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Above: A Egyptian Fruit Bat (*Rousettus aegyptiacus*) caught in the Pufuri area, Kruger National Park, South Africa.

Inside this issue:

Recent Literature	2
Conferences	2
Zoological Society of Southern Africa Conference	2
16 th International Bat Research Conference	5
Published Books / Reports	16
Published Papers	16
Notice Board	26

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Recent Literature

Conference

Zoological Society of Southern Africa 2013

Below are abstracts that are specifically related to African bat species.

Papers

The importance of ecology and physiology in a changing world: Wahlberg Epauletted Fruit Bat (*Epomophorus wahlbergi*) as an example

Colleen T. Downs - School of Life Sciences, University of KwaZulu-Natal,

Globally the biggest threats to mammal and bird populations in the short-term are human development, population growth, urbanisation, alien invasions and land transformation resulting in habitat loss for species. In addition climate change is another threat in the long-term. However, to assess how these threats impact on a species and how they may survive both ecological and physiological studies are required. The importance of interdisciplinary studies is highlighted using the example of Wahlberg's epauletted fruit bat *Epomophorus wahlbergi*. A summary of how these bats use urban environments, are important frugivores and dispersal agents, and are affected by changing temperature extremes is presented. The bats showed seasonal variation in home range size, movements and foraging dynamics in the urban environment of Pietermaritzburg, South Africa. This seasonal variation in home range size can possibly be explained by a reduced amount of fruiting species during winter resulting in bats having to move greater distances to search for food. They have high assimilation efficiencies on both glucose and sucrose irrespective of concentration. As they used both sugars efficiently to maximize and maintain energy gain, it is expected that they feed opportunistically on fruit in the wild depending on temporal and spatial availability to obtain their energy requirements. Furthermore, fruit with high sucrose or glucose content will be consumed. In urban environments they feed extensively on alien fruits which they disperse. In fruit bats with high energy requirements, dietary flexibility may be an advantage when faced with seasonal and unpredictable fruit availability. There was a significant seasonal variation in the thermoregulatory abilities of *E. wahlbergi*. The importance and consequences of roost temperature on extreme hot days is highlighted.

Using high-throughput sequencing in diet analyses

Kristine Bohmann - Centre for GeoGenetics, Natural History Museum of Denmark, University of Copenhagen.

Even a tiny faecal sample from an animal contains DNA traces of what the animal has been eating, and when this DNA is extracted and sequenced, it can reveal prey remains in the faecal samples that are not even identifiable under a microscope. When sequencing of faecal samples is performed on a high-throughput sequencing platform, it can be used as a cost efficient and effective way to conduct diet analyses as it allows for many samples to be sequenced in one go and generates millions of reads in just one sequencing run.

We are currently using these techniques in studies of bats' diet, and depending on the bat species in question, we use them to identify everything from mammal and bird to insect prey. In this talk, I will talk about using high-throughput sequencing in diet studies and discuss its advantages and limitations.

Do patterns of divergence amongst vagile taxa support vicariant evolution in Southern African taxa?

David Jacobs, Hassan Babiker, Anna Bastian, Teresa Kearney, Rowen van Eeden and Jacqueline M Bishop - Department of Biological Sciences, University of Cape Town; Ditsong Museum of Natural History

