing kinematics. We hypothesized that each style would always be associated with two features: characteristic patterns of body rotation and a particular range of peak impact forces. For example, four-point landings would uniformly involve simple rotations (pitch only) and be associated with relatively high peak impact forces, whereas two-point landings would involve a characteristic combination of pitch, yaw, and roll to enable the bat to contact the ceiling with only the hindlimbs, enacting landing at lower peak impact forces. We tested this hypothesis using a combination of kinematic analysis of multi-camera high speed videography to record and quantify body rotations and force plate analysis to quantify the magnitude and orientation of impact forces. We extended the range of taxa sampled from three species, representing two of nineteen extant bat families to a larger and more diverse range of bat species. We compared two-, three-, and four-point landings and a failed landing attempt. Our results show that as the complexity of body rotations during landing increases, peak impact forces consistently decrease across all sample species. This suggests that increased control over the body's rotational degrees of freedom permits more complex landing maneuvers, and that a primary function of controlling body rotation during landing may be to reduce impact forces.

Poster 5: Bat flight in conflicting sensory flow fields

KUGLER KATHRIN[1], LUKSCH HARALD[2], FIRZLAFF UWE[2], WIEGREBE LUTZ[1]

[1] Division of Neurobiology, Department Biology II, LMU Munich, Großhaderner Str. 2, 82152 Planegg-Martinsried, GERMANY
[2] Lehrstuhl für Zoologie, Technische Universiät München, Liesel-Beckmann-Str. 4, 85354 Freising, GERMANY

Flying animals face the challenge to navigate fast in highly structured environments. Sensory flow has been shown to affect flight guidance across the animal kingdom: visually guided animals use optic flow to adjust their flight trajectory as well as flight velocity. Bats, flying in complete darkness, use echo-acoustic flow to adjust their flight trajectory and echolocation behavior to their surroundings.
However, depending on the species, bats are not only active during complete darkness, but also in half- or even daylight. It is known that bats use visual information in various contexts, especially when tasks like landmark detection exceed the working range of echolocation. Furthermore, the availability of visual cues can enhance performance during prey detection or obstacle avoidance. In this experiment we aim to titrate visual flow against echo-acoustic flow: Specifically, we want to test which sensory modality dominates flight guidance when both visual and echo-acoustic cues are available. To this end, we monitor the flight and echolocation behavior of the little spear nosed bat, *Phyllostomus discolor*, while flying through conflicting visual and echo-acoustic flow fields. The intensity and wavelength of illumination of the flight path allows manipulating the relative perceptual salience of putative visual flow against the echo-acoustic flow of fixed salience.

Poster 6: The use of high-resolution mobile radar and ultrasound detectors for tracking foraging activity of bats over the water reservoir in Eastern Poland

ZEGAREK M. [1], HAŁAT Z.[1], GAJKO K.[2], KSEPKO J.[2], KSEPKO M.[2], RUCZYŃSKI I.[1]

[1] Mammal Research Institute, Polish Academy of Sciences, Poland
[2] 3Bird Radar System, 3Gsc, Białystok, POLAND

Radar gives the possibility to track single bats. Post processing analysis allows for classifying detected objects by size. In this study we tested if combination of data collected with the use of bat detectors and radar can provide relevant ecological data on density, changes in temporal and spatial activity and distribution of bats at the open foraging sites. Our observation method combined data from two different tools: (1) mobile horizontally scanning X-band high-resolution radar and (2) ultrasound bat detectors (Anabat Express, Titley Scientific). Our study site was a shallow, large, eutrophic Siemianowka water reservoir (E Poland). Data were collected during the mass swarming of Ephemenoptera and Diptera insects. Observations took place from dusk till dawn. We registered all moving objects above the water surface in a 2 km radius from the radar, which was situated on the dam in the middle of the reservoir. We registered GPS coordinates of the objects, their size and the speed of movement. Ultrasound bat detectors were located on floating platforms to record echolocations of bats flying over the lake. Recordings revealed that *Nyctalus noctula*, *Pipistrellus nathusii* and *Pipistrellus pygmaeus* consisted most of the bat calls (93 %), the rest were identified as *Myotis* spp. (mostly *M. daubentonii*) or were unidentified. Since wingspan of *Nyctalus noctula* and *Pipistrellus* spp. are clearly different, we classified flying objects into two size classes: big (wingspan above 320 mm) and small (wingspan below 320 mm). The only member of the first group was *N. noctula*. The second group included mainly two *Pipistrellus* species. Preliminary analyses indicated that the combination of radar and detector methods can be successfully used for measuring density, distribution and temporal and spatial activity changes in both size classes of bats. However, this method is limited to open areas, such as water reservoirs and rivers. The project was funded by the Polish National Science Centre (grant number: DEC-2013/10/E/NZ8/00725).

Poster 7: Seasonal and daily movements of *Lasiurus blossevillii* in California

JOHNSTON DAVE S. [1], RAINEY WILLIAM E. [2], SCHWARZ SUSAN K. [1], WYATT DAVID[4], PIERSON ELIZABETH D. [2]

[1] H. T. Harvey & Associates, Wildlife Department, Los Gatos, USA; djohnston@harveyecology.com
[2] Rainey and Pierson Consultants,2556 Hilgard, Berkeley, USA
[3] Sacramento City College, Sacramento, Ca USA

We modelled the seasonal distribution by sex of the western red bat (*Lasiurus blossevilli*) to infer seasonal movements using GIS-based ArcView 9 and 527 western red bat location records from the California Natural Diversity Data Base, museum records, and capture and acoustic data from E. Pierson, W. Rainey, C. Corben, D. Johnston, D. Stokes, S. Whitford, and S. Remington and various reports. Land cover attributes, political boundaries, and records were combined into a single table. GAP polygons that showed only the primary wildlife habitat relationship (WHR) vegetation community were used to generate the GIS-based range maps. The breeding (summer female and young) range comprised valley foothill woodland habitats in the Central and Salinas Valleys, and in coastal areas of Southern California. The male summer range included the Sierra Nevada and other mountainous regions adjacent to the female – young summer range. The winter range for both sexes was mostly limited to the San Francisco Bay Area, the Delta, the central portion of the Central Valley, and coastal areas with valley foothill riparian habitat. These range maps suggest males disperse from coastal and Delta wintering areas into a wide range of forested areas up to a several hundred kilometres away and up to 2427 metres above sea level during summer months whereas females migrate shorter distances as a group from coastal wintering areas to raise young at low altitudes along the main stems of rivers and creeks in the Central Valley and inner coastal areas of Southern California. At Sutter Buttes located in the Central Valley, radio-tracking of a combined 20 nights of foraging by 3 females and 1 male suggested relatively long commute distances from roosts to foraging areas n = 20, Mean 7.94 km, SE 1.52 km. Maternity roosting sites were located in undisturbed hilly areas with native vegetation and without non-native predators. Foraging areas comprised agricultural and anthropogenic habitats with non-native predators (e.g., *Rattus rattus*). Although both areas appeared to provide appropriate vegetation structure to support maternity roosts, females raising young may prefer locating maternity roosts in areas without non-native predators, even with commute distances of 10 km.

Poster 8: Links between bat sonar and flight height

ROEMER CHARLOTTE[1,2], DISCA THIERRY[2], BAS YVES[1], COULON AURÉLIE[2,3]

[1] CESCO UMR 7204, Bases écologiques de la conservation, Muséum national d'Histoire naturelle, 43 rue Buffon CP 135, 75005 Paris, FRANCE; croemer@biotope.fr
[2] Research and Development Department, Biotope, 22 Boulevard Maréchal Foch, 34140 Mèze, FRANCE
[3] CEFE UMR 5175, CNRS - Université de Montpellier - Université Paul-Valéry Montpellier - EPHE, Laboratoire Biogéographie et Ecologie des Vertébrés - 1919 route de Mende, 34293 Montpellier, FRANCE

Bat species differentiate from each other in the preys they are foraging, in their physiology and in their behaviour. Over time, their sonar has evolved, matching the requirements of these features, in such a way that today, most of the European species may be identified acoustically. But to what extent are sonar and behaviour linked to one another?
To answer these questions, flight heights of more than 20 bat species were observed with acoustic flight path tracking in France and Belgium. The first set of observations was performed during one to six months on more than 20 wind masts and produced information on the proportion of time spent above 25 m. It was thus possible to order bat species on a gradient from low to high flight species. However, species within Rhinolophus and Myotis genera demonstrate no or very little flights above 25 m. It was possible to order them on this gradient so as to distinguish them from high flight species, but not among each other. We obtained a much more precise localisation of flight heights thanks to a second set of observations that was gathered with material installed at ground level on more than 40 study sites for two nights. With a three-dimensional reconstruction of flight paths, the resulting flight gradient permitted a better ranking within Myotis species.
We then evaluated the predictability of flight behaviour on the basis of acoustic features. We tested correlations between flight height and species mean peak frequency, bandwidth and duration. As expected, peak frequency is the best predictor of flight height and duration divided by peak frequency was an even better predictor.
The flight height gradients established in this study represent in our knowledge the most complete and precise dataset on bat altitudinal behaviour considering the number of species and bat passes gathered (more than 300,000). The gradients may be particularly useful for estimating the specific susceptibility of bats to anthropogenic collision risks such as those caused by vehicles and wind turbines.

SESSION III: BAT LONGEVITY

Poster 9: Bechstein's bat: A candidate for negligible senescence?

FLEISCHER TONI[1,3], GAMPE JUTTA[2], SCHEUERLEIN ALEXANDER[3], KERTH GERALD[1]

[1] Applied Zoology and Conservation, Zoological Institute, University of Greifswald, Johann, Sebastian Bach-Strasse 11/12, 17487 Greifswald, GERMANY
[2] Statistical Demography, Max Planck Institute for Demographic Research, Konrad-Zuse-Str. 1 D-18057 Rostock, GERMANY
[3] Evolutionary Biodemography, Max Planck Institute for Demographic Research, Konrad-Zuse-Str. 1 D-18057 Rostock, GERMANY

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

Poster 10: Contribution to bat longevity studies in Ukraine

VLASCHENKO ANTON[1,2], KRAVCHENKO KSENIIA [1,2,3], HUKOV VITALII[1,2], PRYLUTSKA ALONA [1,2], RODENKO OLENA [1,2,4]

[1] Bat rehabilitation center of Feldman Ecopark, Kharkiv, UKRAINE; vlaschenko@yandex.ru
[2] Ukrainian Independent Ecology Institute, Kharkiv, UKRAINE
[3] Leibniz-Institute for Zoo and Wildlife Research
[4] University of Silesia in Katowice

One of the phenomena of bat's life-history is longevity. Bats have extremely long life span among the mammals of the same body size. The main method of age identification for free-living bats is banding (mostly ringing). However, this method became less popular 20-30 years ago, because of injury cases of bats. The modern types of bat-rings are safety and the number of injuries because of rings is infrequently. On this reason the bat ringing programs are renewed in Europe for the last 10 years. There were two waves of bat ringing in Ukraine: the first one in 1940-1960 and the second one were started in 1990th after 30 years gap. Currently the largest scale bat ringing program in Ukraine is provided by Kharkiv Bat Group in the North-Eastern part of the country. Our team concentrate the ringing efforts in four main locations: Kharkiv city, hibernation and swarming places (the ringing activity is provided in warm season of a year only), and summer habitats. For the first ten years of ringing program (2002-2011) the following results were obtained: 6935 individuals of 12 bat species were ringed and 299 individuals were recaptured. From 2012 to September 2016 yet around 7750 bats were ringed. We have obtained the following results of bat lifespan: *M. brandtii* – 8 years, female, hibernation mine; *M. daubentonii* – 8 years, female, hibernation mine; *M. dasycneme* – 9 years, female, hibernation mine; *M. nattereri* – 8 years, male, swarming place; *N. noctula* – 8 years, male, hibernation site in Kharkiv city; *E. serotinus* –12 years, female, breeding colony; *Pl. auritus* – 5 years, male, hibernation mine.
For other 5 species (*N. leisleri*, *P. nathusii*, *P. pygmaeus*, *P. kuhlii* and *V. murinus*) which are known for the Kharkiv region we have obtained 2-3 years old recaptures only.

Poster 11: Tooth wear patterns and longevity of *Myotis myotis* in the Holocene site of El Conejar Cave (Cáceres, Spain)

SEVILLA PALOMA[1], LAPLANA CÉSAR, CANALES-BRELLENTHIN PATRICIA, MODESTO MARIO, CANALS ANTONI

[1] Paloma Sevilla, Departamento de Paleontología, Facultad de Geología, Universidad Complutense de Madrid. C/ José Antonio Novais, 12. 28040 Madrid, SPAIN; psevilla@ucm.es

Among small mammals, bats stand out for having a series of features that make them look as special. Flight, ability to hibernate, lack of specialized predators and cave-dwelling are some of these features. Another particular feature of bats refers to the origin of their fossils in cave assemblages. Although frequently found together with other fauna, in most cases the bat remains come from *in situ* death, whereas the remaining small mammals become part of the cave sediments as the result of predatory activity. Because of this, certain characteristics concerning bat populations in the past may be obtained, which cannot be inferred for the other small mammals found in these assemblages. For instance, differential representation of tooth wear degrees may be used to provide insight concerning longevity and death profiles.

Although tooth wear in bats shows variability and cannot be used as a precise estimate of age, four categories can be easily established to refer individuals to age groups and analyze the representation of each group in fossil bat death assemblages. Here we present the results we obtained from studying the wear shown in the bat teeth collected in El Conejar Cave, which have provided a basis for discussion on bat longevity in the past. El Conejar Cave is a small-sized cave in the city of Cáceres (Extremadura, Spain). Sediments have been excavated since 1916, yielding abundant archaeological remains ranging in age from the Upper Paleolithic to the Bronze Age. The breccias excavated at different parts of the site yielded abundant small vertebrate remains, bats being the best represented group. Remains of the Greater Mouse-eared bat (*Myotis myotis*) dominate the small mammal assemblage. All wear stages are represented in the material: a) teeth with unworn cusps and cristas, belonging to unborn and/or unweaned individuals; b) teeth with a slight degree of wear located on the cusps, belonging to young individuals that have started to hunt; c) teeth with wear both on cusps and cristas, belonging to a wide range of mature individuals; d) flattened teeth in which wear is so advanced that there is practically no difference in the height of the crown between the cristas and the cusps, the dentine of each tooth widely exposed. An unexpected result was obtained for the intensely worn teeth: numbers were higher than expected, compared to other sites where *M. myotis* is abundant. The different explanations to these results are discussed, dwelling on longevity.

Poster 12: To fly the inflammation: Potent anti-inflammatory response in bat macrophages linked to extended longevity and viral tolerance

KACPRZYK JOANNA[1], HUGHES GRAHAM[1], PALSSON-MCDERMOTT EVA M.[2], QUINN SUSAN R.[2], PUECHMAILLE SEBASTIEN J.[1,3], O'NEILL LUKE AJ[2], TEELING EMMA C.[1]

[1] School of Biology and Environmental Science, University College Dublin, Belfield, Dublin 4, IRELAND; joanna.kacprzyk@ucd.ie
[2] School of Biology and Immunology, Trinity Biomedical Sciences Institute, Trinity College Dublin, Dublin 2, IRELAND
[3] Applied Zoology and Nature Conservation, Greifswald University, J.-S.-Bach-Str. 11/12, 17489 Greifswald, GERMANY

Bats are the reservoir hosts for a number of deadly viruses, have exceptional longevity and are the only mammals capable of sustained flight. To explore the role of the innate immune system in these unique adaptations, we challenged macrophages from the greater mouse-eared bat, *Myotis myotis* and the house mouse, *Mus musculus* with TLR ligands, Poly(I:C) and LPS. Macrophages from both species presented a high level of mRNA induction of anti-viral *INF-β* and proinflammatory *TNF* and *Il -1β*. However, in bats this antiviral, proinflammatory response was balanced by a sustained high level transcription of the anti-inflammatory cytokine *Il-10*, which was not observed in mouse, potentially resulting from adaptive regulation in bats. Additionally, phylogenomic selection tests across the basal divergences in mammals (N=39) uncovered six immune genes under positive selection in bats. We propose that bats may have evolved unique anti-inflammatory responses, to counterbalance inflammation resulting from flight, which consequently drives their extraordinary longevity and viral tolerance by limiting inflammaging and infection-induced immunopathology.

Poster 14: Mitochondrial heteroplasmy in long lived bats

JEBB DAVID[1], FOLEY NICOLE M.[1], PUECHMAILLE SÉBASTIEN J.[1,2],
KERTH GERALD[2],. TEELING EMMA C[1]

[1] University College Dublin, Belfield, Dublin 4, Ireland; Emma.Teeling@ucd.ie
[2] Greifswald University, Greifswald, GERMANY

Mitochondrial heteroplasmy is the presence of multiple non-identical copies of the mitochondrial genome within an individual. Heteroplasmy has important implications for mitochondrial diseases and has been shown to increase with age with humans. The Free Radical Theory of Ageing posits that mitochondrial mutations and increased heteroplasmy, due to oxidative damage, contribute to the familiar gradual, physical deterioration with age. The Chiroptera, bats, have been shown to have highly heteroplasmic mitochondrial DNA, yet also exhibit extreme longevity. However, previous studies have been restricted to small, repeat containing, loci in the Control Region. For the first time, we sequenced whole mitochondrial genomes from two long lived bat species and measured heteroplasmy on a population level. Wing tissue from *Myotis myotis* and *M. bechsteinii*, were sequenced, as well as blood from *M. myotis*. Both populations show similar levels of heteroplasmy to each other and to those previously reported in humans. There was also an extremely low rate of GC-TA transversions, characteristic of oxidative damage. There was also no correlation between the number of heteroplasmies and age in either species. Analysis of protein coding genes showed positive selection for certain heteroplasmies in *Myotis myotis*. Our findings suggest bats defy the Free Radical Theory of Ageing, and oxidative stress induced by flight is not the primary cause of mtDNA mutations. Intra-individual selection and efficient mitochondrial quality control may explain the exceptional longevity of this genus.

Poster 15: The mircobiome of the exceptionally long–lived *Myotis myotis*

HUGHES GRAHAM M. [1], LEECH JOHN[1]. PUECHMAILLE SÉBASTIEN J[3],
LOPEZ JOSE V.[2], TEELING EMMA C.[1]

[1] School of Biology and Environmental Science, University College Dublin, Belfield, Dublin 4, IRELAND; G.hughes@ucd.ie
[2] Department of Biological Sciences, Nova Southeastern University, Fort Lauderdale, Florida, USA
[3] Zoology Institute, Greifswald University, Greifswald, GERMANY

The importance of the gut microbiome, the collection of microbiota inhabiting regions of the GI tract, has become apparent in recent years. In addition to nutrition, health and behavior, the composition of the mammalian gut microbiome has also been linked to the process of biological ageing. Aging is characterized by the progressive decline of physiological function, increased frailty and an increase in chronic disease. Studies of the human microbiome have observed shifts in the microbial composition across different stages of life. The accumulation of potentially pathogenic gut flora with age has been associated with a range of clinical problems such as infection, frailty, cancer and problems relating to the immune response. Similar microbial shifts are also observed in mice.
The question of whether or not such microbial shifts are a symptom rather than a causative mechanism of ageing has yet to be conclusively answered. To explore the ageing-microbiome link further, we investigate the anal microbiome of a population of the wild, long-lived mammal species, the bat *Myotis myotis*. *M. myotis* is one of the few mammals demonstrating exceptional longevity (37 years), given their body mass (45g). We have used Illumina sequencing of the 16S rRNA bacterial gene to characterize the anal microbiome of more than 80 individual *M. myotis* bats through non-lethal sampling. This is one of the largest population-level microbiome studies to date, with juvenile to adult age ranges spanning the entire life span of a mouse or similar sized mammal (0-4 years).
Using the QIIME bioinformatics software suite and the Greengenes Bacterial database, microbial diversity across each individual was classified and compared to investigate *M. myotis* microbial patterns. We have characterized the composition of anal flora between juvenile and adult bats showing a lack of the microbial shifts observed in humans and mice. Additionally, we have used the PICRUSt software to predict what genes are expressed in the different bacteria present in the *M. myotis* microbiome. Our results highlight the potential role of stable gut flora in exceptional longevity.