Similar patterns of evolutionary diversification amongst co-distributed taxa suggest that vicariance may have shaped their evolution. Several co-distributed non-vagile taxa in southern Africa display similar patterns of evolutionary diversification as a result of a common biogeographical history. We test whether the increased dispersal ability of co-distributed vagile taxa have prevented the formation of similar patterns of diversification. We tested the above hypothesis on the bat species *Rhinolophus darlingi*. We sampled populations from localities throughout its distribution and used phylogenetic reconstruction to identify and date lineage divergence. We also used phenotypic comparisons and ecological niche modelling to identify morphological and geographical correlates of those lineages. Our results indicate that *R. darlingi* is in fact paraphyletic, the eastern and western parts of its distribution forming two distinct lineages associated with different clades in the phylogeny. The two clades diverged ~9.68 Ma. On the basis of the localities of the type specimens we retained the name *R. darlingi* for the eastern group and elevated the western group, currently regarded as the sub-species *R. darlingi damarensis*, to full species status. *R. damarensis* was associated with arid biomes and *R. darlingi* with more mesic biomes. *R. damarensis* was comprised of two lineages that diverged ~5 Ma. The timing of the divergence coincided with increased aridification between 7-5 Ma and was probably due to populations becoming isolated in different biomes as a result of the expansion of savannas, grasslands and shrublands. The pattern of evolutionary diversification in *R. damarensis* was temporally similar to those of non-vagile taxa but spatially different. Evolutionary diversification in several southern African taxa appears to have been influenced by similar environmental changes during the Miocene, suggesting vicariant evolution. However, differences in spatial patterns of diversification may be explained by differences in dispersal ability.

Phylogeography of *Hipposideros commersoni* (Chiroptera: Hipposideridae) in the dry forests of Madagascar

Andrinajoro R Rakotoarivelo, Sandi Willows-Munro, Corrie M Schoeman, Jennifer M Lamb and Steven M Goodman - School of Life Sciences, University of KwaZulu-Natal; Field Museum, Chicago, USA and Association Vahatra

The Commerson leaf-nosed bat (*Hipposideros commersoni*) is an endemic species to Madagascar and is particularly common in the western portion of the island in forested areas from sea level to 1150 m. Extensive exploitation for bush meat is probably the most important cause for this species' decline. Seasonal variation has been recorded in its activity and diet, and during the austral winter, at certain sites these bats are not observed exiting caves at dusk to forage. It is not clear if populations undergo a form of torpor or whether they are partially migratory. No information is previously available on the phylogeography of this species and such studies might provide insights into dispersal patterns and gene flow. In this study, we examined the phylogeographic patterns of *H. commersoni* across the dry forest areas of Madagascar using the hypervariable mitochondrial control region gene. Preliminary analyses indicate some geographical structure within this species, with evidence of seasonal movements, consistent with previous morphological studies.

Evidence for ecologically mediated perception of species specific signatures in echolocation calls of the same peak frequency

Anna Bastian and David Jacobs - University of Cape Town, Biological Sciences

Rhinolophus capensis uses peak echolocation frequencies which range from 75 kHz at one end of its coastal distribution in South Africa to 85 kHz at the other end. We tested whether peak frequency was the only acoustic parameter used to discriminate between conspecifics and other species. In habituation-dishabituation playback experiments we exposed 75-kHz and 85-kHz *R. capensis* individuals to a set of acoustic test stimuli each consisting of echolocation calls of the same peak frequency namely *R. capensis* calling at 85 kHz and another species, *R. damarensis*, calling also at 85 kHz. The two test groups differed in their behavioural responses to the test stimuli. The 85-kHz group discriminated between calls from conspecifics (85 kHz) and calls from *R. damarensis* (85 kHz) despite both stimuli having the same peak frequency. This indicates that other components besides peak frequency may contain species specific signatures. In contrast, the 75-kHz test group did not discriminate 85-kHz *R. capensis* from 85-kHz *R. darlingi*. This group is isolated from other *R. capensis* populations but co-occurs with *R. damarensis* and, in its habitat, 85-kHz calls likely represent another species. Furthermore, the 85-kHz *R. capensis* co-occurs with *R. clivosus*, the juveniles of which use similar echolocation frequencies of about 88 kHz and it has to regularly use other acoustic cues to avoid making recognition errors. We discuss our findings in the context of a multilayer recognition system which is required in the presence of other species using similar frequencies.