Poster 16: Bats' Ageing Patterns are unique among Mammals

SCHEUERLEIN ALEXANDER[1] , SEMPF CAROLINE, DANKO MACIEJ,
REUSCH CHRISTINE, FLEISCHER TONI, KERTH GERALD

[1] Max- Planck Institute for Demographic Research, Konrad-Zuse-Straße 1, 18057 Rostock, GERMANY; scheuerlein@demogr.mpg.de

Lifespan in mammals ranges from months to approximately 300 years. Drawing on mortality data from ~400 mammalian species from the DATLife database we found that the proportion of age-related deaths increases with generation time. This effect has been previously described using widely available data on stage-specific survival, and maximum observed lifespan. Here we show that this pattern is robust, using high-quality age-specific mortality data. Bats, however, do not follow this mammalian pattern. Using survival and lifespan data from over 80 species, and high-quality age-specific mortality data for more than 20 species, we found that adult mortality in bat species does not increase with age.

We discuss this result in the light of life history theory, and test the role of phylogenetic constraints that shaped the evolution of bats' vital rates.

Poster 17: Evolution of movement mode and of longevity

RUCZYŃSKI IRENEUSZ[1], BARTOŃ KAMIL A.[2], KOSELJ KLEMEN[3]

[1] Mammal Research Institute PAS, Białowieża, POLAND;
iruczyns@ibs.bialowieza.pl
[2] Institute of Nature Conservation PAS, Kraków, POLAND
[3] Max Planck Institute for Ornithology, Seewiesen, GERMANY

According to evolutionary theory of aging, longevity can only evolve in species with low mortality due to extrinsic factors. Namely, if early death by predation, disease etc. is probable, the animals with costly adaptations for longevity are mostly prevented to receive their fitness benefits. After correction for the low body size, bats are the record holders in longevity among mammals. Together with lifespans of other endotherms capable flight or climbing (birds, arboreal and gliding mammals), the longevity of bats appears to support evolutionary theory of aging. Aging rate is directly related to mortality risk in birds and mammals and active flight enables birds and bats to be more successful at avoiding predators. But is this the only mechanism by which flight can contribute to the evolution of longevity? We used individual-based models to disentangle confounded effects of flight on life span evolution. We tested if increased foraging efficiency and resource availability enable flying animals to reduce the risk of starvation, thereby favouring longevity evolution. In our simulations alleles determining movement mode, offspring size and longevity were allowed to mutate. Aerial foragers had higher metabolic cost of movement per unit time and lower per unit distance than ground foragers and were moving faster. We manipulated energy content and regrowth time of prey, energy capacity of foragers, offspring cost, prey distribution (patchiness) and predation rate. Foragers could die either of age, by predation or by starvation. Evolution of longevity was connected with high costs of offspring and was more likely in aerial than ground foragers. We found that beside high predation, intense competition for food can prevent evolution of longevity. Our results demonstrate that the interplay of factors ranging from environmental parameters to movement mode and physiology, influences evolution of life histories in a more complex manner than previously assumed.

SESSION IV: BAT HETEROTHERMY

Poster 18: Temperature dynamics during torpor

BECKER NINA I. [1,2], OTTO MATTHIAS S.[1], EKSCHMITT KLEMENS[3], ENCARNAÇÃO JORGE A.[12]

[1] Mammalian Ecology Group, Department of Animal Ecology and Systematics, Justus-Liebig-University of Giessen, Giessen, GERMANY; nib@inatu.re
[2] inatu.re, Institute for Applied Animal Ecology and Ecoinformatics
[3] Research Centre for Biosystems, Land Use and Nutrition, Justus-Liebig-University of Giessen, Giessen, GERMANY

Bats are heterothermic endotherms and use torpor to save energy during diurnal inactivity and in periods of inclement weather or food shortage. Entry into torpor is characterized by reduced metabolic rate and declining body temperature. During torpor, body temperature is low and follows the ambient temperature at the roosting site. To exit torpor, the body must rewarm to normothermic levels, which is the energetically most costly phase of torpor. In this study we hypothesized that temperature dynamics during torpor under field conditions are species-specific and vary with reproductive status. Thermo-sensitive radio transmitters were used to measure skin-temperatures for six bat species (*Myotis bechsteinii, M. nattereri, M. daubentonii, Nyctalus noctula, N. leisleri* and *Plecotus auritus*). Preliminary results show species-specific differences in cooling but not in rewarming rates. We tentatively assume that the cooling and warming processes of torpor are driven by different factors. Microclimatic conditions within roosts appear to drive cooling rates, whereas fetal development seems to trigger faster warming rates.
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Poster 19: Plasma proteomic analysis of active and torpid greater mouse-eared bats (*Myotis myotis*)

HECHT ALEXANDER M. [1], BRAUN BEATE C.[1], KRAUSE EBERHARD[2],
VOIGT CHRISTIAN C.[1,3], GREENWOOD ALEX D.[1,4], CZIRJÁK GÁBOR Á.[1]

[1] Leibniz Institute for Zoo and Wildlife Research, Alfred-Kowalke-Str. 17, 10315 Berlin, GERMANY; hecht@izw-berlin.de, czirjak@izw-berlin.de
[2] Leibniz Institute for Molecular Pharmacology, Robert-Rössle-Str. 10, 13125 Berlin, GERMANY
[3] Department of Animal Behaviour, Freie Universität Berlin, Takustraße 3, 14195 Berlin, GERMANY
[4] Department of Veterinary Medicine, Freie Universität Berlin, Oertzenweg 19b, 14163 Berlin, GERMANY

Hibernation is a physiological adaptation to overcome extreme environmental conditions. It is characterized by prolonged periods of torpor interrupted by temporary arousals during winter. During torpor, body functions are suppressed and restored rapidly to almost pre-hibernation levels during arousal. Although molecular studies have been performed on hibernating rodents and bears, it is unclear how generalizable the results are among hibernating species with different physiology such as bats. As targeted blood proteomic analysis are lacking in small hibernators, we investigated the general plasma proteomic profile of greater mouse-eared bats (*Myotis myotis*) and hibernation associated changes between torpid and active individuals by two-dimensional gel electrophoresis. Results revealed an alternation of proteins involved in transport, fuel switching, innate immunity and blood coagulation between the two physiological states. The results suggest that metabolic changes during hibernation are associated with plasma proteomic changes. Further characterization of the proteomic plasma profile identified transport proteins, coagulation proteins and complement factors and detected a high abundance of alpha-fetoprotein. We were able to establish for the first time a basic myotid bat plasma proteomic profile and further demonstrated a modulated protein expression during torpor in *Myotis myotis*, indicating both novel physiological pathways in bats in general, and during hibernation in particular.

Poster 20: Effect of food restriction on thermoregulatory behavior and adipose tissue development in male parti-coloured bats *Vespertilio murinus*

KOMAR EWA[1], ZEGAREK MARCIN[1], DECHMANN DINA K. N.[2], RUCZYŃSKI IRENEUSZ[1]

[1] Mammal Research Institute PAS, Białowieża, POLAND; ekomar@ibs.bialowieza.pl
[2] Max Planck Institute for Ornithology, Radolfzell, GERMANY

In reaction to unfavorable environmental conditions bats, as heterothermic animals, can reduce metabolic rate and decrease body temperature to allocate more energy towards body reserve deposition. However, torpor also affects and slows down other important metabolic processes, e.g. rates of fetus development or potentially reduced sperm production. This can be crucial for male reproductive success due to high sperm competition. However, high insect abundance during summer allows males to invest in adipose tissue, which is critical for winter survival and probably also for mating activity in autumn. We experimentally manipulated food availability for captive male parti-coloured bats, to verify the effect of food limitation on their thermoregulatory patterns. We also investigated if and how the amount of available food affects the development of testes, filling of the epididymis and body condition of the bats as an indicator for the amount of adipose tissue. We found significant correlation between food intake, depth and duration of torpor bouts, and the timing of sperm production. In early summer, individuals provided with higher amount of food maintained higher and more stable skin temperature than food restricted ones. Animals in better body condition finished spermatogenesis up to half a month earlier and after it entered longer and deeper torpor bouts than food restricted animals. More intensive reduction of body temperature contributed to the increased fat accumulation. Our results indicate that bats under limited food availability are forced to trade-off between investment into reproductive tissue or fat. The project was funded by the Polish National Science Centre grant: DEC-2013/10/E/NZ8/00725.

Poster 21: Postnatal thermoregulation of Noctule bat (*Nyctalus noctula*) in captivity: veterinary and physiological aspects

ZUKAL JAN[1], PIKULA JIRI[2], BANDOUCHOVA HANA[2], KOVACOVA VERONIKA[2], LINHART PETR[2], PIACEK VLADIMIR[2]

[1] Department of Ecology and Diseases of Game, Fish and Bees, University of Veterinary and Pharmaceutical Sciences Brno, CZECH REPUBLIC
[2] Institute of Vertebrate Biology, Academy of Sciences of the Czech Republic, Brno, CZECH REPUBLIC

Regulation of body temperature is an important aspect of vertebrate evolution that allows the animal to maintain homeostasis in its physiological functions. Temperate Vespertilionid bats have adapted to seasonal and daily changes in climate food availability by becoming heterothermic, i.e. their body temperature varies with that of the environment.
Daily thermal profiles were undertaken in order to evaluate the physiological condition of the captive female Noctules during lactation and the pups during early postnatal growth. Thermal imaging during the four weeks *post partum* revealed a mean temperature for lactating Noctule females of 34°C. Female Noctules were observed lowering their body temperature and using daily torpor when weaning the young. Neonatal thermoregulation development depends on interaction between the mother and it's young. Young bats were incapable of thermoregulation for at least six days *post partum*; after six days, however, high body temperature and competent homeothermic thermoregulation resulted in rapid growth in the young. Importantly, juvenile Noctule bats seem capable of torpor, i.e. active lowering of body temperature, from around day 20 to 25, which coincides with a reduction in body mass growth rate.

Poster 22: Comparison of Liver Tissue and Mitochondrial Proteomes between Torpid and Active Bats

HUANG WENJIE[1], HAN YIJIE[2], LV QINGYUN[1], ZHANG SHUYI[3], LIAO CHEN-CHUNG[4], PAN YI-HSUAN[1]

[1] Laboratory of Molecular Ecology and Evolution, School of Life Science, East China Normal University, Shanghai, CHINA
[2] Key Laboratory of Protein and Peptide Pharmaceuticals, Institute of Biophysics, Chinese Academy of Sciences, Beijing, CHINA
[3] College of Animal Science and Veterinary Medicine, Shenyang Agricultural University, Shenyang, CHINA
[4] Proteomic Research Center, National Yang-Ming University, Taipei 11221, TAIWAN

Some bats survive extreme cold by hibernation that is composed of the repeated cycles of torpor-arousal. Previous studies suggested that liver plays basic role in metabolism and detoxification during bat torpor and mitochondria are critical organelles in torpid *Myotis ricketti* bats. To learn the molecular mechanism in regulation of liver activities and bat torpor, we compared liver tissue and mitochondrial proteomes between torpid and active *M. ricketti* bats. We found that 17% of identified proteins (135 proteins) with significant changes were associated with lipid metabolic process, citric acid cycle, and respiratory chain. The expression levels of 23% proteins (181 proteins) involved in amino acid metabolism, mitochondrial translation, and protein quality control systems were also significantly altered in torpid bats. Approximately 13% of differentially expressed proteins (99 proteins) were associated with mitochondrial apoptosis, signals, and morphology. Results of *gene ontology* and ingenuity pathway *analysis* indicated that signaling pathways involved in PI3K/AKT and EIF2 could be pivotal in control of cell survival and death of torpid bats. This study provides insights in liver protection during bat hibernation.

Poster 23: Higher Expression of Warm-sensitive Transient Receptor Potential Vanilloid Superfamily Members in the Bain of Torpid Bats

LIU DI, ZHENG SHENGHUI [1], PAN YI-HSUAN

[1] Laboratory of Molecular Ecology and Evolution, School of Life Science, East China Normal University, Shanghai, CHINA

Some small mammals hibernate to survive the harsh environment. During torpor, the body temperature of these hibernators are reduced to an extremely low level that is lethal for euthermic animals. The molecular mechanisms involved in control of thermal sensation in hibernating mammals are not yet clear. Temperature-sensitive transient receptor potential channels, i.e., thermo-TRPs, are critical factors for thermal sensation. Because torpid bats maintain their ability in response to elevated temperature, we hypothesized that warm-sensitive TRPs are highly expressed in bats during torpor. We compared gene expressions of ten thermo-TRPs, including TRPV1, TRPV2, TRPV3, TRPV4, TRPM2, TRPM4, TRPM5, TRPM8, TRPC5, and TRPA1 in the brain between torpid and active bats using quantitative RT-PCR. Results showed that the mRNA level of warm-sensitive TRPV1, TRPV2, TRPV3, and TRPV4 and cold sensitive TRPA1 was significantly higher in torpid bats. In contrast, cold sensitive TRPM8 and TRPC5 and the thermo-sensitive TRPM2, TRPM4, and TRPM5 had lower expression in torpid bats. The data imply that warm-sensitive vanilloid receptors have indispensable roles in bats during torpor. The regulatory mechanism for expression of these thermo-TRPs remains to be investigated.

SESSION V: BAT VOCALIZATIONS

Poster 24: Echo-acoustic flow determines object representation in complex spatial layouts

GREITER WOLFGANG[1,2], FIRZLAFF UWE[1]

[1] Chair of Zoology, Technical University of Munich
[2] Chair of Zoology, Technical University of Munich, Liesel-Beckmann-Str. 4
85354 Freising, GERMANY; greiter@wzw.tum.de

Echolocating bats use the echoes of their sonar emissions to determine position and distance of objects or prey. Target distance is represented in a chronotopically organized map of echo delay in the auditory cortex (AC) of bats. During flight in complex environments streams of echoes are reflected from multiple objects along the flight path. To separate sounds from specific objects in such streams is a challenging task for the auditory system of bats as well as many other animals.
We combined naturalistic call/echo sequences simulating a bat's flight in virtual acoustic space with extracellular recordings in the AC of anaesthetized bats (*Phyllostomus discolor*). We found neurons that selectively focused to echoes from only one object in a complex stream of echoes originating from two different objects along a virtual flight path. The objects were processed sequentially in the order of object approach. We further varied the temporal pattern of sonar emission during the simulated flight sequences to test its influence on cortical object representation. The detailed representation of an object in the cortical target range map was not fixed but could be dynamically adapted depending on temporal patterning of call/echo pairs during target approach within the flight sequence.
Our results show that neurons in the AC of bats can separate different streams of echoes and focus their response to specific objects in a complex naturalistic flight sequence, depending on the dynamic variation of sonar information (i.e. echo-acoustic flow) during flight. Therefore stream segregation in mammals can be based on the integration of multiple dynamically changing acoustic parameters.

Poster 25: Phonological syntax in babbling bouts of *Saccopteryx bilineata* pups

FERNÁNDEZ AHANA AURORA[1], KNÖRNSCHILD MIRJAM[1]

[1] Institute of Biology, Free University of Berlin, GERMANY

Animal communication can range from simple, stereotypic calls to complex and variable songs. Vocalizations can be composed of different syllable types which are arranged into sequences. This arrangement of smaller units (usually defined as syllables) into larger sequences (motifs or bouts) is defined as phonological syntax. Current analyses of phonological syntax in animal communication focuses on vocalizations of adults, e.g. primate alarm calls, whale song or bird song. Ontogenetic development of phonological syntax, however, has not been studied so far. In our present study, we investigate whether babbling bouts of *Saccopteryx bilineata* bat pups possess a syntactical structure and how it changes throughout vocal ontogeny. This bat is a highly social species with a complex vocal repertoire consisting of different call and song types. Pups learn at least one song type, the territorial song, by imitating tutor songs during ontogeny. Vocal imitation is achieved by conspicuous vocal practice in the form of babbling bouts, which bear a certain resemblance to the canonical babbling of human infants and the plastic song of songbirds. We recorded the babbling bouts of 31 pups belonging to 9 different colonies throughout their ontogeny (10-12 weeks from birth to weaning). Isolation and echolocation calls are emitted immediately after birth and both call types remain part of the species' adult vocal repertoire. Starting about 13 -15 days of age, pups of both sexes also produce syllables belonging to male adult territorial songs. Pup song renditions become more stereotypic during ontogeny until they resemble adult territorial song at approximately 10 weeks of age. Babbling bouts contain isolation calls, territorial song renditions and other syllables from the entire adult vocal repertoire. A network analysis revealed that isolation calls function as important nodes in the syntax network of babbling bouts and facilitate the transition from one vocalization type to the next. Moreover, the analysis suggests that the phonological syntax changes throughout ontogeny because older pups produce babbling bouts with more different vocalization types than those of younger pups.

Poster 26: Vocal Production Learning in Adult *Phyllostomus discolor*

LATTENKAMP ELLA Z. [1], VERNES SONJA C., WIEGREBE LUTZ

[1] Ludwig Maximilians University Munich, Division Neurobiology, Großhaderner Straße 2, 82152 Planegg-Martinsried, GERMANY; lattenkamp@bio.lmu.de

Bats have a highly specialized audio-vocal system, which allows not only for echolocation but also for rich acoustic communication. Most research has focused on bat echolocation, but recently bats have started to attract attention for being a well-suited animal model for vocal learning. Several bat species are known to have an extensive call repertoire and to exhibit a rich pallet of communicative interactions. Not only sophisticated syllable- and song formation was demonstrated, but some bat species have also shown indications of vocal production learning, i.e., the acquisition of non-innate communication calls, which further adds to the flexibility of the vocal repertoire.

Here we aim to establish a psychophysical behavioral paradigm that allows testing for vocal production learning in adult *Phyllostomus discolor* under fully controlled laboratory conditions: we developed a multistage training plan, in the course of which adult bats will be trained via an ultrasonic intercom to adjust their calls according to real-time manipulated auditory feedback. With the help of food reward, adult bats will be trained to adjust parameters of their own calls to match or compensate real-time modified playbacks of their calls. Modifications include changes of the fundamental frequency (‘pitch’) or energy content of the harmonics (‘formants’), among others. Via multivariate call analyses, we will assess the calls before and after the training period and will thus be able to detect significant changes in call parameters upon occurrence.

Targeted real-time modifications will allow investigating the ability of adult *P. discolor* to imitate artificially modified calls by independently adjusting properties of their phonatory system (the vocal folds for e.g. fundamental frequency) and filter system (the vocal tract for e.g. formant formation).

Poster 27: Full-spectrum characterisation of the vocal repertoire of the ghost bat (*Macroderma gigas*)

HANRAHAN NICOLA[1], TURBILL CHRISTOPHER, ARMSTRONG KYLE N., DALZIELL ANASTASIA H., WELBERGEN JUSTIN A.

[1] Hawkesbury Institute for the Environment, Western Sydney University Hawkesbury Campus, Science Road, Richmond, New South Wales 2753, AUSTRALIA; n.hanrahan@westernsydney.edu.au

Interest in the study of social communication in bats has grown substantially in recent years, facilitated by advances in recording and playback technologies as well as analytical techniques. Bats have been found to possess complex vocal repertoires of calls and even songs similar to birds; however, little is known at present about the functional significance of bat non-echolocation vocalisations. The ghost bat (*Macroderma gigas*) is a highly social, cave-dwelling, carnivorous bat that produces a range of vocalisations in the roost and while foraging, the functions of which are mostly unknown. Here, we characterise the vocal repertoire of this iconic bat as a first step to determining the functions of the vocalisations in the social organisation of the species. Ghost bat vocalisations were recorded at a maternity roost located in Pine Creek, Northern Territory, Australia over a 12-month period. Vocalisations were recorded remotely using a passive sound recorders installed within the roost (SM3Bat; Wildlife Acoustics) recording in full-spectrum format. Call element exemplars were identified by eye and the groupings confirmed using cluster analysis, incorporating frequency, slope, entropy and bandwidth variables. Next, thousands of call elements were extracted using a band limited energy detector designed in Raven Pro (Cornell Lab of Ornithology), and these elements were then classified using Discriminant Function Analysis based on the reference set previously identified. The analysis revealed that ghost bats have a remarkably rich repertoire of calls, comprising, chirps, trills, rasps, and melodious whistles, sometimes presented in a highly variable order akin to birdsong. The results show that the vocal repertoire of the ghost bat is much more variable than previously appreciated. This highlights the need for the study of social calls in full-spectrum in other species, and the potential conservation management application of remote acoustic recording as a low-disturbance tool for monitoring specific activities in bat roosts.

Poster 28: Sensory Collision Avoidance in Bat Aggregations: an empirico-theoretical approach

BELEYUR THEJASVI[1], GOERLITZ HOLGER R.[1]

[1] Acoustic and Functional Ecology Group, Max Planck Institute for Ornithology, Eberhard-Gwinner-Straße, Seewiesen, GERMANY; tbeleyur@orn.mpg.de, hgoerlitz@orn.mpg.de

Active sensing animals like echolocating bats are ideal to understand how organisms adapt their sensing strategies to maximise the information they gain about their environment. Individual bats emit very loud calls and rely on the faint returning echoes to sense their surroundings. Studies of individual bats have revealed how they alter their calling strategies during prey capture or in response to cluttered environments. Though bats can process complex trains of returning echoes, the presence of other echolocating conspecifics could cause detrimental 'sensory collisions' – where a loud call from another individual masks incoming echoes.

Many echolocating bats are social and are known to alter aspects of their call structure like call duration, inter-pulse interval, frequency content or a combination of these. Although empirical observations exist on the variety of call strategies that bats adopt against sensory collisions, a generalised conceptual framework is still missing. We present an empirico-theoretical approach to understand the underlying sensory basis of these behaviours by simulating how the various call strategies may reduce sensory collisions, and by testing these expectations against experimental data.

In our agent-based simulations we investigate the effect of altering the temporal structure of calls on sensory collisions by simulating bat agents calling at a variety of call durations, inter-pulse intervals and duty cycles. We also quantify the effect of spatial heterogeneity in hearing and calling by incorporating experimentally derived head-related-transfer-functions and call directionality data. To simulate a range of behavioural contexts we simulate bat agents echolocating at various group sizes, inter-individual distances and trajectory types. These simulations provide an understanding of which call strategies could potentially reduce sensory collisions in the presence of conspecifics.

On the experimental side, we present plans for our field-based tracking setup. Using a combination of 3 thermal cameras and a 12 microphone array, we will record the positions, calling directions and spectro-temporal call parameters in free flying *Myotis daubentonii*. This rich dataset will allow us to infer the time of arrival of calls from conspecifics and own echoes to derive the extent of sensory collision potentially experienced by each individual in the field with reference to the calling behaviour they adopt.

Our combined empirico-theoretical methodology presents a formal approach to reveal the underlying basis of call strategies adopted by bats when flying with conspecifics, and provides a flexible multi-species framework to do so.

Poster 29: What good are harmonics?

BEEDHOLM KRISTIAN[1]

[1] Aarhus University, Department of Bioscience, CF. Moellers Allé 3; kristian.beedholm@bios.au.dk

Since bat calls, like human speech are voiced vocalizations, they are inherently multiharmonic. The consequence of this fact is that the bats using echolocation calls that sweep over a frequency span of more than exactly one octave will experience some overlap between the frequency ranges covered by at least two of the resulting harmonics. In fact only the components of the call that lie within the lowest octave are guaranteed to occur only once within the call duration. Since it is well established that echolocating bats evaluate the delay between their outgoing emissions and the echoes returning to their ears in order to establish the range to objects in the surroundings, such multiple occurrences of frequency elements is bound to lead to ambiguities: harmonics may simply be mistaken for echoes. This is the case regardless of which perceptual mechanisms one assumes to be underlying the evaluation of the delay, and certain gleaning species like Natterer's bat seem to make an effort to diminish the harmonic content of their calls, strengthening the case for the idea that harmonics can be a problem to bats that need good resolution in time. Several researchers have pointed to the fact that bat calls appear to be Doppler tolerant (hyperbolic), at least for some species. This explanation for the concave time-frequency structure of the typical call is surprising in that the error in delay measurement would mostly appear to be tiny compared to the error introduced by the distance travelled between emitting the call and reception of the echo. I present here the idea that bats may in fact use calls that are optimal for measuring the delay between the different harmonic components in their calls particularly accurately. By comparing the local sweep rate in the overlapping portions of harmonics of calls from four captive *Eptesicus fuscus* recorded in a laboratory setting, it is found that these sweep rates are more similar between harmonics than is the case for the same calls modelled as a hyperbolically sweeping waveform. Thus, the actual data are better explained by the hypotheses that bats optimize their calls to detect Doppler induced delays within the calls than by the assumption that their calls are optimized to make them blind to the Doppler effect imposed by their flight speed.

Poster 30: Biosonar gone wrong: When bats cannot avoid colliding with recording equipment

LINNENSCHMIDT MEIKE[1], WIEGREBE LUTZ

[1] Ludwig-Maximilians University Munich, Division of Neurobiology, Dept. Biology II, Großhadernerstr. 2, 82152 Planegg-Martinsried, GERMANY; linnenschmidt@bio.lmu.de

The Mexican free-tailed bat (*Tadarida brasiliensis*) is known to aggregate in colonies of over one million individuals. Typically around sunset the bats leave the roost to fly to their feeding grounds. All bats emerge during a short time window creating a constant and dense stream of bats flying in the same direction. As all the bats use echolocation simultaneously to navigate while flying, one can imagine that the acoustic scenery is dense, loud and complex. We aim to understand how bats navigate with sonar under these extremely challenging circumstances. Emerging bats were recorded at a lava tube and canyon cave system on private land in New Mexico, USA, on three evenings between 19:30 and 22:00 pm in June 2015. Using a six-channel ultrasonic microphone array, placed directly in the pathway of the bats' flight, most bats managed to avoid the recording equipment. However, occasionally bats hit parts of the array construction (1 m long flexible metal poles with 6 mm diameter), tumbled shortly and continued flying. Some of these collisions can be identified in the array recordings. Here we investigate the acoustic scenery in a 0.5 s window before each collision to evaluate why and under which acoustic conditions bats collided with the array. By reconstructing the flight paths, we found that these bats fly at a speed of approximately 10 m/s (36 km/h). In most cases, the analyzed acoustic window (on the microphone that is closest to the collision) contained echolocation call sequences that show a reduction in inter-pulse interval, call duration, and an increase in frequency modulation, similar to when bats approach an object. Simultaneously, many calls without such a change were recorded. Further analysis will reveal whether these sequences belong to the colliding bat, or to another one that managed to avoid the structure. We will discuss the findings in the light of the following possibilities. In the case of the first scenario, the question remains "Why did the bat collide although the structure was obviously detected? In the second scenario, the question remains "Did the colliding bat echolocate at all?" The data will allow quantifying a reaction time and – distance in this extremely crowded echo-acoustic scene.

Poster 31: ABR derived audiograms and directional hearing of *Myotis daubentonii*

BRINKLØV SIGNE[1], WILSON MARIA, CHRISTENSEN-DALSGAARD JAKOB

[1] Department of Biology, University of Southern Denmark, Campusvej 55, 5230 Odense M, DENMARK; brinklov@biology.sdu.dk

Their auditory adaptations make echolocating bats hearing specialists and, as such, ideal model organisms for studies of general hearing mechanisms. The echolocation behavior and sound production physiology of *Myotis daubentonii*, one of the most common bats in Europe, has been studied in great detail, but with emphasis on the emitter, rather than the receiver, perspective. Yet, to fully understand the behaviour of the echolocator and the capacity of the echolocation system as a whole, the hearing characteristics of the echolocator must also be considered. To investigate pure tone thresholds and directional characteristics of their hearing, we established a protocol for anesthesia in *M. daubentonii* and measured the auditory brainstem response (ABR) of the bats using small (30G) sub-dermal needle electrodes. Once anesthetized, bats were placed on a turntable in front of an ultrasound speaker with the head exposed and ears in a natural position. We derived audiograms from bats facing the speaker by playing pure tones at different intensities within the relevant range of frequencies covered by the bats' echolocation signals. We then plotted the amplitude of the ABR, recorded at different sound intensities, and derived the threshold for each frequency by extrapolation. We used playback of the bats' own echolocation signal, a short, frequency-modulated sweep, to determine their directional hearing. For this purpose we used the input-output function to determine the hearing threshold and then used a signal intensity of 20 dB above threshold to compare the directional hearing response at six different angles ipsi and contralateral relative to the speaker. We found that, consistent with the peak frequencies of their echolocation signals, *M. daubentonii* have best auditory sensitivity from 45-60 kHz. Our measurements of directional hearing in *M. daubentonii* indicate nearly equal sensitivity at 0 and 60 degrees with a slight increase between 15 and 45 degrees, likely resulting from the resting position of the pinnae. We hypothesize that they can further hone their directional hearing by active movements of the outer ears. Our results contribute novel knowledge about the hearing characteristics of *Myotis daubentonii*, of use not only to enhance understanding of habitat use and anthropogenic noise effects and inform conservation initiatives but also in technologica l applications such as human hearing aids and biomimetics.

Poster 32: The impacts of acoustical interference from conspecifics on capture success of *Myotis daubentonii*

OLSEN MADS[1], SURLYKKE ANNEMARIE, JAKOBSEN LASSE

[1] University of Southern Denmark, Institute of Biology, Campusvej 55, 5230 Odense M, DENMARK; madsolsen@biology.sdu.dk

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Echolocating bats often encounter and interact with conspecifics in their search for food. This has long been believed to be problematic for the bats due to acoustical interference. Several theories explaining how to adapt and avoid this problem have been proposed, especially the use of jamming avoidance response (JAR). Recent studies have questioned this theory and conclude that some species of bats are not actively using JAR [1][2]. Our study focuses on how the water bat (*Myotis daubentonii*) overcomes the issue of acoustical interference from conspecifics and how this affects its capture success during hunting. Observations made in the field seem to support the newly concluded hypothesis and indicate that *Myotis daubentonii* does not use JAR. For our study we recorded several wild *M. daubentonii* in its natural habitat hunting over open water and supplemented the data with recordings of *M. daubentonii* hunting over an artificial pond in the lab. We analyzed the acoustical behavior and capture success of bats flying alone and bats hunting in groups. Preliminary data indicate that *M. daubentonii* does not use any clear JAR. Furthermore the data indicate that the presence of conspecifics does not influence the capture success. Further analysis is needed to clarify our observations. If in fact the bats do not use JAR and their hunting success is not affected it strongly indicates that the echolocation system is more robust than previously assumed.

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Poster 33: Acoustic and ecological similarity as factors for echolocation-call mediated interspecific information transfer in wild Myotis bats

HÜGEL THERESA[1,2,3], VAN MEIR VINCENT[1,2], MUÑOZ-MENESES AMANDA, CLARIN B.-MARKUS[1], SIEMERS BJÖRN M.[1,†], GOERLITZ HOLGER R.[1,2]

[1] Sensory Ecology Group, Max Planck Institute for Ornithology, Eberhard-Gwinner Straße 11, 82319 Seewiesen, GERMANY; hgoerlitz@orn.mpg.de
[2] Acoustic and Functional Ecology Group, Max Planck Institute for Ornithology, Eberhard-Gwinner Straße 11, 82319 Seewiesen, GERMANY
[3] Department of Animal Ecology and Tropical Biology (Zoology III), Julius-Maximilians-University, Am Hubland, 97074 Würzburg, GERMANY

Recognizing species identity is crucial for many aspects of animal life and directly relevant to fitness. A strong selection pressure exists in mating to distinguish conspecifics from sympatric similar species. Additionally, distinguishing between sympatric heterospecifics should be beneficial, for example for following ecologically similar heterospecifics to suitable roosting and foraging sites. The information transfer required for this ability might be mediated by multiple cues and signals, with acoustic signals playing a major role in many taxa including insects, anurans, birds and mammals. In bats, echolocation evolved for sound-based orientation and foraging of the calling individual, yet it also contains diverse information about the calling individual with can be perceived by close-by individuals. Increasing evidence supports the communicative function of echolocation within species, yet data about the role of echolocation calls for interspecific information transfer is scarce. Here, we asked if bats extract information from heterospecific echolocation calls, which information they extract, and if they use it for their own decision making during foraging. We tested the ecological similarity and the acoustic similarity hypothesis that propose different sensory and cognitive mechanisms underlying this information transfer. In three lab- and field-based playback experiments, we tested if foraging bats (*M. capaccinii* and *M. daubentonii*) approached the foraging calls of conspecifics and four heterospecifics that were similar in foraging ecology only (ecological similarity hypothesis), acoustic call structure only (acoustic similarity hypothesis), both, or none. In the lab, bats only approached calls of *M. capaccinii* and *M. daubentonii*, and only showed a very weak positive response to these species in the field. Our results confirm information transfer across species boundaries, yet cannot decide on the underlying mechanism which might be based on acoustic similarity only or on a combination of acoustic and ecological similarity. Furthermore, the mostly lacking response in the field highlights the importance of environmental factors and the need for studying animal behaviour where it really happens, in the field.

Poster 34: Tell me how aggressive you are: encoding the aggression level in bat vocalizations

WALTER MICHAEL[1], SCHNITZLER HANS-ULRICH[1]

[1] Animal Physiology, Institute for Neurobiology, University of Tübingen, GERMANY; mic.walter@student.uni-tuebingen.de

Bats are special compared to (some) other mammalian orders as they rely heavily on acoustic signals in order to communicate across social contexts. Among those, agonistic interactions and accompanying vocalisations have received comparatively little study. The usage and acoustic structure of such vocalisations is known to encode the emotional and motivational state of the caller. We studied the communicational behaviour between male greater mouse-eared bats (*Myotis myotis*) during agonistic encounters. Two randomly paired adult males were placed in an observation box that allowed us to record video and sound synchronously. We describe their vocal repertoire and compare the acoustic structure of vocalisations across two aggression levels, as quantified by the behaviour in the video. By inspecting thirty, one-minute long encounters we identified a rich variety of social calls that can be described as a signal continuum reaching from low-frequency sweeps to long, broadband squawks. Squawks were the most common vocalisation, often exhibited a chaotic spectral structure and presumably convey the highest level of aggression. We provide evidence for the presence of multiple types of nonlinear phenomena in this species' vocal repertoire, which further increased the spectral diversity. As predicted, the aggression level of the caller was encoded in the structure of squawks: increased aggression resulted in an increase in call frequency and was positively correlated with tonality. We argue that the extreme variability between and within squawks can be explained by small fluctuations in vocal control parameters which are likely a direct effect of the animal's increased level of arousal. Our assumption explains the described repertoire of aggressive calls as a continuum of signals that are influenced in graded fashion by the level of the sender's motivational state. Our approach potentially makes the definition of an extensive number of different call types redundant.

Poster 35: Bats and Bytes: echolocation producing Big Data for large-scale acoustic monitoring

BAS YVES[1], NEWSON STUART, JULIEN JEAN-FRANÇOIS, KERBIRIOU CHRISTIAN

[1] CESCO, National Museum of Natural History, 43, rue Buffon, 75005 Paris – FRANCE; ybas@mnhn.fr

Monitoring biodiversity over large spatial and temporal scales is crucial for assessing the impact of global changes and environmental mitigation measures. Bats often have high conservation prioritisation owing to their trophic position, habitat associations and threat level, and many have dedicated management plans. However, poor knowledge of species' ecology, identification issues and surveying challenges mean that large-scale monitoring to produce required distribution and abundance information is less developed than for some other taxa. Exciting possibilities applicable to professional and citizen science are offered by new recording techniques and methods of semi-automated species recognition based on sound detection. Static detectors deployed to record bats throughout whole nights have been recommended for standardised acoustic monitoring but until recently cost and lack of software to support the analyses of such data has prohibited wide uptake. Such monitoring schemes have recently been deployed in both Britain and France allowing the fast and standardized collection of millions of bat records together with very interesting data on non-targeted taxa such as bush-crickets. On the basis of a newly developed open software toolbox, we describe a semi-automated stepwise method for processing this large volume of recordings to assign identity to species or genus level with low error rates. We demonstrate how such data can accurately describe pronounced ecological patterns for numerous bat species at different scales: spatial variation in activity as a proxy for relative abundance, habitat selection and phenology of seasonal and nocturnal activity. If maintained in the long term, such schemes will also greatly improve estimates of species temporal trends and hence the assessment of conservation priorities.
The feedback produced by these two monitoring schemes allows us the opportunity to provide recommendations for the sustainability of long-term acoustic monitoring of bats. These include a database that is adaptively managed to allow all raw data to be re-analysed every time automatic identification makes significant progress, while keeping the link with expert validation to ensure consistency in the semi-automated process. More importantly, there are real benefits of developing long-term acoustic monitoring within a collaborative framework. Specifically, (1) for collaboration among bat scientists for the collection of reference sound data, because diversity and quantity of the reference library remains a limiting factor for automatic identification, and (2) for work on bats to consider the wider acoustic monitoring of other species groups by working with other zoologists to share resources and costs.

Poster 36: Not so special after all: Environmental acoustic cues guide the biosonar attention of the greater horseshoe bat

LATTENKAMP ELLA Z. [1], KAISER SAMUEL, KAUČIC ROŽLE, GROßMANN MARTINA, KOSELJ KLEMEN, GOERLITZ HOLGER R.

[1] Acoustic and Functional Ecology, Max Planck Institute for Ornithology, Eberhard-Gwinner-Straße, 82319 Seewiesen, GERMANY

Echolocation is a highly sophisticated sensory system specialized for actively probing light-deficient environments. However, due to the directional and stroboscopic emission of calls and the strong attenuation of ultrasonic frequencies, sensory acquisition by biosonar is limited both spatially and temporally. We hypothesise that this limitation will favour the opportunistic use of additional information for general perception of surroundings, and that mammals that use biosonar to hunt likely exploit a wider range of environmental information than previously believed. We tested this hypothesis in greater horseshoe bats (*Rhinolophus ferrumequinum* (Schreber, 1774)), whose echolocation is specialised for the detection of fluttering insects, but spatially strongly limited due to high call frequencies. We predicted that bats will react to passive acoustic cues, such as prey-generated rustling sounds, by steering their sonar beams towards the origin of the sound for further biosonar-based evaluation. In our first experiment, bats heard the sound of a moth fluttering in vegetation (or phase-randomised or amplitude-inverted versions of the recording to control for temporal and spectral cues). In our second experiment, we simultaneously presented a rustling sound with one of the control stimuli. Bat echolocation calls were recorded on a spatial microphone array to evaluated the number, intensity and direction of calls. Generally, bats scanned the room with their sonar beam, but directed it towards the sound source during playback; some individuals even towards the control sounds. Our results show that passive acoustic information guides the spatial pattern of information acquisition by echolocation. Akin to cross-modal integration, these echolocating mammals thus possess cognitive mechanisms to integrate environmental cues with actively generated echo-information, enlarging perceived space beyond the reach of their biosonar. Thus, despite the special and unique adaptations required for echolocation, it is integrated with and rooted in the phylogenetically older ‘passive’ hearing.

Poster 37: Loud Escapades during Cold Nights: Vocal Courtship of the Parti-coloured Bat

LADEGAARD MICHAEL[1], BEEDHOLM KRISTIAN[1], TEGLBERG MADSEN PETER[1,2]

[1] Zoophysiology, Department of Bioscience, Aarhus University, 8000 Aarhus, DENMARK; michael.ladegaard@gmail.com
[2] Murdoch University Cetacean Research Unit, School of Veterinary and Life Sciences, Murdoch University, South Street, Murdoch, Western Australia 6150, AUSTRALIA

As autumn progresses the soundscape of Danish cities is enriched by the parti-coloured bat's (*Vespertilio murinus*) display call which males cry out night after night even in temperatures below freezing. The parti-coloured bat's display call is easily audible to most humans, unlike its echolocation calls which have peak frequencies around 26 kHz. Lower frequencies suffer much less attenuation in air than do higher ones and hence travel further. That begs the question of how much the parti-coloured bat actually gains in active space by decreasing the frequency of its calls when communicating? To test this, the parti-coloured bat's display call was recorded in Aarhus University Park, Denmark, using a linear microphone array allowing for acoustic localisation and hence estimation of source levels. Transmission loss between array and sound source was estimated by calculating spherical spreading loss and correcting for frequency dependent attenuation. The display calls were characterised by mean peak and centroid frequencies of 13.5 and 17.5 kHz, respectively, and mean source levels at 10 cm of 113 dB re. 20 µPa (peak to peak), 100 dB re. 20 µPa (rms), and 82 dB re 20 $\mu Pa^2 s$ (energy flux density). A display call is thus an octave lower in peak frequency than an echolocation call and might be detected by another bat at ranges up to 200 metres in front of the caller assuming a detection threshold of 0 dB re. 20 µPa. By further assuming these bats are flying at the same height and taking directivity into account, the area of the parti-coloured bat's active space is about six times larger when emitting the display call compared to a call made at the usual echolocation frequency at the same peak to peak source level. It is suggested that parti-coloured bats incorporate the for bats unusually low 13.5 kHz component in their display call to maximise the chances of an encounter with a mate in the dark.