The influence of habitat on echolocation call design of insectivorous bats in Swaziland

Machawe Innocent Maphalala

Echolocating bats emit sounds and then analyze the returning echoes to get information about their immediate surroundings. Factors that influence echolocation call design in bats include habitat change and activity of bat. In this study the design of echolocation calls was examined using a frequency-time structure display from anabat II detector. The study compares echolocation calls of five species recorded in two adjacent foraging habitats: savanna and sugarcane plantation in the lowveld of Swaziland. The five species are *Chaerephon pumilus*, *Mops condylurus*, *Scotophilus dinganii*, *Neoromicia nana* and *Miniopterus natalensis* and they were identified based on reference calls provided by Taylor et al (2013). Each species was tested for variation in echolocation call design in each habitat. The call parameters compared were minimum frequency, maximum frequency, frequency of the knee and call duration and results show that all species show difference in at least one of the parameters. The two Molossidae bats *C. pumilus* and *Mops condylurus* varied their frequency components, minimum frequency and frequency of the knee respectively. *Miniopterus natalensis* of the Miniopteridae family varied only the call duration parameter. Calls of Vespertilionidae bats *S. dinganii* and *N. nana* showed more flexibility, they changed both their frequency and time parameters. It can be concluded from the results of this study that all five species alter their calls with habitat. The bats alter their calls to enhance foraging in a more open habitat if they were foraging in a closed habitat and vice versa. Some of the changes could be due to different prey encounter rates in each habitat even though this could not be verified in this study.

Morphometric variation in *Mops condylurus* (Chiroptera: Molossidae) from Sub-Saharan Africa

Tarin L Ramsaroop - School of Biological & Conservation Sciences, University of KwaZulu-Natal

The molossid genus *Tadarida* was considered to comprise the subgenera *Chaerephon*, *Mops* and *Mormopterus*. Traditional morphometric analyses of the cranial morphology of molossid species provided evidence for the recognition of *Chaerephon*, *Mops* and *Mormopterus* as separate genera to *Tadarida*. *Mops* species were distinguished from congeners based on several cranial characters and the characteristic band of skin connecting the ears at their bases. *Mops condylurus*, the Angolan free-tailed bat, is the most widespread African *Mops* species. It is an ecologically and economically important species in agricultural regions throughout sub-Saharan Africa where it is known to forage on crop pests. Recent molecular studies strongly support a monophyletic *Chaerephon-Mops* clade, with the exception of *Chaerephon jobimena*. *Mops* species generally appeared ancestral to *Chaerephon* species. On the basis of external morphology, some authors have recommended the inclusion of *M. condylurus* within the genus *Chaerephon*. Ambiguity regarding the taxonomic status of *M. condylurus* warranted a more detailed investigation of the morphological diversity of this widespread molossid species. The aim of this study was to explore geographic variation in the cranial morphology of *M. condylurus* throughout sub-Saharan Africa using landmark-based geometric morphometric techniques. Skull shape and size differences between individuals from southern, southeastern and western Africa were investigated using 14 dorsal, 17 ventral and 14 lateral landmarks. Morphometric data revealed clinal variation in both cranial size and shape, with populations from western Africa noticeably larger southern African forms. Partial least squares analysis revealed morphological diversity of *M. condylurus* was correlated with ecogeographic variables. Clarification of morphological variation amongst geographically segregated populations of *M. condylurus* will help to advance our understanding of the evolutionary history of the species, and will provide useful information for future conservation management of Angolan free-tailed bat populations throughout Africa.