Poster 38: Never hold up travellers? – A playback study on the eavesdropping behaviour of migrating Nathusius‘ bats on feeding buzzes and courtship vocalisations

MARGGRAF LARA[1,2], VOIGT CHRISTIAN C.[1,3], PĒTERSONS GUNĀRS[4], VOIGT-HEUCKE SILKE L.[1,3]

[1] Department of Evolutionary Ecology, Leibniz Institute for Zoo and Wildlife Research, Alfred-Kowalke-Str. 17, 10315 Berlin, GERMANY; lmarggra@uni- potsdam.de
[2] Animal Ecology, Institute for Biochemistry and Biology, University of Potsdam, Maulbeerallee 1, 14469 Potsdam, GERMANY
[3] AG Verhaltensbiologie, Institute of Biology, Freie Universität Berlin, Takustr. 6, 14195 Berlin, GERMANY
[4] Faculty of Veterinary Medicine, Latvia University of Agriculture, K. Helmana Street 8, LV-3004 Jelgava, LATVIA

During autumn, migratory bats of the temperate zone face the challenge of accomplishing two things almost at the same time: migration and mating. These two life-history stages most likely require different sensory systems in bats. For example, during energy-demanding long-distance flights bats should eavesdrop on conspecific feeding buzzes to localise profitable and suitable foraging patches for refuelling efficiently, whereas the task of finding a mating partner demands listening for courtship vocalisations to spot potential mating areas. Yet, the knowledge on the use of eavesdropping during bat migration and mating is scarce. During autumn migration, we studied the eavesdropping behaviour of Nathusius' bats (*Pipistrellus nathusii*) at a major migratory corridor, at the coastline of the Baltic Sea and subsequently at sites in Germany where Nathusius' bats are known to court and probably also mate on their journeys to hibernation areas. We presented two vocalisation types (feeding buzzes and courtship calls) of their own species and as a control, a heterospecific species (*Nyctalus noctula*) to wild Nathusius' bats. We hypothesized that the response of bats differed with respect to place and time due to context-specific differences in motivation and energetic needs. At the migration corridor, the echolocation call activity of *P. nathusii* decreased in response to the broadcast of all stimuli types. The same pattern was evident later on at mating sites in response to the broadcast of conspecific courtship calls, yet, with a higher proportion of recorded social calls compared to the migration corridor. Concluding, we found no support for the hypothesis that bats differ in their eavesdropping behaviour during migration and mating periods. Nathusius' bats were not attracted to feeding buzzes and courtship calls during migration. Our experimental findings provide new insight into the use, or rather non-use, of bat vocalizations for eavesdropping in a migrant bat species.

SESSION VI: BAT IMMUNITY AND PATHOGENS

Poster 39: Novel highly divergent reassortant bat rotaviruses in Cameroon, without evidence of zoonosis

YINDA CLAUDE KWE[1,2], ZELLER MARK[1], CONCEIÇÃO-NETO NÁDIA[1,2], MAES PIET[2], DEBOUTTE WARD[1], BELLER LEEN[1], HEYLEN ELISABETH[1], MBIGHA GHOGOMU STEPHEN[3], VAN RANST MARC[2], MATTHIJNSSENS JELLE[1]

[1] KU Leuven - University of Leuven, Department of Microbiology and Immunology, Laboratory of Viral Metagenomics, Rega Institute for Medical Research, Leuven, BELGIUM; kweclaude.yinda@kuleuven.be
[2] KU Leuven - University of Leuven, Department of Microbiology and Immunology, Laboratory for Clinical Virology, Rega Institute for Medical Research, Leuven, BELGIUM
[3] University of Buea, Department of Biochemistry and Molecular Biology, Molecular and cell biology laboratory, Biotechnology Unit, Buea, CAMEROON

Bats are an important reservoir for zoonotic viruses. To date, only three RVA strains have been reported in bats in Kenya and China. In the current study we investigated the genetic diversity of RVAs in fecal samples from 87 straw-colored fruit bats living in close contact with humans in Cameroon using viral metagenomics. Five (near) complete RVA genomes were obtained. A single RVA strain showed a partial relationship with the Kenyan bat RVA strain, whereas the other strains were completely novel. Only the VP7 and VP4 genes showed significant variability, indicating the occurrence of frequent reassortment events. Comparing these bat RVA strains with currently used human RVA screening primers indicated that most of the novel VP7 and VP4 segments would not be detected in routine epidemiological screening studies. Therefore, novel consensus screening primers were developed and used to screen samples from infants with gastroenteritis living in close proximity with the studied bat population. Although RVA infections were identified in 36% of the infants, there was no evidence of zoonosis. This study identified multiple novel bat RVA strains, but further epidemiological studies in humans will have to assess if these viruses have the potential to cause gastroenteritis in humans.

Poster 40: Molecular evidence of Chlamydia-like organisms in the faeces of the bat *Myotis daubentonii*

VESTERINEN EERO J. [1], HOKYNAR KATI[2], LILLEY THOMAS M.[1,3], PULLIAINEN ARTO[4], KORHONEN SUVI[2], PAAVONEN JORMA[6], PUOLAKKAINEN MIRJA[2]

[1] Department of Agricultural Sciences, Latokartanonkaari 5, FI-00014 University of Helsinki, Helsinki, FINLAND; eero.z.vesterinen@helsinki.fi
[2] Virology, University of Helsinki and Helsinki University Hospital Helsinki, PO Box 21, 00014 University of Helsinki, FINLAND
[3] Biology Department, 1 Dent Drive, Bucknell University, Lewisburg PA, 17837 USA
[4] Institute of Biomedicine, University of Turku, FI-20520, Turku, FINLAND
[5] Obstetrics and Gynecology, University of Helsinki and Helsinki University Hospital, Helsinki, FINLAND

In this study we screened bat faeces and potential bat prey items for the presence of CLOs – recently identified members of the Chlamydiales order – by molecular analysis. CLOs share intracellular lifestyle and biphasic developmental cycle and they have been detected in environmental samples as well as in various hosts like amoebae, arthropods, fish and mammals. Targeting the *16S rRNA* gene, Chlamydiales DNA was detected in 55% of the bat specimens. PCR amplification, sequencing and phylogenetic analysis of the 16S rRNA and 23S rRNA were used to classify positive specimens and infer their phylogenetic relationships. Most sequences matched best with *Rhabdochlamydia* spp. or with uncultured *Chlamydia* sequences identified in ticks. Another set of sequences matched best with *Chlamydia* genus or with uncultured *Chlamydia* from snakes. To gain evidence of whether CLO in bat faeces is merely diet-borne, we analyzed insects trapped from the same location where the bats foraged. Interestingly, the CLO sequences resembling *Rhabdochlamydia* spp. were detected in insect material as well, but the other set of CLO sequences was not, suggesting that this set might not originate from prey. Thus, bats represent another potential host for Chlamydiales and could harbor novel, earlier unidentified members of the order.

Poster 41: Effect of sex and reproductive status on the immunity of the temperate bat, *Myotis daubentonii*

RUOß SARA[1], BECKER NINA INGA[1,2], OTTO MATTHIAS SEBASTIAN[1], CZIRJÁK GÁBOR-ÁRPÁD[3], ENCARNAÇÃO JORGE ANDRÉ[1,2]

[1] Mammalian Ecology Group, Department of Animal Ecology and Systematics, Justus-Liebig-University of Giessen, Heinrich-Buff-Ring 26 (IFZ), 35392 Giessen, GERMANY; J.Encarnacao@bio.uni-giessen.de
[2] inatu.re, Institute for Applied Animal Ecology and Ecoinformatics, 35457 Lollar, GERMANY
[3] Department of Wildlife Diseases, Leibniz Institute for Zoo and Wildlife Research, Alfred-Kowalke-Str. 17, 10315 Berlin, GERMANY

Immunity is highly variable within and between species and can be influenced by both internal (e.g. hormone levels, energy demand) and external (e.g. pathogens, climate) factors. Especially in bat species a profound understanding of immunology is needed as they are known reservoirs for numerous emerging zoonotic pathogens. In addition, bats have remarkable ecological and energetic characteristics making them outstanding study organisms for the field of ecoimmunology. Thus, we aimed to examine the variability of a temperate bat's immunity assessing the humoral and cellular effectors of innate and adaptive immune system of male and female *Myotis daubentonii* during different reproductive states. After sampling female (N = 46) and male (N = 40) *M. daubentonii* , we estimated their bacterial killing activity, complement and natural antibody titers, immunoglobulin G concentration and the total and differential white blood cell counts. Reproductively active males had lower cellular immunity compared to non-reproductive individuals. Pregnant females had increased IgG concentrations while hemolysis was enhanced during lactation. No clear trade-off between immunity and reproduction was found; instead immunity of male and female bats seems to be modulated differently most probably due to varying hormonal and energetic states. Our data suggest that both adaptive and innate immunity as well as individual differences, i.e. sex and reproductive state need to be considered to get a comprehensive overall picture of immunity in wild mammals.

Poster 42: Monoclonal antibodies for the specific detection of immunoglobulins (IgM and IgG) from *Eidolon helvum* and *Rousettus aegyptiacus* fruit bats

BALKEMA-BUSCHMANN ANNE[1], KLEY NILS[1], GROSCHUP MARTIN H.[1], KELLER MARKUS[1], SCHMIDT KRISTINA M.[1], KOELLNER BERND[2]

[1] Friedrich-Loeffler-Institut, Institute of Novel and Emerging Infectious Diseases, Greifswald-Insel Riems, GERMANY; anne.buschmann@fli.de
[2] Friedrich-Loeffler-Institut, Institute of Immunology, Greifswald-Insel Riems, GERMANY

Fruit bats have moved into the focus of infectiology research due to their postulated role as competent reservoir species for a variety of viruses. The precise analysis of their actual role in certain disease outbreaks is often hampered by the lack of specific diagnostic tools, eventually resulting in the dissemination of uncertain assumptions. To close this gap, we aimed at generating monoclonal antibodies (mabs) for the specific detection of IgM antibodies that are exclusively produced in the very early phase of an infection, and IgG antibodies, indicating that the infection lies at least several weeks, sometimes even years before the actual analysis of the samples. Our target species are *Eidolon helvum* and *Rousettus aegyptiacus* fruit bats, as both species have been shown to play an important role in the transmission of a number of disease agents. These species have been kept as productive breeding colonies at the Friedrich-Loeffler-Institut for a number of years.

In this project, IgG and IgM of both fruit bat species were purified by affinity chromatography and used for the immunization of Balb/c mice. Screening of the resulting clones was performed using sera from bats immunized with bovine serum albumin (BSA). Doing so, we were able to identify a panel of mabs that specifically bind to either IgG or IgM derived from *Eidolon helvum* or *Rousettus aegyptiacus*.

These newly generated mabs will considerably improve the diagnostic situation for the analysis of fruit bat samples by enabling the determination and differentiation of an early and late humoral immune response in animals that may have been in contact with infectious agents. This will considerably facilitate elucidating the role of bats in certain disease outbreaks.

Poster 43: When a virus uses another entrance - Immune mechanisms involved in innate anti- Lyssaviruses immune response in nasal cavity of European bats

ZHU YAQING[1], HE XIAOCUI[2], SCHÄFER ALEXANDER[3], PIKULA JIRI[4], KÖLLNER BERND[1]

[1] Institute of Immunology, Friedrich-Loeffler-Institute, Greifswald-Insel Riems
[2] Max-Planck-Institute for Immunology, Freiburg
[3] Department of Natural Sciences, University Greifswald
[4] University of Veterinary Sciences, Brno

Lyssaviruses are neurotropic viruses causing fatal encephalitis of central nerve system, rabies. In Europe, bats act as reservoir hosts for two specific types of Lyssaviruses, European Bat Lyssavirus (EBLV-1 and -2). Although cases of rabies in bats caused by and transmission to humans of EBLV 1 or 2 are described, there are no reports about epidemics in bats. Moreover, Lyssavirus specific antibody titers in European bat colonies were only rarely detected. This indicates that innate immune pathways might be responsible for the observed resistance without contribution of adaptive immune mechanisms in bats.
Therefore, we characterized the interferon Type I and III family of two European bats species *E.serotinus* and *M.myotis*. Both species do have a typical IFN structure with Type I IFN β, δ, ε, κ, ω and τ and Type III IFN λ. Until now there are no evidences for an active IFN α as only one pseudogene could be sequenced yet. Using established cell lines from nasal epithelium (*Mm*Nep) nervus olfactorius (*Mm*Nol), *M. myotis* brain (*Mm*Br) we analyzed in-vitro the IFN responses along the aerosol infection route by investigation of IFN-specific signaling pathways, induction of interferons (IFNs)/interferon stimulated genes (ISGs) and anti-viral effects in correlation to the expressions of viral receptors in each cell line.
Interestingly, we found a gradual decreased susceptibility along the aerosol route combined with an increased IFN response indicating that the observed resistance of bats is based on a specific co-evolutionary relation between Lyssaviruses and there reservoir hosts.

Poster 44: Phylodynamic studies on astrovirus sequences detected in German bats as a model of agent transmission within and between bat species

KÖHLER ARIAN[1], ZEUS VERONIKA[2], FISCHER KERSTIN[1], KERTH GERALD[2], GROSCHUP MARTIN[1], BALKEMA-BUSCHMANN ANNE[1]

[1] Friedrich Loeffler Institut, Institute of Novel and Emerging Infectious Diseases, Greifswald – Insel Riems, GERMANY
[2] Ernst-Moritz-Arndt Universität Greifswald, Institute for Zoology, Greifswald, GERMANY

In recent years, bats have received increased attention from virologists for harbouring a huge variety of viruses, including some viruses with zoonotic potential, especially in the tropics. A better understanding of virus transmission routes and the role of bats as possible vectors would be desirable. In order to elucidate the routes and frequencies of virus transmission within and between bat colonies, we selected astroviruses (virus family *Astroviridae*) as a model agent for our study. Astroviruses are found in numerous mammalian and avian species in a large variety of sequence variations. Though bat-astroviruses exhibit a relatively high prevalence, there was no pathogenic effect observed so far, neither on bats, nor on other animals. However, other specific animal astrovirus variants were described in humans and other animals, that could be linked to diarrhoea, and more recently also hepatitis, nephritis and encephalitis. In bats, astrovirus sequences were first detected eight years ago, but little is still known about the course of infection, possible routes of virus dissemination, as well as the transmission mode of astrovirus infections in bats. We analysed faecal and urine samples of individually tagged bats of the species *Myotis nattereri*, *Myotis bechsteinii*, *Myotis daubentonii*, and *Plecotus auritus* collected at three different sampling sites in Germany for the presence of astrovirus nucleic acids by hemi-nested conventional PCR and sequencing. Additional genetic studies including Next Generation Sequencing (NGS) and newly established PCR assays were conducted to reveal more of the genetic background of the viruses. The phylogenetic proximity of the virus sequences detected in bats of different colonies, different species, and different geographical regions within Germany were analysed in order to increase our understanding of the possible virus transmission modes between these animals. Our first results indicate a seasonal fluctuation in the prevalence of astroviruses in bats. Furthermore, detected variants show a high diversity (especially in the Natterer's bat, *Myotis nattereri*) and cluster in a mainly species-specific manner, whereas other sole variants seem to be genetically very distinct to other clusters of bat-associated astrovirus sequences. Some variants have been detected regularly throughout our study (2011-2016), while others are predominantly present in specific years.

Poster 45: Endogenous retrovirus mining in bat transcriptomes

LEVANTIS ILYA[1], POTTER JOSHUA, WARREN KIM, YOHE LAUREL,
DÁVALOS LILIANA, KATZOURAKIS ARIS, ROSSITER STEPHEN

[1] School of Biological and Chemical Sciences, Queen Mary University of London, London, UK; i.levantis@qmul.ac.uk

Retroviruses have been infecting mammals for at least 100 million years, leaving descendants in host genomes known as endogenous retroviruses (ERVs). A marked difference in the activity of retroviruses among species has been observed; for example, humans largely contain inactive lineages of ERVs, while the mouse contains numerous lineages of active ERVs. The increasing quantity of genomic data for mammalian species now allows the study of ERV features more broadly across this well-studied clade. This study focuses on bats, which number >1200 species, and which are the natural hosts of multiple zoonotic viruses of public health concern, including Ebola, Nipah, Hendra and SARS.

Most ERV derived sequences found in host genomes are inactive 'viral fossils', however, previous studies have shown that these endogenous viral elements (EVEs), occasionally maintain open reading frames and show evidence of purifying selection. A number of cases have been described in the literature where EVEs have been co-opted in host immunity pathways giving rise to EVE-derived immunity (EDI). In these cases EVEs either acting as regulatory elements, or as part of expressed transcripts.

This study is a pilot report describing initial findings from analysis of ERVs across multiple tissue transcriptomes across multiple species. We used high-throughput sequencing to generate transcriptomic data from tissue specific samples (including spleen samples) of 15 species of phyllostomid bats. Assembled transcriptomes are first analysed to catalogue the diversity of ERVs and ERV fragments present, thus outlining the retrovirus pathogen landscape in each studied species. Addiotionally, we investigate ERV derived sequences present in spleen transcriptomes for signs of co-option by the host species as EDI genes.

Poster 46: White-nose syndrome infection intensity in Palearctic and Nearctic bats

PIKULA JIRI[1,2], AMELON SYBILL K.[3], BANDOUCHOVA HANA[1], BARTONIČKA TOMÁŠ[4], BERKOVA HANA[5], BRICHTA JIRI[1], HOOPER SARAH[3], KOKUREWICZ TOMASZ[6], KOLARIK MIROSLAV[7], KÖLLNER BERND[8], KOVACOVA VERONIKA[1], LINHART PETR[1], PIACEK VLADIMIR[1], TURNER GREGORY[9], ZUKAL JAN[4,5], MARTÍNKOVÁ NATÁLIA[5,10]

[1] Department of Ecology and Diseases of Game, Fish and Bees, University of Veterinary and Pharmaceutical Sciences Brno, Brno, CZECH REPUBLIC; pikulaj@vfu.cz
[2] CEITEC - Central European Institute of Technology, University of Veterinary and Pharmaceutical Sciences Brno
[3] United States Department of Agriculture Forest Service, University of Missouri, Columbia, MO, USA
[4] Department of Botany and Zoology, Masaryk University, Brno, Czech Republic
[5] Institute of Vertebrate Biology, Academy of Sciences of the Czech Republic, Brno, CZECH REPUBLIC
[6] Institute of Biology, Department of Vertebrate Ecology and Paleontology, Wrocław University of Environmental and Life Sciences, Wrocław, POLAND
[7] Laboratory of Fungal Genetics and Metabolism, Institute of Microbiology, Czech Academy of Sciences, Prague, CZECH REPUBLIC
[8] Institute of Immunology, Friedrich-Loeffler-Institute, Federal Research Institute for Animal Health, Greifswald-Insel Riems, GERMANY
[9] Pennsylvania Game Commission, Harrisburg, PA, USA
[10] Institute of Biostatistics and Analyses, Masaryk University, Brno, CZECH REPUBLIC

White-nose syndrome (WNS) decimates populations of hibernating bats in the Nearctic, yet species from the Palearctic seem to cope better with identical skin invasion by the fungal pathogen causing WNS. The discrepancy encourages a plethora of hypotheses on mechanisms leading to differential species survival of the same disease. To address the issue of intercontinental comparisons of WNS, we developed a novel grading scheme from a series of periodic acid–Schiff stained sections according to presence of distinct microscopic lesions consistent with the histopathologic criteria for WNS diagnosis. The proposed WNS grading scheme provided good agreement between raters in a crowd-sourcing experiment, making it a powerful and widely applicable tool. We sampled Nearctic and Palearctic bats using non-lethal, ultraviolet light guided biopsy. The findings of *Pseudogymnoascus destructans* infection and WNS were ordered with increasing severity from presence of the fungus on the wing surface to replacement of tissues in the whole wing thickness by the fungus. Occurrence of surface fungal skin colonization, multiple and confluent cupping erosions, basement membrane breach, the full-thickness invasion, inflammatory response and fungal sequestration in *M. lucifugus* was at least 10 to 30 % higher than in Palearctic bats. Overall accumulative grading score was significantly higher in North America compared to

Europe and Asia, indicating that Nearctic bats develop more severe pathology when infected with *P. destructans*. The accumulation of wing damage likely influences mortality in affected bats as we demonstrate in a fatal case in *Myotis daubentonii* with natural WNS infection and a healing process in *Myotis myotis*.

Poster 47: Virus Diversity in bats from the Daintree Rainforest

KOHL CLAUDIA[1], KURTH ANDREAS[1], BURROUGHS AMY[2], CLAYTON BRONWYN[2], NITSCHE ANDREAS[1], TODD SHAWN[2], SPENCER HUGH[3], CRAMERI GARY[2], SMITH INA[2], WANG LIN-FA[4]

[1] Robert Koch Institute, Centre for Biological Threats and Special Pathogens, Nordufer 20, 13353 Berlin, GERMANY
[2] CSIRO Health and Biosecurity, Australian Animal Health Laboratory, Geelong, Victoria 3220, AUSTRALIA
[3] Austrop Foundation, Cape Tribulation, AUSTRALIA
[4] Programme in Emerging Infectious Diseases, Duke-NUS Medical School, SINGAPORE 169857

Viruses responsible for disease outbreaks in humans naturally emerge either from the human population itself or by spill-over events from animal hosts (zoonoses). Despite all differing possibilities of virus emergence, seventy-five per cent of emerging viruses have a zoonotic origin, thus highlighting spill-over events from animals to humans as a major threat to public health. Consequently, it has become evident that surveillance and long-term monitoring of viruses prevalent in wildlife is of particular importance. Hereby it is important to focus on apparently healthy animals in their natural habitat to maximize discovery potential and understand environmental disease factors, biology and ecology (heat, stress, nutrition deficiencies) that are further influencing the risk of virus spreading and shedding. In this collaborative pilot study the Tropical North Queensland (TNQ) rainforest has been chosen because it is the oldest rainforest in the world and comprises a unique diversity of bats. We investigate how the biodiversity of bats, the second largest order of mammals, influences the evolution of highly pathogenic viruses and vice-versa. To assess the viral diversity we are using metagenomic sequencing, serology and virus isolation. Results obtained so far from this collaborative project will be presented and discussed in comparison to similar work with European bats and the viruses they carry.

SESSION VII: BATS AS CONSERVATION TARGETS

Poster 48: Adverse effects of artificial illumination on bat drinking activity

RUSSO DANILO[1, 2], CISTRONE LUCA[3], LIBRALATO NOEMI[4], KORINE CARMI[5], JONES GARETH[2], ANCILLOTTO LEONARDO[1]

[1] Wildlife Research Unit, Laboratorio di Ecologia Applicata, Sezione di Biologia e Protezione dei Sistemi Agrari e Forestali, Dipartimento di Agraria, Università degli Studi di Napoli Federico II, via Università 100, I-80055 Portici (Napoli), ITALY; danrusso@unina.it
[2] School of Biological Sciences, University of Bristol, UK
[3] Forestry and Conservation, Cassino), ITALY
[4] Dipartimento di Biologia e Biotecnologie "Charles Darwin", Università degli Studi di Roma La Sapienza, Roma, ITALY
[5] Mitrani Department of Desert Ecology, Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, ISRAEL

Artificial illumination at night (ALAN) alters many aspects of animal behaviour. Commuting and foraging bats have been found to be affected by ALAN, but no study has yet addressed the impact of lighting on drinking activity, despite its critical importance for bats. We experimentally illuminated cattle troughs used by drinking bats at four forest sites in Italy, and compared drinking activity and foraging activity under lit and dark conditions. We predicted that 1) the number of bat species and drinking events will be lower under illumination and 2) forest bat species will be more affected than edge specialists. We recorded 2549 drinking events from 12 species or species groups, most of which decreased drinking activity under illumination. The effects of ALAN on drinking were stronger than on foraging. Forest species never drank when the light was on. Edge-foraging species reduced drinking activity while also increasing foraging under lit conditions. We highlight a previously overlooked negative effect of ALAN on bats, whose implications may be locally catastrophic. Given the importance of water sites for both bat foraging and drinking, their illumination should be forbidden or, if necessary, mitigated or compensated for with the creation of alternative drinking sites or part-time lighting.

Poster 49: Diversity and activity patterns of bats from Northeastern Algeria.

FARFAR AMRANE[1], BENDJEDDOU MOHAMMED LAMINE[1], BOUKHEROUFA FERIEL[1], METALLAOUI WASSIM[1], KORBA RAOUF AMARA[1], BAKER MOHAMMAD ABU[2], AMR ZUHAIR[3], BOUSLAMA ZIHAD[1]

[1] Ecology of Terrestrial & Aquatics Systems Laboratory (EcoSTAq), Department of Biology. BP 12 Bloc F. Badji Mokhtar University, Annaba 23200, ALGERIA
[2] Department of Biological and Environmental Sciences, Qatar University, Doha, QATAR
[3] Department of Biology, Jordan University of Science & Technology. P. O. Box 3030, Irbid, JORDAN

Diversity, Species richness, activity patterns and association of 13 bats species representing four families (Rhinolophidae, Miniopteridae, Vespertilionidae and Molossidae) from nine different habitats at El Kala Biosphere Reserve, North-eastern Algeria were studied. *Nyctalus leisleri* and *Myotis emarginatus* were found in five different habitats, while *Rhinolophus ferrumequinum Rhinolophus mehelyi* and *Pipistrellus pipistrellus* were found in three habitat types. Species richness (total number of species within a site) ranged between 1 and 9 with an average species richness is 4.78. *Rhinolophus ferrumequinum*, was netted during March until September with peaks in May and July. Activity pattern for *Rhinolophus hipposideros* continued from March until December, with a peak in July with no activity during January and February. For *Rhinolophus blasii*, a steady activity almost all year round, with exception of January with a peak noted in July. Maximum number of *Rhinolophus euryale* was observed during July, and then declined after August to appear again in good numbers in March. *Rhinolophus mehelyi* individuals was similar from April to September, and then declined with no records from December and January. *Myotis punicus* was captured all year round expect in February, with highest number collected in July. *Myotis emarginatus* was absent from October to February, then appeared from March to September with a peak in July. *Eptesicus isabellinus* was captured from February to November. Highest number of individuals for *Pipistrellus kuhlii* was recorded during April and August. *Pipistrellus pipistrellus* were captured over the duration of the study. Two periods of activity were noted for *Nyctalus leisleri*, the first from February to March, then from October to November. *Miniopterus schreibersii* was absent during December to February, then became active in March and their after. Two activity periods are noted for *Tadarida teniotis*, one in February and March, then in September to December, with no activity during spring and summer months.

Key words: Chiroptera, El Kala, Algeria, diversity, activity patterns, species richness.

Poster 50: The influence of weather on a population of *Pipistrellus pygmaeus* in West Wales, U.K.: a mammalian indicator of changes in climate

ANDREWS PETER T. [1], CRUMP ROBIN G.[2], HARRIES DAVID J.[3],
ANREWS MARGARET M.[4]

[1] The University of Liverpool, Liverpool L69 3 BX, UK., [1] deceased;
[2] Orielton Field Centre, Pembrokeshire SA71 5EZ;
[3] Somerton Cottage, Hundleton Pembrokeshire, SA71 5RX, UK.
[4] School of Biomolecular Sciences Liverpool John Moores University, Liverpool L3 3AF; m.m.andrews@livjm.ac.uk

A nursery roost of the soprano pipstrelle bat *Pipistrellus pygmaeus* has been monitored continuously between 1 April and 27 September (Weeks 1-26) for 20 years to promote conservation of the species, which declined over the last century. The long-term study, essential to estimate a reliable population trend, is linked to environmental changes as possible causes of decline. Criteria for an assessment and conservation of an indicator species are that a population should be sampled quickly with reasonable effort on a regular basis. The use of weekly exit counts of bats from a nursery roost during May, June and July fulfilled those criteria and enabled predictions of year to year populations to be made for *Pipistrellus pygmaeus.* The main emergence was from May to July (Weeks 6–18) when 550 ± 190 (SD) *P. pygmaeus* were counted. Analysis showed that the year-to-year change in population size of female *P. pygmaeus* (ΔN) and the time of the peak exit count of the females from the roost in May to June could be predicted from the integrated air temperature (degree days, D) between 1 January and 31 March. The regression of ΔN on D showed a statistically significant linear regression line defined by $\Delta N = 1.31 - 0.0015\ D$ ($R^2 = 38.4\%$; $p = 0.005$). $\Delta N = 1.04$ to 1.33 reflected a stable to increasing population (Years 1–7 and 15–20). $\Delta N = 0.78$ to 1.00 reflected a stable to decreasing population (Years 8–14). The regression of the time of the first peak exit count, calculated as the number of weeks from 1 April on D showed a statistically significant linear regression line defined by Weeks = $12.75 - 0.020\ D$ ($R^2 = 32.8\%$; $p = 0.008$). Rising temperatures between January and March would be detrimental to *P. pygmaeus* populations and rising temperatures due to climate change would cause a higher number of degree days between January and March. The findings of this study revealed the environmental factors that are relevant to the design of appropriate conservation strategies. Although *P. pygmaeus* prey includes Nematocerean Diptera, the preference is for Chironomidae, whose larvae are found in stagnant or slow moving water. *P. pygmaeus* has an advantage in that the foraging range is relatively small but has limitations as a specialist, foraging mainly in riparian woodland and over water. The conservation approach for *P. pygmaeus* needs to be specific since they are susceptible to anthropomorphic changes.

Reference: Andrews, P. T., Crump, R. G., Harries, D. J & Andrews, M. M. (2016). *Endang. Species Res.*, *30*: 19-28, doi: 10.3354/esr00720.

Poster 51: High resolution MaxEnt Modelling of Habitat Suitability for Maternity Colonies of the Barbastelle Bat (Barbastella barbastellus Schreber, 1774) in Rhineland-Palatinate

GOTTWALD JANNIS, ADORF FRANK, HILLEN JESSICA

The Barbastelle bat (Barbastella barbastellus , 1774), probably one of western Europes rarest bat species, suffered from substantial population declines in the last decades and was believed to be extinct from the federal state Rhineland-Palatinate (Germany) until the discovery of a maternity colony in the year 2004. Proof of reproduction sites is growing ever since, demonstrating the substantial lack of knowledge about the actual distribution and abundance of the species. Suitable habitats for maternity colonies are crucial for the survival of a population and knowledge of their location is substantial for their conservation. We modelled the suitability of habitats for the federal state based on high resolution data of the forest structure and roosting sites of maternity colonies, using the presence-only machine learning approach MaxEnt. Besides statistical testing of the model performance we surveyed two selected sites with high suitability, resulting in the discovery of new maternity colonies in both cases and analyzed surveys we performed in the last years for evidence of occurrence assessed via acoustic monitoring of the barbastelle bat. Results of these analyses together with the dispersal of potentially suitable habitats over the federal state challenge the previous assumption of the geographic range of the barbastelle bat and lead to the suspicion that the species is more abundant than previously thought. We could show that habitat suitability modeling is able to make an important contribution to the enlightenment of the situation of endangered species and stress that our results should be considered as a base for future conservation strategies.

Keywords:
species distribution modelling, barbastelle bat, barbastella barbastellus, MaxEnt, conservation

Poster 52: Bats are special – why bat boxes are not effective as compensation for the loss of roost trees

ZAHN ANDREAS[1], HAMMER MATTHIAS[2]

[1] Koordinationsstelle für Fledermausschutz Südbayern – LMU München, H. Löns Str.4 , 84478 Waldkraiburg, GERMANY; Andreas.Zahn@iiv.de
[2] Koordinationsstelle für den Fledermausschutz in Nordbayern, Universität Erlangen, Staudtstraße 5, 91058 Erlangen, GERMANY; fledermausschutz@fau.de

If hollow trees or other potential bat roosts in/on trees are to be removed during a project or due to pending adverse impact, they often have to be replaced by continuous ecological functionality measures (CEF). In many cases bat boxes are used to compensate for felling. Their effectiveness was reviewed by the Bavarian Coordination Centre for Bat Protection by analysis of a survey on the use of bat boxes in forests and parks. Data were collected from box groups (several boxes in a spatial network) in 146 forest areas or parks with a total of around 6,500 boxes, in which 13 species of bats occur.
The results show that the box groups are rarely used for reproduction: nursery roosts or groups of young animals were only detected in 17 % of all box groups. A further 42 % were at least regularly used by individual bats or mating groups. In the remaining cases (41 %), individuals could be found only sporadically. Many box groups were never used by bats. Decisive factors for colonization were shown to be size and age of a box group, as well as the availability of existing older boxes: small box groups (up to ten boxes) are used much less frequently by bats than large groups (over 30 boxes). Older groups (six to ten years or older) showed higher colonization levels than newer ones. If old boxes (for birds or bats) were absent before new bat boxes were installed, bats were detected in considerably fewer cases in the first ten years and nursery roosts did not occur at all.
This study suggests that in areas without existing boxes, new boxes cannot sufficiently replace the loss of nursery roosts in trees, even in the long term. Losses of other types of roosts (for example, individual or mating roosts) can be compensated for by boxes, but here it can also be assumed that there is a time delay of several years. Protection of roost trees and the development of new roost trees areas is therefore of crucial importance in project planning. In many cases it will not be possible to compensate for loss of roost trees for years to come.

Poster 53: Bat rehabilitation for welfare and research: results from Ukraine

POLIAKOVA DARIA[1,2], ZOZULIA VITALII[1,2], VLASCHENKO ANTON[1,2], KRAVCHENKO KSENIIA[1,2], PRYLUTSKA ALONA[1,2], HUKOV VITALII[1,2], RODENKO OLENA[1,2,3], ZHILKINA NATALIA[1], ZHILKIN ALEXANDR[1]

[1] Bat rehabilitation center of Feldman Ecopark, Kievskoje shosse 12, Kharkiv reg., 62340, UKRAINE; daria.poliakova.mail@gmail.com
[2] Ukrainian Independent Ecology Institute, P.O. Box 2385, Kharkiv, 61001, UKRAINE; vlaschenko@yandex.ru
[3] University of Silesia in Katowice, Faculty of Biology and Environmental Protection, Studentska st., 15, 40-743 Katowice, POLAND

Urbanization increases conflicts between human and bats, that causes numerous cases of bats' injuries and death. There are many Bat Rehabilitation Centres in countries of EU, USA and Australia. But in countries of former Soviet Union currently exists only one Bat Rehabilitation Center that is situated in Kharkiv, Ukraine. The Bat Rehabilitation Center (BRC FE) is special project of private Zoo - Feldman Ecopark founded in 2013.

Main aims of BRC FE are supporting of wild bats population that inhabit urban territories preserving their roosts, resolving conflicts between human and bats and rehabilitation of exhausted and injured individuals.

Each year BRC FE saves thousands of bats. The majority of bats need help and rehabilitation in winter. Hundreds of injured bats are provided with necessary treatment. But only 1 of 10 seriously injured bats survives after surgical intervention. Volunteers keep disabled bats in captivity for a lifelong rehabilitation.

Insectivorous bats have covert and complicated behavior that is hard to study in wild nature. Bats on rehabilitation allow studying bats behavior at close range: how they go into hibernation, communicate, take care of offspring etc. The adaptation process of disabled bats can also be studied.

The BRC FE plays significant eco-educational role and concerns numerous ethical questions about citizens' attitude to wildlife nature. Citizens science increases consciousness among different social groups.

There's much to be studied about bats and it would be incredibly important and helpful if bat volunteers created an international association and exchanged their experience of feeding, treatment and baby bats rescue. It is very important to create all-Europe data base of bats on lifelong rehabilitation that are kept at Wildlife Rescue Centers.

However, there are legislation boundaries for transboundary collaboration of Bat Rehabilitation Centers even within Europe. Successful bat conservation and welfare should be broadly discussed by bat research community.

Poster 54: The results of all-winter rehabilitation of *Nyctalus noctula*: a case study (Kharkiv, NE Ukraine)

KRAVCHENKO KSENIIA[1,2,3], VLASCHENKO ANTON[1,2], RODENKO OLENA[1,2,4], HUKOV VITALII[1,2], BELOVETSKAYA SVETLANA[5]

[1] Bat rehabilitation center of Feldman Ecopark, Kharkiv, UKRAINE; vlaschenko@yandex.ru
[2] Ukrainian Independent Ecology Institute, Kharkiv, UKRAINE
[3] Leibniz-Institute for Zoo and Wildlife Research, GERMANY
[4] University of Silesia in Katowice
[5] V.N. Karazin Kharkiv National University

Nyctalus noctula is one of the species which readily occupies European cities since XX, XXI century. In Eastern Europe this species uses urban areas for hibernation. Since 1990th there are a lot of records of *N. noctula* which hibernates in crevices of old prefabricated blocks of flats. It causes multiple conflicts between bats and citizens. Quite frequently during reparatory or rebuilding works in such buildings the roosts are destroyed and bats are thrown away. In most cases without rapid help of animal care and bat specialists, such individuals are doomed in condition of harsh winters of eastern Europe. 2 December 2014 such group of abandoned *N. noctula*, from the destroyed cavity, was saved by staff of Bat Rehabilitation Center (BRC) of Feldman Ecopark (Kharkiv, Ukraine) and was kept in artificial hibernation conditions from December 2014 to March 2015. The study presents the results of rehabilitation of group of *N. noctula* (N=95) during the winter 2014/2015 in BRC. For each individual sex, age and reproductive status if possible were evaluated. Forearm length and body mass (by digital scale to 0.1 gram) were also measured. All individuals were surveyed for presence of any injures or traumas. After 37-48 days of hibernation all individuals were weighted again. The bats which had insufficient weight were additionally hydrated and fed during several continuous days and then were moved again for hibernation in artificial conditions. Since then, such checkup take place in average each two weeks. For each individual was made data base, where the information about weight check, feeding or hydration actions was fixed. After analyses of obtained data we estimated the survival rate of the *N. noctula* during hibernation, their weight dynamics and effect of additional feeding and hydrating. The survival rate of rehabilitated individuals was 70%.

Poster 55: Site fidelity, seasonal movement and genetic diversity of the lesser horseshoe bat *Rhinolophus hipposideros* in Western Carpathians – implications for bat conservation in Natura 2000 sites

MYSŁAJEK ROBERT[1], KUREK KORNELIUSZ[2], SZEWCZYK MACIEJ[2], NIEDŹWIECKA NATALIA[2]

[1] Faculty of Biology, Institute of Genetics and Biotechnology, University of Warsaw
[2] Association for Nature Wolf

Lesser horseshoe bat *Rhinolophus hipposideros* (Bechstein, 1800) have undergone a severe decline in Europe. The same dramatic population decrease was recorded in Poland, where the species is still critically endangered according to the Polish Red Data Book. Network of Natura 2000 sites is the most important conservation effort being implemented in Europe, although the effectiveness of Special Areas of Conservation (hereinafter SAC) regarding the protection of bats, remains to be evaluated. We investigated patterns of site fidelity, seasonal movement, as well as genetic diversity in a population of the lesser horseshoe bat inhabiting the western-most edge of Polish Western Carpathians. Gap analyses indicate that the most important summer roosts, swarming sites and hibernacula of the lesser horseshoe bat are not protected by SAC sites. Bats seasonally move between summer roosts and caves at distances more than 10 km, but individuals from summer roosts protected as SAC frequently winter in unprotected caves and *vice versa*. Nonetheless, marked bats exhibited high degree of fidelity for swarming sites and caves where they hibernate. Our genetic analyses, based on 8 microsatellite markers, revealed that bats from unprotected sites have great genetic diversity, thus its protection is crucial for the entire local population. Our results indicate that the Natura 2000 network in Western Carpathians does not guarantee the protection of the lesser horseshoe bat population. We recommend the designation of new sites or enlargement of already established ones to complement the existing network and to help guarantee bat fauna protection in this area.