Morphometric variation in *Tadarida aegyptiaca* (Chiroptera: Molossidae) across Africa

Sylvana Reddy - School of Biological and Conservation Sciences, University of KwaZulu-Natal

There is much debate regarding morphological- and genetic-based research into the evolutionary relationships amongst and within molossid genera, particularly the genus *Tadarida*. There are six *Tadarida* species that occur throughout the Afro-Arabian region. *Tadarida aegyptiaca*, the Egyptian free-tailed bat, is the most wide-spread species occurring mainly throughout southern Africa, to the Arabian Peninsula and south-western regions of Asia. Recent molecular studies have revealed paraphyly within the genus *Tadarida*, with *T. aegyptiaca* more closely related to *Chaerephon jobimena* and *Sauromys petrophilus* than other congeners. Such findings have raised questions concerning the taxonomic status and species limits of *T. aegyptiaca* throughout Afro-Arabia. I used geometric morphometrics to investigate morphological variation amongst geographically segregated populations of *T. aegyptiaca*. Sixteen dorsal, 12 lateral and 17 ventral landmarks were used to describe cranial size and shape variation amongst Egyptian free-tailed bats. Multivariate analyses of landmark data sets revealed significant inter-population size and shape divergence. Thin plate splines were utilised to demonstrate several population-specific cranial characteristics. These preliminary findings indicate that the morphological diversity of *T. aegyptiaca* is underestimated.

Activity patterns of bats in an African Savanna

Fezile Mtefetswa and Ara Monadjem - Department of Biological Sciences, University of Swaziland.

Bat distributions remain poorly known in southern Africa compared to other small mammals, this is because previous studies have utilized mist-netting and trapping techniques which can easily be detected by insectivorous bats through the use of echolocation. The activity of bats was studied in an African savanna site (Simunye, Swaziland) and compared with that of neighboring sugar cane fields. ANABAT II detectors were used to record echolocation calls and the activity was calculated as the number of passes. Results of the study showed the presence of three foraging groups in the study area which were identified by their frequency of the knee (Molossidae; open air foragers Fk<32 kHz, Vespertilionidae/Minioptreidae; clutter-edge forages, Fk 72<31> kHz and Hipposideridae/Rhinolophidae; Fk>72 kHz). Bat activity showed variation with habitat and with season; highest activity was observed in winter and was negatively affected by the high amount of rainfall received in summer. Composition of families also varied with season and with habitat. There was some variation in activity patterns observed and those observed in previous studies (Monadjem *et al.*, 2008); i.e. increase in bat activity was observed during winter instead of summer. Variation was due to environmental factors such as temperature, humidity and amount of daily rainfall received. More studies need to be done to determine if these irregular patterns persist as these results could mean a lot for Swaziland; i.e could be an indicator of maybe a shift in time of seasonal change or some change in the climate itself

Wind energy and South African bats: implementation of proactive mitigation measures

Kate MacEwan

Several applications are in progress for Wind Energy Facility developments in South Africa. Whilst most biologists would support the development of clean, renewable energy sources, such as wind energy, studies conducted internationally at established WEFs have demonstrated numerous bat fatalities, with fatalities predicted to be several hundreds of thousands per annum in the USA alone. Natural Scientific Services CC has been conducting long-term pre-construction bat monitoring at 13 proposed Wind Energy Facility sites in South Africa over different periods since May 2011, in accordance with the South African Good Practice Guidelines for Surveying Bats in Wind Farm Developments. We have discovered interesting temporal and spatial bat activity patterns at the different study sites in terms of varying activity levels per site and across sites, peak activity times of night and activity levels related to different weather variables. We aim to share some of these findings to date and also to describe the potential challenges faced by bats in terms of the rapid expansion by South Africa into the wind energy sector. There are potential major direct and indirect impacts on bats associated with these developments, if appropriate measures are not put in place. However, developers, authorities, environmental assessment practitioners and specialists have the opportunity and responsibility to integrate renewable energy with the least environmental impact. We can gain from the lessons hard-learned internationally, and together with local assessments and knowledge, apply appropriate measures to reduce direct impacts on bats and hence, lesson effects on the ecosystem services that bats provide. Through detailed pre-construction bat monitoring assessments, Natural Scientific Services has presented various actions that developers can implement to result in reduced bat fatalities. Such actions will be subject to post-construction monitoring verification.