Poster 56: Global transition from conventional to LED street lighting may be advantageous for light-averse bats, but disadvantageous for light-tolerant species

LEWANZIK DANIEL[1], VOIGT CHRISTIAN C.[2]

[1] Department of Animal Behaviour, Freie Universität Berlin, Takustraße 6, 14195 Berlin, GERMANY
[2] Department of Evolutionary Ecology, Leibniz Institute for Zoo and Wildlife Research, Alfred-Kowalke-Straße 17, 10315 Berlin, GERMANY

Light pollution is rapidly increasing and can have deleterious effects on biodiversity, yet light types differ in their effect on wildlife. Among the light types used for street lamps, light emitting diodes (LEDs) are expected to become globally predominant within the next few years.
In a large-scale field experiment, we recorded bat activity at 46 street lights for 12 nights each and investigated how the widespread replacement of conventional illuminants by LEDs affects urban bats: we compared bat activity at municipal mercury vapour (MV) street lamps that were replaced by LEDs with control sites that were not changed.
Pipistrellus pipistrellus was the most frequently recorded species; it was 45% less active at LEDs than at MV street lamps, but the activity did not depend on illuminance level. Light type did not affect the activity of *Pipistrellus nathusii*, *Pipistrellus pygmaeus* or bats in the Nyctalus/Eptesicus/Vespertilio (NEV) group, yet the activity of *P. nathusii* increased with illuminance level. Bats of the genus Myotis increased activity 4.5-fold at LEDs compared with MV lights, but illuminance level had no effect.
Decreased activity of *P. pipistrellus*, which are considered light tolerant, probably paralleled insect densities around lights. At LEDs, the competitive advantage – the exclusive ability to forage on insect aggregations at lights – may be reduced for light-tolerant bats. Further, our results suggest that LEDs may be less repelling for light-averse *Myotis* spp. than MV lights. Accordingly, the transition from conventional MV lighting to LEDs may greatly alter the anthropogenic impact of artificial light on urban bats; it might lead to a more natural level of competition between light-tolerant and light-averse bats and could eventually affect the resilience of urban bat populations. Yet, the potential benefits of LEDs could be negated if low costs foster an overall increase in artificial lighting.

Poster 57: Egyptian fruit bat of Cyprus: A story of survival effort

AŞAN BAYDEMIR NURSEL[1], TÜZMEN ŞÜKRÜ[2]

[1] Department of Biology, Faculty of Arts and Sciences, University of Kırıkkale, Kırıkkale, TURKEY; nurselasan@yahoo.com
[2] Department of Biological Sciences, Faculty of Arts and Sciences, Eastern Mediterranean University (EMU), TRNC, Mersin 10, TURKEY, sukru.tuzmen@emu.edu.tr

Thus far, 22 bat species were recorded from Cyprus by various authors. The Egyptian fruit bat, *Rousettus aegyptiacus*, is the only fruit bat on the island. The aims of this study were to determine the current distribution and conservation status related to the geography of the species in Northern Cyprus, and to present recommendations regarding prioritization of the habitats in which the species existed, for an effective conservation. New distribution localities of the fruit bat from Morphou, Famagusta, the Pentadactylos mountains have been determined in the present study. Some roosts in Morphou are used by individuals of both sexes throughout the year. Besides, the Egyptian fruit bat populations in North Cyprus are dramatically decreasing because of various anthropogenic threats; increased tourism activities, intense lighting, improperly designed gates, poisoning, illegal killing, cutting of fruit trees and limestone quarries.

Poster 58: The importance of artificial roosts for rhinolophid and vespertilionid bats in Central Anatolia

AŞAN BAYDEMIR NURSEL[1], ŞIMŞEK GÜR MERVE, GENÇ MERYEM

[1] Department of Biology, Faculty of Arts and Sciences, University of Kırıkkale, Kırıkkale, TURKEY; nurselasan@yahoo.com, merveeesimsek@hotmail.com, meryem.genc01@gmail.com

This study is an examination of the summer and winter colonies of some vespertilionid and rhinolophid bats that had clustered in an abandoned tunnel in Kırıkkale province, Central Anatolia. Between 2014 and 2016 a total of 38 field trips were made during which the population density of hibernating bats and maternity colonies, together with the temperature and relative humidity of the tunnel, were regularly recorded. Greater horseshoe bat (*Rhinolophus ferrumequinum*), Lesser horseshoe bat (*Rhinolophus hipposideros*), Greater mouse-eared bat (*Myotis myotis*) and Lesser mouse-eared bat (*Myotis blythii*) colonies sympatrically existed in this tunnel. *Myotis myotis/blythii* species roost in the tunnel throughout the year with the largest population densities identified in April, May and June, as a colony of 600-800 individuals comprising females and jveniles. Only males formed the winter swarming, as the females abandoned the tunnel in September after mating. The highest temperature and relative humidity in winter and summer months were recorded as 16 °C and 64 % and 19.6°C and 70 %, respectively. Furthermore, the tunnel is located in a public place and therefore subject to various threats. We began to study by contacting the people authorized with protecting the tunnel.

Poster 59: The costs of leaving early: Mortality costs associated with departure from the hibernaculum in bats

REUSCH CHRISTINE[1], SCHEUERLEIN ALEXANDER[2], GROSCHE LENA[1,3], MEIER FRAUKE[1,3], GAMPE JUTTA[2], KERTH GERALD[1]

[1] University of Greifswald, Zoological Institute and Museum, Johann-Sebastian-Bach-Str. 11-12, 17489 Greifswald, GERMANY; christine.reusch@uni-greifswald.de
[2] Max Planck Institute for Demographic Research (MPIDR), Konrad-Zuse-Straße 1, 18057 Rostock, GERMANY
[3] Echolot – Büro für Fledermauskunde Landschaftsökologie und Umweltbildung, Eulerstr. 12, 48155 Münster, GERMANY

It is well documented that hibernation is crucial for temperate bat species to survive periods with low food availability during the winter. However, how differences in individual hibernation behaviour influences mortality and whether individuals are plastic with respect to their hibernation behaviour are largely unknown. Because bats are of high conservation concern it is of prime importance to understand factors that might influence mortality during hibernation.
In this study we used an individual based data-set of the two bat species *Myotis nattereri* and *Myotis daubentonii* at a hibernaculum. Each PIT-tagged individual was automatically recorded while passing the entrances and, therefore, can be followed at the hibernaculum over its life time. We investigated the impact of their individual hibernation behaviour, precisely the timing of departure in late winter and early spring, on mortality, as well as differences within and between the two species from 2011 until 2015.
Our results show that an early departure from the hibernaculum is associated with a high mortality risk that however varies among years. In general, as time progressed into late winter and early spring, this mortality risk declined. The rate of this decline differed among both species. Furthermore, the time of departure from the hibernaculum varied within, as well as among individuals. Variance within individuals was unexpectedly large which suggests that phenotypic plasticity is high with respect to the duration of the hibernation of individuals.
Our results suggest considerable differences among individuals within as well as between bat species with respect to emergence behaviour from the hibernaculum. Hence, our study highlights the necessity to further investigate the phenotypic plasticity of hibernation behaviour and to understand its effects on the demography of bats. We conclude that it is important for the conservation management of bat species to identify key factors for the survival of individuals during hibernation and to distinguish between species to select the best management tools for bat hibernacula.

Poster 60: Predicting times of high collision risk for bats at wind turbines from regional phenological and ecological data

BEHR OLIVER[1], KORNER-NIEVERGELT FRÄNZI[2], SIMON RALPH[1], BAUMBAUER LOTHAR[1], HOCHRADEL KLAUS[1], WEBER NATALIE[1], BRINKMANN ROBERT[3], REERS HENDRIK[3], NAGY MARTINA[1]

[1] Sensory technology, FAU Erlangn
[2] oikostat GmbH
[3] FrINat GmbH

Stopping the rotors of wind turbines during times of high collision risk is the mitigation method most commonly used to reduce the number of bat fatalities at wind turbines in Central Europe and is also applied in other parts of the world. It has been shown that by doing so, bat fatalities at a specific turbine can be reduced to a number previously defined by the relevant authorities. The crucial point of this method is to reliably predict times of high bat activity at the nacelle of turbines and to quantify the resulting collision risk. Therefore, understanding the ecology and activity patterns of bats in the rotor-swept area of wind turbines (at modern turbines this may include altitudes of more than 150 m above ground level) is vital for taking efficient actions to protect bats and to reduce the loss in revenue resulting from mitigation measures. Currently, phenological (season, time of night) and meteorological (wind, temperature, rain) parameters are being used to predict the level of bat activity during a specific time period. Here we present an improved statistical model based on a large data-set from several years that also accounts for differences in regional bat phenology and species composition. We also show how the improved models are implemented in the free software tool ProBat that is widely used in Germany for calculating bat friendly curtailment algorithms for wind turbines.

Poster 61: The barbastelle bat – a high flying species?

HURST JOHANNA[1], BIEDERMANN MARTIN, DIETZ MARKUS, KARST INKEN, KRANNICH ELENA, SCHAUER-WEISSHAHN HORST, SCHORCHT WIGBERT, BRINKMANN ROBERT

[1] Freiburger Institut für angewandte Tierökologie, Dunantstr. 9, 79110 Freiburg, hurst@frinat.de

For precautionary reasons the rare barbastelle bat (*Barbastella barbastellus*) is ranked as high flying species and therefore considered to be at risk of collision with wind turbines. In this study, acoustic recordings were made on measuring masts at three areas of known barbastelle nurseries to investigate the activity of barbastelle bats at height. Nursery roosts were identified and acoustic recordings were made on the ground to aid the interpretation of activity measurements at height. In all cases the measuring masts were situated no more than 1 km away from colony roost trees. Activity close to the ground was detected regularly over the whole active season from April until November. A stratification of activity was recognised at different heights: at a height of 30 m and in the area around the tree canopy occasional activity was detected, considerably less than activity close to the ground. At heights of 50 m and above activity was so seldom recorded that it was considered to be an absolute exception.

Based on these results in three different nursery habitats it can be assumed that barbastelle bats don´t regularly fly above the forest canopy and therefore an increased collision risk is not present for this species, the one exception to this being small wind turbines where rotor blades pass close to the ground or just above the tree canopy. In such cases very intensive monitoring and the development of tailored mitigation measures for the barbastelle bat, and for other species, is essential to avoid an increased risk of collision. Nevertheless, considering the particular habitat demands of the barbastelle bat, the construction of wind turbines should be avoided in forest areas with numerous roosts or very suitable potential roosts.

Poster 62: Challenges posed by newly discovered cryptic species: a case study with european *myotis nattereri* species complex

RUEDI MANUEL[1], JAN CAMILLE M. I., BUTLIN ROGER K., GLOVER ANITA M., ALTRINGHAM JOHN D.

[1] Natural History Museum of Geneva, P.O. Box, 1211 Genève 6, SWITZERLAND; manuel.ruedi@ville-ge.ch

The existence of major cryptic mitochondrial lineages has been evidenced in many taxonomic groups, following the increased use of molecular surveys in natural populations. These cryptic lineages are generally based on sequences of the mitochondrial genome, which is essentially transmitted clonally by the females, without recombination. In bats, such phylogeographic surveys suggest that the species diversity in European bats might increase by 40% if the unravelled cryptic lineages turn to be new biological species. Such discoveries pose important new challenges for protection of bat diversity, as new cryptic species complexes are by definition difficult to identify with conventional methods, and also because they might question previous estimates of potential threats affecting apparently common or widespread species. By using a combination of mitochondrial and highly variable nuclear markers, we explore various components of the *Myotis nattereri* species complex in Western Europe with the aim (1) to identify the nature of biological interactions between evolutionary components, (2) to understand their current geographical distribution, and (3) identify the conservation challenges they pose for their protection. The two classes of markers indicate that little, if any, geneflow exists among the three evolutionary units investigated, but that ancient hybridization events related to past changes in geographic ranges led to a complete mitochondrial introgression between two of them. This complicates the molecular identification of the different cryptic species though simple barcode approaches.

Poster 63: Wind energy impact on bat activity: an omitted long-distance concern

BARRE KEVIN[1], JULLIARD ROMAIN[1], LE VIOL ISABELLE[1], BAS YVES[1], KERBIRIOU CHRISTIAN[1]

[1] National Museum of Natural History, Center for Ecological and Conservation Sciences (CESCO), UMR 7204 MNHN-CNRS, 61 rue Buffon, 75005 Paris, FRANCE; kevin.barre@mnhn.fr

Wind farm developers have to provide an effective mitigation hierarchy: an avoidance and a reduction of negative impacts of wind farm on biodiversity (bats in our case), and to implement offsetting measures when residual impacts persist. Offsetting consists in implementing measures (e.g. hedgerows) that counteract residual losses of biodiversity and generate gains in order to achieve a no net loss or a net environmental benefit. Indeed, due to the reluctance of local people to install wind turbines near their homes, project developers often attempt to install wind energy facilities on agricultural land, particularly in arable land dominated by open fields or wooded countryside. Research and ecological impact assessments studies are focused for many years on bat mortality impact, without really know if the mitigation hierarchy applied is effective. Mortality is often describe as a significant negative impact on bat population, even though population parameters are poorly known, but what about habitat losses by revulsion?

To our knowledge no study attempts to evaluate impact distance of wind turbines on bat activity. To determine the loss of number of bat passes according to distance to wind turbine, we performed a sampling design focused on hedgerows. We simultaneously recorded activity on 10 points per night, at 10 different distances to wind turbine. We studied one wind farm per night, and each record point was chosen in order to minimize differences in local and landscape characteristics with other simultaneous points. Sampled distances were between 0 and 1000 meters to wind turbines, thus, we did not use controls. A total of 36 wind farms were studied using 280 record points in north-west France.

Results show for all species/species groups, for which statistical analysis were possible, a significant negative impact of wind farms on bat activity. We found quadratic or linear positive relationship between bat activity and distance to wind farm, without threshold effects, except for Plecotus sp (around 750 meters). Predicted number of bat passes from models reveals a loss of a minimum of 50% within a range from 1000 to 0 meters. Amongst these species, some are known to be less sensitive to wind turbines in literature (i.e. mortality) are affected by long distances. Results indicates that loss of foraging and moving habitat is very important and could play an important role on population dynamics. This concern should therefore be taken into account in mitigation reflections and implementation ways, especially in wooded countryside regions.

Poster 64: Bat activity at nacelle height over forests

REERS HENDRIK[1], BRINKMANN ROBERT

[1] Freiburg Institute of Applied Animal Ecology (FrInaT GmbH), Freiburg, GERMANY, reers@frinat.de

The rising numbers of wind turbines in Germany is increasingly affecting bats, especially onshore. Currently, forested areas are regarded as suitable sites to further increase renewable energy production through wind energy. Forests play a crucial role for most bat species as hunting grounds and/or roost sites. Knowledge about how wind turbines in forests affect bats, however, is rudimental. Besides the obvious destruction of roost sites and hunting habitat, collision with operating wind turbines is likely to be the most problematic effect.

Recent studies on the effect of wind turbines on bats focused on open landscape, mainly because forested areas were not yet considered for wind energy production. In recent years however, wind turbines are constructed in forests more commonly, mainly in the forest-covered hillsides of Western and Southern Germany. Up to now, data collected at forest sites was not analysed in a large scale. In the research project “Construction and operation monitoring of wind energy in forests”, funded by the Federal Ministry for Economic Affairs and Energy (BMWi), a large set of acoustic monitoring data was gathered and analysed, collected at 130 wind turbines at nacelle height over forests and open landscapes from all over Germany.

The results show that bat activity over forests shows very little differences to open landscapes. Daily and annual phenologies, as well as species composition, are similar in forests and open landscapes, however, depending on geographical region. As in open landscapes, bat activity over forest decreases with increasing wind speed and decreasing temperature. These results suggest that mitigation measures, developed to reduce bat fatalities in open spaces, are also applicable to wind turbines placed in forests.

Poster 65: Inside-out: bat activity and diversity from the forest interior to forest gaps

ERASMY MAUDE[1], DIETZ MARKUS[2], LEUSCHNER CHRISTOPH[1]

[1] Department for Ecology and Ecosystem research, University of Göttingen; merasmy@gwdg.de
[2] Institute for Animal Ecology and Nature Education, Gonterskirchen

Habitat heterogeneity is often considered to be an essential driver of biodiversity, offering more opportunities for resource partitioning within and between habitats. Canopy gaps as temporal disturbances in forests are known to increase habitat diversity by altering the light regime, nutrient cycling and species diversity. Therefore, they are considered to be important habitats for different animal groups, including birds and arthropods. In closed forest stands, the relationship between bat diversity and vegetation structure has been analysed in several studies, but so far no conclusive results have been reached. In this study, we included natural gaps as essential elements of the horizontal structural heterogeneity, and combined research on bat activity and diversity in closed forest stands and in adjacent gaps of the near-natural forests of the National Park "Beloveshskaya Pushcha" in Belarus.
We hypothesize that the three bat guilds considered (narrow-space foragers, edge-space foragers and open-space foragers) benefit from the presence of gaps depending on gap size: small gaps possess structural elements both from the forest edge and the forest interior. They offer foraging habitats for narrow-space foragers, but also enhance the activity of edge-space foragers. Medium-sized gaps mainly provide foraging grounds to edge-space foragers. Big gaps can be considered as islands of open habitat, and open-space foragers penetrate these gaps for foraging activities. Therefore, small gaps are expected to present the highest species diversity, since they incorporate aspects of the forest interior and of open habitats. We expect these general turnover in species community to take place independent of the forest type considered.
We studied bats acoustically on twelve forest plots in two different forest types (six oak-dominated and six pine-dominated plots with the help of 'batcorders' during 8-17 nights in a gap situation and in the adjacent forest interior as subplots. The acoustic sampling was accompanied by the collection of forest structure variables describing the forest and the gap situation respectively. These structure variables will be used to explain shifts in bat activity and diversity from the forest interior to the gap.
We present the results of our study on guild and on species level. Our findings on gaps as natural disturbances and on the dependence of forest bats on vegetation structures will allow us to express suggestions how forest management practices can maintain or augment bat species diversity.

Poster 66: Mating patterns, relatedness and population structure of the Leisler's bat (*Nyctalus leisleri*)

KOHNEN ANNETTE[1], EBERT CORNELIA, SCHORCHT WIGBERT, DIETZ CHRISTIAN, HURST JOHANNA, BRINKMANN ROBERT

[1] Freiburg's Institute of Applied Animal Ecology (Frinat), Dunantstr. 9, 79110 Freiburg, GERMANY; kohnen@frinat.de

Species with long distance migration between reproductive and wintering sites require special conservation efforts and management strategies. Especially in bat species only few is known about migration routes and the connectedness between individuals of different nursery roosts. Therefore a possible decline of a local community may be caused during migration and hibernation. For example bat fatalities induced by wind turbine blade rotation are regularly described and concerns not only local but especially migrating individuals. Here, we used a combined approach of individual marking with forearm bands and microsatellite markers to assess familiar relationships within and between nursery roosts and nearby mating and wintering sites of the Leisler's bat (*Nyctalus leisleri*) in Southwest Germany. We surprisingly found no relationships between individuals of the nursery and the mating roosts, neither by switching individuals nor by genetic relatedness. Instead the mating roosts genetically resemble nursery roosts in Thuringia. Individuals reproducing in Thuringia thus seem to migrate to our study site during winter whereas the wintering sites of our local nursery colonies remain unknown. Unraveling the patterns of bat migration can help decision making in several planning topics, e.g. windfarm construction.