Poster

The utility of geometric morphometric data in discerning species within the Afrotropical *Hipposideros caffer-ruber* complex (Chiroptera: Hipposideridae)

Leigh R Richards, Peter J Taylor & Ara Monadjem - Durban Natural Science Museum; School of Environmental Sciences, University of Venda; All Out Africa Research Unit, Department of Biological Sciences, University of Swaziland

Systematic relationships amongst Afrotropical insectivorous bats belonging to the genus *Hipposideros* have often been questioned due to the difficulties in species delimitation and the existence of morphologically similar cryptic species. One particularly challenging group is the *Hipposideros caffer-ruber* complex. Recent genetic studies have begun to clarify the phylogenetic and phylogeographic patterns within this species complex and have revealed cryptic lineages within *H. caffer* and *H. ruber*. The Critically Endangered *H. lamottei* falls within the *H. caffer-ruber* group, yet the taxonomic identification of this species remains unclear and the distinction of *H. lamottei* from *H. caffer* and *H. ruber* has not been fully investigated. We used geometric morphometric approaches to investigate cranial size and shape variation amongst five Afrotropical hipposiderid species, including those formerly attributed to the *H. caffer-ruber* complex in attempts to a) assess the validity of the recently described genetic lineages within the complex, b) provide possible lineage-specific cranial characters to aid in taxonomic diagnoses, and c) determine the adaptive role of cranial size and shape variation. Principal component analysis of landmark data revealed four distinct morphological groups corresponding to the species

H. beatus, *H. caffer*, *H. lamottei*, *H. ruber*. Shape variation was, in part, explained by overall cranial size. Multivariate analyses of landmark data demonstrated significant cranial size and shape divergence between the morphological groups. Understanding the ecological and physiological adaptive value of morphological variation can provide valuable insights into the evolutionary history of this diverse Afrotropical species complex.

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Complete abstract book can be downloaded as PDF [3.2 Mb] from http://www.ibrc2013.com/pdf/ibrc_2013_abstracts.pdf

Below are abstracts that are specifically related to African bat species.

Do Bats Talk Funny In Helium? A Test of Echolocation Flexibility

Eran Amichai and Yossi Yovel - Tel-Aviv University, Israel

Our study aimed to test the extent of flexibility in an active sensory system - echolocation, in insectivorous bats. We conducted flight experiments with *Pipistrellus kuhlii* in a helium-enriched environment to test two aspects of flexibility: **1. Speed-of-sound:** As target ranging depends largely on measuring the time interval between an emission and its echo, an accurate reference of the speed-of-sound is crucial to an echolocating bat. Our goal here was to test the bats' ability to deal with changes in speed-of-sound which also occur in the natural environment. **2. Call parameters:** echolocation calls are produced by the vocal cords, and are then filtered by the vocal tract. The lower density of helium should thus increase the frequency of the emitted call, and our goal here was to check whether bats cope with the altered calls or try to actively compensate. Bats were held in a flight tank containing either regular air or 80% heliox, in which speed-of-sound was increased by 20%-25%, and were required to fly a short distance and land on a target. We analyzed echolocation parameters and target ranging (hits or misses) to assess heliox effects and bats' responses to them. While echolocation appears to be unaffected, target ranging was severely impaired and bats repeatedly underestimated target distance even after long periods in heliox and much training. Our results show flexibility is limited when faced with drastically altered speed-of-sound. The exact limits and the reason for lack of effect on emission parameters are currently under further research.

Marburg Virus Outbreaks: Understanding Virus Spillover from the Natural Reservoir

Brian Amman, Serena Carroll, and Jonathan Towner - Centers for Disease Control and Prevention, USA

Marburg virus (MARV) causes sporadic outbreaks of Marburg hemorrhagic fever (MHF) in Africa. The Egyptian fruit bat (*Rousettus aegyptiacus*) has been identified as a natural reservoir based most recently on the repeated isolation of MARV directly from bats caught at the Kitaka mine and Python Cave (~50km apart) in southwestern Uganda where miners and tourists separately contracted MHF from 2007-08. A long-term study of *R. aegyptiacus* at these locations determined that 2-5% of the population was actively infected, that bat and human virus sequences were genetically similar, and that twice-yearly birthing seasons produced pulses of juvenile bats that, when ~6 months old, were 5-6 times more likely to be infected than adults. These seasonal pulses coincide with the dates of 83% (54/65) of all known MARV bat to human spillover events. These data are the first to forecast periods of increased-risk for human infection. There are still many unanswered questions however; how is the virus shed? Are there symptomatic infections in bats? Can experimental infection on captive bats be achieved? To answer these questions and more, we captured, tested, and imported a breeding colony of *R. aegyptiacus* to perform experimental infections with filoviruses in a high containment setting. Experimental infections with Marburg virus and captive *R. aegyptiacus* are currently being conducted. Preliminary results reaffirm conclusions from our field data, which indicates these bats are capable of maintaining the virus within a population. Further analysis of experimental infection data hopefully will elucidate more aspects of virus spillover from this reservoir host.

Phylogeography of the European Free-tailed Bat in the Western Palearctic

Francisco Amorim, Raquel Godinho, Javier Juste, Carlos Ibañez, Stephen Rossiter, Pedro Beja, and Hugo Rebelo - Universidade do Porto, Portugal; Estación Biológica de Doñana, Spain; Queen Mary University of London; University of Bristol, UK

The European free-tail bat *Tadarida teniotis* is one the most northerly distributed member of the Molossidae yet almost nothing is known about its population history and genetic structure. The importance of unraveling complex historical events that may explain current species distribution patterns is paramount for guiding conservation. Here we combined results from the analysis of two mtDNA fragments and nuclear DNA with species distribution modeling to determine *Tadarida teniotis* glacial refugia and postglacial colonization routes. For mtDNA we sequenced fragments of cytochrome *b* and the hypervariable domain (HVII) of D-loop, while for nuclear DNA we genotyped a set 14 microsatellites. Overall 150 samples covering the west Palearctic range of the species and a few from the Far East were used for DNA analysis. For modeling purposes we used a maximum entropy modeling technique to calculate bioclimatic models for the present and projected them to the last glacial maximum (LGM; 23 000–18 000 years BP). We used two different general circulation models (GCM) for this latter period, the Community Climate System Model (CCSM) and the Model for Interdisciplinary Research on Climate (MIROC). Microsatellites showed very high allelic diversity within the species range but no population structure was detected across European and North Africa. Palaeodistribution models predicted that suitable climatic conditions probably existed during LGM in southern Europe and North Africa. Our early results suggesting a panmictic population across a wide area highlight the need for international policies for conservation management of this taxon.

The Revolutionary Foraging Niche of the Barbastelle Bat

Raphaël Arlettaz, H. Goerlitz, G. Jones, P. Jones, S. Puechemaille, J. Rydell, D. Schmieder, B. Siemers, and D. Russo - University of Bern, Switzerland; Max Planck Institute for Ornithology, Germany; University of Bristol, UK; University of Texas, USA; Ernst Moritz Arndt University, Germany; Lund University, Sweden, Università degli Studi di Napoli Federico II, Italy