Poster 67: Vertical distribution of bat activity changes seasonally and depends on weather conditions

BLOMBERG ANNA[1], VASKO VILLE, LILLEY THOMAS, NORRDAHL KAI

[1] Department of Biology, University of Turku, 20014 Turku, FINLAND, asblom@utu.fi

The growing demand for renewable energy has led to a dramatic increase in wind power development, but at the same time concerns have been raised about bat fatalities associated with poorly located wind farms. We wanted to investigate which bat species in Finland are most susceptible to wind power and determine the time period and weather conditions during which they are most active at high altitudes. Furthermore, we wanted to investigate if acoustic monitoring under the canopy gives an accurate impression of bat activity at the rotor blade height. We conducted our study during 2013 and 2014 on the island of Kemiö in South-Western Finland. We studied both migrating and foraging bats simultaneously on ground level and at a height of 60 meters on 10 GSM-masts using acoustic monitoring. The most abundant species observed at 60 meter height was the Northern bat (*Eptesicus nilssonii*). The Northern bats were particularly active at high altitudes at the end of July and beginning of August during nights with low wind speed and high ambient temperature. Activity observed at high altitudes largely reflected the activity of Northern bats underneath the canopy. The second most abundant bat species observed at 60 meter height was the Nathusius' pipistrelle (*Pipistrellus nathusii*). The spring migration of Nathusius' pipistrelles took place at the end of May and the much more prominent autumn migration at the end of August and beginning of September. The odds of observing Nathusius' pipistrelles at 60 meter height were increased by low wind speed whereas the ambient temperature alone did not affect the activity at high altitudes. However, during cold nights Nathusius' pipistrelles were only observed at 60 meter height if the wind speed remained low. Given that the activity peaks of these two species differ, the timing of possible mitigation measures should depend on the target species. The target species on the other hand will most likely be determined by the location of the wind farm, since Nathusius' pipistrelles in Finland are mostly observed close to the shore line whereas the Northern bat occurs all over Finland.

Poster 68: Gain and loss of habitat – the response of different bat species to experimental light at night varies with spectral composition

SPOELSTRA KAMIEL[1], VAN GRUNSVEN ROY H. A., RAMAKERS JIP, FERGUSON KIM, DONNERS MAURICE, VEENENDAAL ELMAR, VISSER MARCEL E.

[1] Department of Animal Ecology, Netherlands Institute of Ecology (NIOO-KNAW), P.O. Box 50, 6700 AB Wageningen, NETHERLANDS; K.Spoelstra@nioo.knaw.nl

Artificial light at night has increased dramatically over the last decades. Effects are known for many species, and include changes in species presence, behaviour and physiology. Bats are strongly affected, but effects vary for different species of bat, and with different light sources. This is a consequence of light colour, hence, the use of different spectra may potentially reduce negative consequences. In order to experimentally quantify the impact of spectral composition on different species of bat in their natural habitat, we used a unique setup in which otherwise dark, undisturbed natural forest edge is illuminated. Over the course of five years, we measured activity of three bat species groups around transects with light posts emitting white, green and red light with a realistic light intensity, with all spectra equally intense for the human eye (e.g. normalized to Lux value). The results reveal a strong and spectrum dependent response for the first species group with the genera *Myotis* and *Plecotus* and the second group with the genus *Pipistrellus*, but not for the third group with the genera *Nyctalus* and *Eptesicus*. Species in the first group are slow-flying, and clearly avoided white and green light. However, they were equally abundant in darkness and red light. The agile, opportunistically feeding *Pipistrelle* species in the second group were significantly more abundant around white and green light, which is most likely a result of increased insect activity around these light sources. Around the red illuminated transects, pipistrelle activity was however comparable to dark control. Forest-dwelling *Myotis* and *Plecotus* species are less abundant than *Pipistrellus* species, which are widespread in urbanized areas and are able to expand their activity in natural area by light. We therefore argue that, for conservation purposes, the use of white and green light should be avoided in and around natural areas.

Poster 69: The importance of coastal lagoons as foraging habitats for local bats and migrating Nathusius' pipistrelles

FRITZÉN NICLAS[1], SCHNEIDER MICHAEL[2]

[1] Metsähallitus, Parks & Wildlife Finland, Wolffskavägen 36, 65101 Vasa, FINLAND; nrfritzen@gmail.com
[2] Länsstyrelsen Västerbotten, Västerbotten County Administration, Storgatan 71 B, 901 86 Umeå, SWEDEN

Coastal lagoons with a shallow threshold facing the sea have been formed as a result of the postglacial land uplift in the Kvarken area, the narrow region in the Gulf of Bothnia between Finland and Sweden at N 63°. These warm, sheltered and nutrient rich bays constitute biogeographical islands with a high biodiversity. They play an ecologically important role as breeding areas of fish populations, as breeding or resting sites for birds, and as nurseries for aquatic insects. A contribution to the conservation of the biodiversity and to the ecosystem services produced by these habitats is the main goal of a three-year (2017–2019) Interreg Botnia-Atlantica project named Kvarken Flada.

Recent passive monitoring of bats with ultrasound detectors indicates a migratory route of *Pipistrellus nathusii* through the Kvarken area between Finland and Sweden. What is of great importance for the survival and reproductive success of migratory bats is that the routes meet the energy demands of their long migration. One of the values of the coastal lagoons is expected to be their importance for foraging bats. Regardless of whether the lagoons are used for fly-and-forage strategies or for stopover feeding, they could provide migrating bats with profitable feeding habitats along the route. Their rich insect production in combination with the short distance of open water in this area might have played an important role in the evolution of this migratory route. However, the lagoons might also serve as important feeding habitats for local bats, or for bats conducting short feeding trips out into the archipelago at a regional scale.

In this study, we will map the activity of bats in coastal areas in Sweden and Finland during three consecutive seasons, using passive bat detectors. We will correlate bat activity with time of the year, microclimate and food resources within and outside ten coastal lagoons. Invertebrate diversity and biomass will be monitored using water and air eclector traps, enabling us to distinguish between food resources that are produced within the lagoons and those that are attracted from the outside. We will investigate the possibility to distinguish between local, regional and migrating bats and their activities (social, feeding or migratory behaviour). In this project the novel use of automated radio telemetry and coded tags for the study of migrating bats between Finland and Sweden will also shed light on the migration behavior of *P. nathusii* in this area.

Poster 70: Bats in the Carpathian mountains – a survey to promote the protection of large forests in Europe

DIETZ MARKUS[1], BASHTA ANDRIY-TARAS[2], BROMBACHER MICHAEL[3], SIMON OLAF[1]

[1] Institut of Animal Ecology and Nature Education, 35321 Gonterskirchen, Hauptstraße 30, GERMANY; Markus.Dietz@tieroekologie.com
[2] Institute of Ecology of the Carpathians, National Academy of Sciences of Ukraine, 4 Koselnytska str., Lviv 79026 UKRAINE
[3] Frankfurt Zoological Society, Bernhard-Grzimek-Allee 1, 60316 Frankfurt, GERMANY

Bats (Chiroptera) are one of the oldest mammalian orders and one of the most diverse in terms of physiological and behavioral adaptations, which enable them to inhabit different ecosystems successfully. Throughout the world, bats are distributed mainly in forests and some species are recognized as key species for ecosystem services.
Forests are however not only used as feeding areas but also as roosting sites. More than two thirds of the European bat species live predominantly in tree cavities such as woodpecker holes, crevices or behind the bark of trees. Therefore, availability and destruction of roosts by forest tree cutting is one of the major factors responsible for population decline in forest-dwelling bat species.
Vice versa, as flagship-species, forest-dwelling bats may support the protection of old growth and primeval woodland areas as we find in the Carpathian mountains of Western Ukraine. Remnants of primeval beech forests and large old growth forests are highly important to protect biodiversity in Europe. Despite the implementation of nine national nature parks (NNPs) in the Carpathians, the immense deforestation induced by international timber industry is growing and huge parts of old growth and primeval woodlands are already lost.
To date bat assemblages have not been studied comprehensively in the large Carpathian forests. Hence, we implemented an acoustic bat survey together with scientists from nine national parks in the Carpathian mountains of Ukraine. Study sites within the parks comprised of old beech forests, small mountain rivers, and in higher altitudes, large old-growth beech-maple-fir forests and spruce forests. With the aid of real-time ultrasound recording systems (Batcorder, EcoObs) we recorded more than 21.000 sequences with bat-calls during 491 nights in the summer months of 2015 and 2016 (2015: 230 nights with 13.904 sequences; 2016: 261 nights with 8.504 sequences). Until now (determination is still ongoing) we identified 19 of 28 known bat species of Ukraine (at minimum 8 – 16 species for each NNP).
Many bat species were initial proofs for some NNPs. The whole data set provides valuable information on the necessity of old growth and primeval forest protection. As representative species of old forests *Barbastella barbastellus* (documented in 6 national parks), *Myotis alcathoe* (in 5 national parks) and *Myotis bechsteinii* (in 8 national parks) were found in more than half of the research areas. More identified forest dwelling bats are *Eptesicus nilsonii*, *Myotis brandtii*, *M. nattereri*, *Nyctalus*

leisleri and *N. noctula* as well as *Pipistrellus nathusii*, *P. pygmaeus* and *Plecotus auritus*.

These results contribute to an enriched state of knowledge about bat communities within the National nature parks of the Ukrainian Carpathian mountains. Furthermore, the results support NNP extension plans to extend the protection areas to old growth forests and primeval forests nearby, which currently have no protection status. This two-year ongoing bat survey study is a well done example of best practice cooperation that achieved a unique record of bat species data and will help to protect old growth and primeval forests.

Poster 71: Natural dynamics in forests increases the roosting possibilities for tree-dwelling bats

DIETZ MARKUS[1], BROMBACHER MICHAEL[2], ERASMY MAUDE[3], FENCHUK VIKTAR[4], SIMON OLAF[1]

[1] Institut of Animal Ecology and Nature Education, 35321 Gonterskirchen, Hauptstraße 30, GERMANY; Markus.Dietz@tieroekologie.com
[2] Frankfurt Zoological Society, Bernhard-Grzimek-Allee 1, 60316 Frankfurt, GERMANY
[3] University Göttingen, Department of Ecology and Ecosystem Research, Untere Karspüle 2, 37073 Göttingen, GERMANY
[4] APB-BirdLife Belarus, 220114 Minsk, Parnikovaya str. 11, of. 4, BELARUS

Forests are the most important key habitat for bats all over the world. In Europe more than two-third of the bat species find crucial roosting and foraging opportunities in forests. Depending on wing morphology, echolocation call structure, sociability and thermal conditions they segregate niches by exploiting different cavity types or feeding grounds. Nearly all European forests have historically been exploited by humans for many centuries and are still strongly influenced by timber harvesting. One of the consequences is the loss of key habitat resources, often making forests inhospitable to bats.

Since primeval and near-natural forests in Europe have become extremely rare and keep shrinking due to forestry, only few studies deal with forest-dwelling bats in these habitats. In 2013-2016 we studied tree-dwelling bats in the National Park "Belaveshskaya Pushcha" in Belarus. The whole forest covers 1.500 km^2 and stretches along the border between Poland and Belarus. Large parts of the forest are strictly protected and characterized by old stands of *Tilio-Carpinetum-*, *Querco-Piceetum-* and *Pino-Quercetum* forests with high amounts of standing dead trees. We investigated the bat species community and bat habitat use by automatic acoustic surveys, mist-netting and radio-tracking.

First results show that the bat community of the National Park "Belaveshskaya Pushcha" (n=16 bat species) comprises nearly all of the bat species of Belarus. In 2015 and 2016, we identified 21 maternity colonies from seven tree-dwelling species (*Barbastella barbastellus, Nyctalus leisleri, Plecotus auritus, Myotis nattereri, Pipistrellus pygmaeus, P. nathusii* and *Eptesicus nilssonii*). The highest proportion of roosts were cavities created by natural forest dynamics, like trunk crevices or loose bark, in dead standing trees caused by storm or lightning stroke. Bats also used woodpecker-made cavities and break-offs of branches. Maternity roosts were found in *Quercus robur, Picea abies, Pinus silvestris, Acer platanoides, Betula pendula* and *Populus tremula.*

In summary, the results reveal that natural processes in forests create highly structured habitats with different roosting niches for a rich bat community. The number of roosting availabilities increases with the age of the trees and decreasing human impacts, like sanitary cuttings of dying spruce, oak and pine trees – a key roosting habitat e.g. for the endangered *Barbastella barbastellus*.

Poster 72: *Nyctalus lasiopterus* in the far north? Population size and habitat use of a very special bat in the Pripiat floodplains (Belarus)[1]

DOMBROVSKI VALERA[1], FENCHUK VIKTAR[1], DIETZ MARKUS [2]

[1] APB-BirdLife Belarus, 220114 Minsk, Parnikovaya str. 11, of. 4, Belarus
[2] Institute of Animal Ecology and Nature Education, 35321 Gonterskirchen, Hauptsraße 30, GERMANY; Markus.Dietz@tieroekologie.com

The Greater Noctule (*Nyctalus lasiopterus*) is the largest and the least studied bat species in Europe. The species distribution shows an insulated pattern, with population centers in the iberian Peninsula and south-eastern parts of Europe. Until now, the northern distribution area of Greater Noctules was determinated by 50 ° North. In 2015 we found a maternity colony in the Pripiat floodplain at the southern border of Belarus which is far north of the known reproduction sites in central Slovakia and northern Hungary. Records of the species in neighbouring countries of Belarus (Ukraine, Poland) are very rare and attributed to non-breeding animals.

Greater Noctules were identified by mist netting and systematic acoustic surveys using real-time ultrasonic systems (Batlogger M, Elekon AG & Batcorder, EcoObs). Tree-roosts of the maternity colony were located by radio-tracking of reproductive females and juveniles (in total 6 individuals).

In total, we investigated 55 potential breeding localities of *N. lasiopterus* in seven districts of Belarusian Polessie. As the core area of the colony's range we identified the territory of Ramsar Site Stary Zhaden (51.9 N; 27.6 E) in Zytkaviči district, Homiel region. The site is entirely located within the area of the Pripyat water-glacial alluvial plain with large mires and numerous dunes, islands of terminal moraines and kames. Key-habitats of the maternity colony are old grown pine forest and open water bodies like small streams and ponds. The maternity colony comprises at least 18 females. All identified roosts (n=9) were situated in old pine trees on small forest islands surrounded by swamps and hardly accessible to humans. Tree-roosts were found in distances between 0.7 and 6 km from the place of mist-netting and had a distance about 0.05 km to 4.6 km from each other. Automatic acoustic monitoring revealed that N. lasiopterus inhabits the area from mid- April to mid- September.

Our study's results should help to develop and implement conservation measures for this important maternity colony at the northern border of the species range. During the cold winter season, the forest in the swamps is very accessible to forestry activities and tree logging is a serious threat.

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Poster 73: The relevance of small water bodies for bats foraging above farmland

HEIM OLGA[1, 2], LENSKI JOHANNES, SCHULZE JELENA, JUNG KIRSTEN, ECCARD JANA A., VOIGT CHRISTIAN C.

[1] Animal Ecology, Institute of Biochemistry and Biology, University of Potsdam, Maulbeerallee 2a, D – 14469 Potsdam, GERMANY
[2] Leibniz Institute for Zoo and Wildlife Research, Alfred-Kowalke-Str. 17, 10315 Berlin, GERMANY; heim@izw-berlin.de

Remnant semi-natural landscape elements, such as hedgerows, forest edges and small ponds, represent important refuge zones for wildlife in intensively used agricultural landscapes. Bats are known to forage and commute close to hedgerows and forest edges when moving across the agricultural matrix, yet it is unclear how small ponds which are often isolated landscape elements within arable fields influence bat activity along the edge-field interface.
Our aim was to investigate whether small ponds within arable fields affect flight and foraging activity of bat species along the edge-field interface. Additionally, we aimed at comparing species-specific activity measures between forest edges and hedgerows/tree lines and at identifying seasonal changes in these effects on activity measures along the edge-field interface.
We repeatedly recorded bat activity using passive acoustic monitoring at hedgerows and forest edges (each N = 10) along a transect leading in a perpendicular direction from the edge structure up to a distance of 200 m into the arable field (edge-field interface). Hereby, a small pond was located close to transects on five sites per edge structure type (total N = 20). Using generalized linear mixed effect models, we analyzed the effects of edge structure type, pond presence and the season on species-specific bat activity and foraging activity along the edge-field interface.
We found a positive effect of small ponds on the activity of *Nyctalus noctula*, *Pipistrellus pygmaeus* and *Myotis* spp. and on the foraging activity of *N. noctula* above the arable field. In addition, we found that bats used forest edges and hedgerows/tree lines largely for commuting, but also for foraging. Furthermore, we found seasonal variation in the use of these linear landscape elements.
We conclude that linear woody vegetation edges are important for all bat species that were investigated here. Additionally, small ponds within the arable field support the interaction of bats from different functional groups with the agroecosystem. Therefore, these remnant semi-natural landscape elements should be preserved, but primarily restored if not intact and better linked to surrounding landscape elements in order to efficiently support biodiversity of bats and wildlife in general within the agroecosystem.

SESSION VIII: OTHERS

Poster 74: Bat activity above 3000 m in the Austrian Alps

WIDERIN KARIN[1], REITER GUIDO

[1] Koordinationsstelle für Fledermausschutz und Forschung in Österreich (KFFÖ), 4060 Leonding, Fritz-Störk-Str. 13, AUSTRIA;
karin.widerin@fledermausschutz.at, guido.reiter@fledermausschutz.at

During the last few years (2013 to 2015) we investigated the migratory behaviour of bats throughout the Alpine Arch. A rather surprising result was that a large number of bats crosses the Alps at an altitude of up to 2500 m. Subsequently, we wanted to know up to which altitude bats can be detected in the Central Alps.
Thus, we investigated bat activity on top of Mt. Sonnblick at an altitude of 3106 m.a.s.l. during the years of 2014 and 2015. This mountain top is located in the South of the province of Salzburg and it is part of the main Alpine Arch. Extreme weather conditions, glaciers and rocks with very rare fragments of vegetation characterize the investigated site and hence, this habitat seemed totally unsuitable for bats.
Bat activity was monitored by automated recording of bat calls (batcorder, ecoObs, Nuremberg) during September and October 2014 and permanently from March to November 2015.
Contrary to our expectations we found bat activity from mid-April to mid-September. There was a little peak of activity in spring, however, the main activity was detectable during August and September. Among the recorded species were all long-distance migrants of Europe, namely *Nyctalus leisleri*, *Nyctalus noctula*, *Pipistrellus nathusii* and *Vespertilio murinus*, but also sedentary species like *Eptesicus nilssonii* and species with more or less unknown migratory behaviour like *Pipistrellus pygmaeus* were found.
Bat activity was strongly linked to milder weather conditions, but activity was still found at relatively high wind speeds up to 16,6 m/s and temperatures as low as –2,5°C.
In the presentation, I am also going to discuss social behaviour of the bats on the peak of this mountain.

Poster 75: City bats vs. country bats: neural differences due to navigation skills in the Egyptian fruit bat *Rousettus aegyptiacus*.

ORIT DASHEVSKY[1], YANIV ASSAF[2,3], YOSSI YOVEL[1,2]

[1] Dept. of Zoology, George S. Wise Faculty of Life Sciences, Tel Aviv University, Tel Aviv 69978, ISRAEL
[2] Sagol School of Neuroscience, Tel Aviv University
[3] Dept. of Neurobiology, George S. Wise Faculty of Life Sciences, Tel Aviv University; oritdash@gmail.com

Rousettus aegyptiacus the Egyptian fruit bat is a social nocturnal mammal that roosts in groups and forages on different fruits. GPS data from our lab shows that there is a difference in foraging behavior in Egyptian fruit bats that live in natural habitats (country bats) vs. those that live in human settlements (city bats). Country bats fly every night to feed on a specific tree, frequently, at a distance of many kilometers from their roost. City bats forage every night at many different trees and spend the night moving from tree to tree, this behavior requires maintaining a spatial representation of their many feeding sites and navigating between them. A classic MRI study compared the brains of London taxi drivers that must navigate to many sites, and London bus drivers that follow the same rout every day. The study showed that taxi drivers had greater gray matter volume in mid-posterior hippocampi (a navigation related area) in comparison to bus drivers. In this study we examined the brains of 30 city and 30 country bats using Diffusion Tensor Imaging MRI scans which reflect differences in neural activity. In addition we conducted a behavioral experiment in these two groups in which they were exposed to a room with many food sources that they could select from. Following this behavioral test, we kept 10 country bats and 10 city bats for a month in the lab in a city-like food setup, and looked for changes in the bats' behavior and brain. The foraging behavior of the bats in this setup was evaluated, and they were MRI scanned at the beginning and at the end of the month. We found multiple brain areas that significantly differed between city and country bats. Country bats that were kept in the setup above for a month showed country like behavior at the beginning of the period and city like behavior at the end of it. In addition, brain areas that differed between city and country bats at the beginning did not differ at the end.

Poster 76: What are they looking at? Ganglion cell density maps in *Myotis daubentonii*

CECHETTO CLÉMENT[1], DE BUSSEROLLES FANNY[2], COIMBRA JOAO PAULO[3], JAKOBSEN LASSE[1], WARRANT ERIC[3]

[1] Sound, Communication and Behaviour group, University of Southern Denmark, Odense, DENMARK
[2] Queensland brain institute, The University of Queensland, Brisbane, AUSTRALIA
[3] Vision Group, Lund University, Lund, SWEDEN; clementc@biology.sdu,dk

Bats are widely known for their use of echolocation to navigate and forage. Echolocation has allowed bats to occupy a wide range of ecological niches with an equally wide range of feeding ecologies (e.g. insectivorous or frugivorous, gleaning or hawking). Even though all species of bats possess eyes, vision has been largely ignored as a sensory modality for bats. Evidence shows that some bats use vision for orientation and even for prey localization (e.g. *Eptesicus nilsonii* gleaning white ghost moths off of leaves[1]). Bats also display a large range of relative eye sizes suggesting differences in the importance of the vision for different bat species. The goal of this study is to use retinal anatomy to investigate the visual performance of *M. daubentonii*, a small trawling vespertilionid that occurs over most of Eurasia.
We estimated spatial resolution and sensitivity from ganglion cell and photoreceptor cell density maps (generated using Stereology). The data collected so far shows that *M. daubentonii's* peak acuity is approximately 0.6 cycles per degree. This is a low value that is in accordance with existing literature[2] (human acuity is around 63 cycles/deg[2]). As expected, we find an area centralis located in the ventral region of the retina, but surprisingly we also have find a second area centralis located in the dorsal retina. We hypothesise that this area may be a specialisation that has evolved in *M. daubentonii* for trawling over water. Our results suggest that *M. daubentonii* likely doesn't use vision to find prey, as it has relatively poor acuity, but instead uses vision to orient itself and control its flight.

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Poster 77: What can we infer from the diet analysis of specialist-bats?

GOITI URTZI[1], ARRIZABALAGA AITOR[1], GARIN INAZIO[1], AIHARTZA JOXERRA[1]

[1] Department of Zoology and Animal Cell Biology, Faculty of Science and Technology, University of the Basque Country UPV/EHU, Sarriena z.g., Leioa, BASQUE COUNTRY; arrizabalaga.aitor@gmail.com

Understanding the degree of prey-specialization and adaptive flexibility of insectivorous bats, as well as their evolutionary relationship with prey is pivotal to assessing their ability to adapt to varying environments. However, this is limited by taxonomy-based diet analyses where the identification and interpretation of functional relationships are restricted due to the vast diversity of consumed prey species and the high diversity of evasive and defensive adaptations of prey. In this study we introduce an innovative approach to analyze and interpret the foraging ecology of insectivorous bats. We aimed to analyze the trophic flexibility of a moth specialist horseshoe bat (*Rhinolophus euryale*) and its evolutionary relationship with prey, by linking prey's functional traits (e.g. mass, wing-loading) and bats' intraspecific variables (i.e. sex, size and ontogeny) through diet and across a spatiotemporal gradient. Diet was analyzed using DNA metabarcoding in combination with RLQ and the fourth-corner analyses. Our trait-based approach showed that prey's traits related to energy content (i.e. mass) and flight performance (i.e. wing loading and maneuverability) changed significantly across seasons and bats' ontogenetic stage. These results showed that a moth-specialist bat is trophically flexible enough to take advantage of seasonally variable moth types. Moreover, we identified functional dietary differences between juveniles and adults hardly possible to identify by taxonomy-based approaches, as both consumed moths. In addition, the eared Arctiine moths seemed to be under-represented in the diet of *R. euryale*, suggesting that these moths developed some effective level of protection against highly specialized moth-eating bats. Our results showed that trait-based approaches open new insights to understanding the foraging ecology, evolutionary relationships and conservation of insectivorous bats.

Poster 78: Challenges of a special sense: Exploring echolocation's encoding of spatial and temporal frequency

BAIER LEONIE[1,2], GOERLITZ HOLGER R.[2], WIEGREBE LUTZ[1]

[1] Ludwig- Maximilians- University Munich, Division of Neurobiology, Department Biology II, 82152 Martinsried, GERMANY
[2] Max Planck Institute for Ornithology, Acoustic and Functional Ecology Group, 82319 Seewiesen, GERMANY; baier@bio.lmu.de

Undoubtedly, one of bats' specialties is their use of echolocation as the main remote sense to image the environment. However, while echoes give direct cues about distance, size, surface properties or position of the targeted objects, there is no simple one-to-one relationship between the acoustic features of the echoes and the spatial layout of the environment. As opposed to the explicit spatial layout of the retina, the bat cochlea represents echoes along an audio-frequency axis. Thus, bats have to construct a spatial representation from the spectro-temporal echo features at their two ears. Another special problem, this time regarding the analysis of temporal frequencies, arises from echolocation being stroboscopic, not continous like vision. In FM bat species the duty cycle of sonar ensonification is typically less than 10%, i.e., bats more often don't call than they do. This sparse temporal sampling of the environment impairs the assessment of changes, as for example the distance of an object over time. For fast periodic changes an echolocating bat may run into aliasing problems, i.e. a systematic perceptual error introduced through too low temporal sampling. On the other hand, slow changes can only be perceived by tracking changes of echoes across a sequence of calls. In two formal psychophysical experiments with the echolocating bat *Phyllostomus discolor*, we have systematically evaluated 1) biosonar sensitivity to spatial frequency (meaning change as a function of space) and 2) sensitivity to the magnitude of an object's temporal frequency. Bats were trained and tested in the discrimination of two targets. In experiment 1), the reference target sported a spatial frequency of 0/m, corresponding to a flat surface, while the test target was covered with waves of varying spatial frequencies. Our results indicate that echolocation in bats is more sensitive to higher spatial frequencies than to lower spatial frequencies, implying that echolocating bats can segregate prey from background according to spatial frequency. In experiment 2), the reference target sported a temporal frequency of 0Hz, corresponding to an immobile target, while the test target's distance was modulated at varying temporal frequencies. Preliminary results show that the sensitivity is highest to periodic changes of 1000Hz, which corresponds to the fastest wing beats of small insects (Sotavalta, 1953), and decreases towards lower temporal frequencies.

Poster 79: The Giant noctule (*Nyctalus lasiopterus*) in the middle of southern France (Puy de Dôme): a five-year study of breeding colonies brings new insights on the ecology of the species

BEUCHER YANNICK[2], GAGER YANN[3]

Our work present the results of a 5-year study (2012-2016) of breeding colonies of the Giant noctule (*Nyctalus lasiopterus*) discovered in 2012 in the middle of Southern France (Puy de Dôme). The discovery was made possible without capture but relying on the development of a new method where observers follow bats back to their roosts in the early morning using both acoustic and visual information. Once the colonies were discovered, we used complementary tools, such as capture / telemetry, night vision tools (infrared camera coupled with light intensifiers) or acoustic data from a network of Batcorders placed in fixed points.
The population of Giant noctule exploits each year a particularly dense network of ancient lodges of Black woodpeckers (*Dryocopus martius*) found in a beech forest located in a deep valley. The breeding roosts (females and offspring) are concentrated in the part of the forest with the richest density in cavities, allowing regular transfers between roosts. Our results also show the presence of more isolated satellite roosts of non-breeding males (likely subadults) remaining in the surroundings of the females before their sexual maturity. These results not only question the hypotheses about latitudinal and altitudinal migrations advanced by the spanish experience but also bring new insights about the notion of sexual segregation at the breeding colonies of giant noctules.

[2] EXEN : RD64, route de Buzeins, 12310 VIMENET, France
ybeucher.exen@gmail.com

[3] Hillerstrasse 3, 04109 LEIPZIG, Germany
yann.gager@gmail.com

Poster 80: Noctule bat (*Nyctalus noctula*) migration in Central Europe: linking summering and wintering grounds

LEHNERT LINN S. [1], KRAMER-SCHADT STEPHANIE[1], POPA-LISSEANU ANA[2], TEIGE TOBIAS[3], HOFFMEISTER UWE[4], VOIGT CHRISTIAN C.[1]

[1] Department of Evolutionary Ecology, Leibniz Institute for Zoo and Wildlife Research, Berlin, GERMANY; lehnert@izw-berlin.de
[2] Estación Biológica de Doñana, Sevilla, SPAIN
[3] Büro für faunistisch-ökologische Fachgutachten
[4] natura - Büro für zoologische und botanische Fachgutachten

European bats are currently threatened by a variety of substantial indirect and direct anthropogenic stressors, such as habitat degradation, climate change and mortality events at wind turbines. Migratory bats are particularly susceptible to habitat changes and require particular protection. However, detailed understanding of migratory behavior and even migratory connectivity between summer and winter habitats of European migratory bats, which is essential for implementing effective conservation measures, is lacking to date. Here we studied a) the geographical origin of noctule bats (*Nyctalus noctula*) from hibernacula across central Europe to illuminate the connectivity between wintering and summering grounds of this facultative migratory species b) morphometric differences between migrant and regional bats, and c) the plasticity in migratory strategies (migration vs. non-migration) on the individual level. We took fur samples of hibernating noctule bats in different European countries and measured stable isotope ratios of non-exchangeable hydrogen in fur keratin to separate migrants from regional individuals. After establishing site specific proportions of migratory bats in the hibernacula we used isoscape origin models (IsoriX) to determine the geographical breeding provenance of the migratory individuals. Data with available information on body mass and forearm length were used to test for morphometric differences between migrants and regionals. For one site with intensive banding efforts over the last decade, we were able to obtain longitudinal data from recaptured individuals and used this unique opportunity to study the plasticity of the individual migration strategy over time. We found migratory individuals in all studied hibernacula across Europe, while proportions differed. No significant difference in forearm length was detected between regional and migratory bats, while migrants were found to be significantly heavier. While most of the individual bats we were able to follow showed consistency in their specific migration strategy over time, we also found evidence for plasticity – not only in terms of strategy itself but also regarding the choice of alternative breeding areas.

Poster 81: Escaping a bat: Behavioural variability as anti-predator adaptation in moths

HÜGEL THERESA[1], TER HOFSTEDE HANNAH M.[2], GOERLITZ HOLGER R.[1]

[1] Acoustic and Functional Ecology Group, Max Planck Institute for Ornithology, Eberhard-Gwinner Straße 11, 82319 Seewiesen, GERMANY; thuegel@orn.mpg.de
[2] Dartmouth College, Department of Biological Science, 78 College St, Hanover, NH, 03755, USA

How to not end up as a predator's meal? This question is crucial for animals of prey; and therefore a multitude of adaptations for avoiding or escaping predators evolved. One of the widespread adaptations is erratic and therefore unpredictable movement known as "protean behaviour". Echolocating bats and eared moths are ideal to study this kind of behaviour. Upon detecting a bat with their ultrasound sensitive ears, many moths engage in evasive flight manoeuvres to escape the attacker. Previous studies already revealed that moths´ escape flight behaviour consists of two stages, directional and erratic flight. Surprisingly however, erratic flight seems to show some degree of stereotypy. As successful defence behaviour is mainly based on unpredictability, an open research question is how such stereotypical behaviour can be effective for avoiding predators. We hypothesize that interspecific variation in evasive flight exists across moth species, causing a masking effect of the stereotypy of the evasive flight of any single moth species. We recorded the evasive flight behaviour of multiple European and North-American moth species using two different approaches. (A) Using an automated force-transducer we recorded behavioural audiograms of stationary flying moths. Pure tone stimuli from 5-90 kHz were presented in randomized order and with increasing intensity of 20-90 dB SPL to flying moths. (B) To observe natural flight behaviour, we recorded 3D trajectories of free flying moths in a sound-attenuated and anechoic acoustic chamber in response to pure tone pulses of 30 kHz at 50, 65 or 80 dB SPL. Analysing behavioural thresholds (A) and the onset and three-dimensional shape of escape trajectories (B) will enable us for the first time to systematically compare moth escape flight across multiple species, to compare behaviour to the underlying neuronal audiograms, and to study additional factors like moth size and echo reflectivity on escape behaviour. In sum, this will shed light on the specialised adaptations that evolved in prey species in response to the threat posed by their highly specialized predators, nocturnal flying echolocating bats.

Poster 82: Benefits and costs of a special mammalian trait: male philopatry in proboscis bats (*Rhynchonycteris naso*)

LINUS GÜNTHER[1], KNÖRNSCHILD MIRJAM[2], NAGY MARTINA[3], MAYER FRIEDER[1]

[1] Museum für Naturkunde, Leibniz Institute for Research on Evolution and Biodiversity
[2] Free University Berlin, Institute of Biology
[3] Friedrich-Alexander University Erlangen-Nuremberg, Department of Sensor Technology

In contrast to the majority of mammals that predominantly exhibit male-biased dispersal, Neotropical bats show an astonishing variability in dispersal behaviour. Currently, we know of only a few bat examples with a reversed dispersal pattern where females leave their natal group and males stay where they were born (e.g. in *Rhynchonycteris naso*, *Saccopteryx bilineata* and *Carollia perspicillata*). While inbreeding avoidance is widely accepted as the major driver for female dispersal, the evolution of male philopatry is still poorly understood and discussed to be driven by male mating strategy, mate competition among male kin and kin cooperation. During a five-year study we gathered detailed data on pedigree, individual roosting and mating behaviour to assess the benefits and costs of male philopatry in proboscis bats and improve the understanding of its evolution. Our behavioural data and genetic paternity show that male proboscis bats adopt a territory based mating strategy with aspects of resource-defence at night and direct female-defence during the day. Further, our results reveal that social groups consist of several males descending from few patrilines and few unrelated male immigrants. By assessing relatedness and competition (i.e. agonistic interactions, same mate pairing and siring success during the same mating periods) of the present adult males we show, that in *R. naso* closely related males face mate competition. However, these costs seem to be outweighed by the benefits of philopatry, since philopatric males become more often territorial and have a higher individual reproductive success compared to male immigrants. Finally, the fact that males frequently tried to immigrate into colonies, but rarely stayed, reproduced or became territorial indicates that male immigration is possible but assumingly difficult. This illustrates how males may benefit from staying in their natal colony despite facing high mate competition with their close relatives – a driver which is discussed to usually prevent male philopatry in mammals.

Poster 83: Hiding in the dark: social foraging networks of vampire bats cracked by miniaturized proximity sensors

RIPPERGER SIMON[1], MAYER FRIEDER[1,2]

[1] Museum für Naturkunde, Leibniz Institute for Evolution and Biodiversity Science
[2] Berlin-Brandenburg Institute of Advanced Biodiversity Research

Bats are extremely diverse, not only in terms of species numbers but also regarding their social lives. Despite the great diversity of social organizations, mating systems and social structures, relatively few species have been studied in detail, so far. Observations on social behavior are time consuming and usually restricted to the roost because of their nocturnal activity, their cryptic lifestyle and their high mobility. In addition, the relatively small average body size of bats restricts the applicability of automated tracking devices to few large-bodied species. We developed a miniaturized and highly automated sensor network that is designed to detect encounters among individual bats both inside the roost and during foraging. We used these light-weight animal-borne devices to track the social behavior of free ranging common vampire bats (*Desmodus rotundus*). Vampire bats show an extraordinary social behavior (allogrooming, food sharing) which has been studied in both captive colonies and natural roosting sites. In our study we asked whether the social bonds that form among individuals inside the roost are also reflected by their foraging behavior. To this end we compare roosting networks that base on close associations inside the roosting site to foraging networks that are built from encounters during foraging bouts. This is the first study that evaluates the social behavior of bats during foraging using proximity sensors which collect quantitative data on associations between individual animals.

Poster 84: Social roosts as a solution to ecological constraints in fruit bats

RAMAKERS JIP[1]

[1] Animal Ecology, Netherlands Institute of Ecology

Animals have to make daily foraging decisions, and in doing so rely on different sources of social information and weight it against their own experience to reduce costs associated with foraging. Social roosts can serve as 'information centres' where roost members communicate with one another, thereby inadvertently transferring information about the location, quality or quantity of food. Relying on others' foraging decisions may be particularly important for energy-constrained foragers with widely dispersed and unpredictable food sources, such as fig-eating bats. In my talk I will elaborate on a series of food-choice experiments done with one such a bat, *Uroderma bilobatum*. In our work, we focused on the question of whether and how bats use information from roost mates to make informed foraging decisions. The results of the experiments reveal that these bats do, with evidence that information transfer effectively takes place in the wild. Our results shed new light on a potential mechanism underlying the evolution of sociality.

Poster 85: Rapid somatic and behavioral development in juvenile tent-making bats

KOHLES JENNA[1-4], PAGE RACHEL[1], DECHMANN DINA[1-3], O'MARA TEAGUE[1-3]

[1] Smithsonian Tropical Research Institute, Balboa, Ancon, REPUBLIC OF PANAMA
[2] Department of Migration & Immuno-Ecology, Max Planck Institute for Ornithology, Radolfzell, GERMANY
[3] Department of Biology, University of Konstanz, Konstanz, GERMANY
[4] jkohles@orn.mpg.de

Juvenile bats develop at exceptional rates relative to other long-lived mammals, quickly reaching adult wing size which is necessary for flight. This rapid morphological development coincides with many behavioral changes that have not been characterized for wild bats. In particular, we know little about behavioral development during pup fledging and weaning. We studied a population of Peter's tent-making bat (*Uroderma bilobatum*) in Gamboa, Panama, a species that naturally roosts in ephemeral tents constructed from palm leaves. In our study site, *U. bilobatum* roosts under the eaves of houses, creating opportunity for detailed observation. We conducted weekly roost surveys to determine the population's size and breeding seasons. We captured juveniles from multiple roosts over the course of two summer breeding seasons, recording mass and forearm length. We video recorded one roosting group for 24-hour periods every two to four days during the fledging period, capturing both diurnal and nocturnal behavior. Female *U. bilobatum* rear single pups in two breeding seasons per year and give birth in relative synchrony with roost mates. Maternity groups remain fairly stable during pup rearing. Adult females leave the day roost for approximately 6-12 hours each night and carry pups during foraging for several weeks after parturition. Pups more than double body mass in less than 60 days and become volant at approximately 4 weeks of age, at which time mothers begin to leave the roost without them. Pups never remain in the roost alone for an entire night, but some delay departure during which mothers return to provision milk. Through behavior coding we show changes in activity budgets and social interaction as pups grow. These results fill gaps for natural history of tent-roosting bats and may give insight into ontogeny of flight, foraging, and social behavior for this species.

Poster 86: Beyond the range of echolocation: Disentangling essential bat senses for long-distance navigation

LINDECKE OLIVER[1], HOLLAND RICHARD A.[2], PĒTERSONS GUNARS[3], VOIGT CHRISTIAN C.[1]

[1] Leibniz Institute for Zoo and Wildlife Research, Department of Evolutionary Ecology, Alfred-Kowalke-Straße 17, 10315, Berlin, GERMANY; lindecke@izw-berlin.de
[2] Bangor University, School of Biological Sciences Deiniol Road, LL57 2UW, Bangor, UNITED KINGDOM
[3] Latvia University of Agriculture, Faculty of Veterinary Medicine, K. Helmaņa 8, LV-3004, Jelgava, LATVIA

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Seasonal migration is a successful example of adaptations of bats to guarantee survival in harsh winters, gene flow over large spatial scales; and effective resource exploitation. Despite millions of bats travel up to thousands of kilometres each year, the mechanisms involved in orientation and navigation over distances beyond their home range are far from understood. The scientific literature on sensory ecology and physiology elucidating this aspect of bats' life is still in its infancy compared to decades of endeavours in ornithology. However, results from bird studies are not easily transferable to mammals and intriguing alternative solutions to deal with way finding can be expected from bats.
Over the last two years, we engaged in three different types of experimental approaches to investigate the sensory ecology of migratory pipistrelles during their autumn passage of the Pape Biological Research Station at the Latvian Baltic Sea coast. The experiments differ in their spatio-temporal design, ranging from simulated in-roost orientation observations to large-scale displacement of individuals and tracking their subsequent navigational decisions.
Here, we outline the principal set-ups and present first findings from either of the experiments. Using selected cues tested so far (vision, olfaction, and magnetoreception), we are able to demonstrate the diversity of sensory inputs putatively relevant for effective long-distance movements performed by temperate bats.

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