Barbastelle bats (*Barbastella barbastellus* and *B. leucomelas*) belong to the long-eared bats (Plecotinae) but have a unique head and face morphology, probably related to an unusual foraging niche. Long-eared bats generally use passive listening to detect prey and faint broad-band echolocation calls mainly for spatial orientation. Nevertheless, adaptive plasticity within the group is shown by the spotted bat *Euderma maculatum*, which uses loud, low-frequency (audible) echolocation calls. In general, long-eared bats, including *E. maculatum*, frequently feed on moths, a prey type usually difficult to capture for species using high-intensity echolocation calls. Indeed, many moths escape bat predation thanks to their ultrasound-sensitive ears by which they detect echolocation calls of approaching bats. Barbastelles feed almost exclusively on moths, and indeed seem more specialized on this prey type than any other European bat. This has been explained by a «stealth strategy» – echolocation calls are weak enough to alert the prey only when the bat is so close that anti-predatory reactions are no longer effective. Here, we propose that a further special, possibly unique and complementary, adaptation in the foraging technique exists. Based on previous findings (diet analyses, description of echolocation calls and field observations of foraging bats) and the above rationale, we experimentally analysed the prey detection technique of *B. barbastellus* in captivity. Results suggest that barbastes listen to the fluttering noise emitted by flying moths to locate and capture them. This behaviour has not previously been described for bats, but may occur in other species, notably those with convergent head morphology.

Ecological Correlates of Coronavirus Dynamics in West African Bats

Heather Baldwin, V. Corman, S. Klose, E. Nkrumah, E. Badu, P. Anti, A. Annan, M. Owusu, O. Agbenyega, S. Oppong, Y. Adu-Sarkodie, P. Vallo, E. Kalko, J. Drexler, C. Drosten, and M. Tschapka - Ulm University, Germany; Macquarie University, Australia; Bonn University, Germany; Kwame Nkrumah University of Science and Technology, Ghana; Academy of Sciences of the Czech Republic, Czech Republic; Smithsonian Tropical Research Institute, Panama

Bats are important reservoir hosts to a number of emerging viruses, including SARS-coronavirus (CoV), Hendra and Nipah viruses, as well as Ebola and Marburg viruses. These pathogens can cause problems for public health, animal industries, and wildlife conservation. To minimize the risk of future epidemics, knowledge about the reservoir hosts is required. We need to understand how ecological factors may influence disease dynamics and drive host-switching and emergence. While numerous studies have aimed at discovery of novel infectious diseases in bat populations, little research has examined the role of host ecology on pathogen dynamics and diversity. We investigated the influence of host phenology and demography on the dynamics and diversity of CoVs in West African cave-dwelling bats. We screened 7,000 bat faecal samples from 15 species, collected regularly over two years at ten bat colonies in Ghana, for CoVs. Four CoV lineages were quantitatively detected using highly sensitive strain-specific real time RT-PCR assays. Here, we report on results on host demographic, phenological and seasonal influences on infection dynamics. Preliminary findings suggest that CoVs were preferentially carried by juvenile bats and lactating females, corresponding to seasonal spikes in virus amplification once per year linked to bat reproductive cycles. These data may imply the potential of host colonies as settings conducive to host-switching events. In sub-Saharan Africa, where bat-human contact is relatively high, these kinds of ecological insights to the study of emerging diseases are crucial to inform decisions about management, conservation and mitigating potential threats to human public health.

Reproductive Biology and Seasonal Dynamics of Spatial Activity of *Rousettus aegyptiacus* in the Eastern Mediterranean

Tomáš Bartonička, R. Lučan, P. Benda, P. Jedlička, Š. Řeřucha, R. Bilgin, M. Abi-Said, M. Porteš, A. Reiter, W. Shohdi, M. Šálek, M. Uhrin, and I. Horáček - Masaryk University, Czech Republic; Charles University, Czech Republic; National Museum, Czech Republic; ASCR Brno, Czech Republic; South Moravian Museum in Znojmo, Czech Republic; Boğaziçi University, Turkey; AUB Beirut, Lebanon; Nature Conservation Egypt, Egypt; Pavol Jozef Šafárik University in Košice, Slovakia

Reproductive cycle of *Rousettus aegyptiacus* has been intensively studied in the years 2005–2012. We analyzed the data from two regions corresponding to two types of environment (biomes): the zone of continuous distribution in the Levant (Turkey, Cyprus, Lebanon, Jordan – 1285 individuals, 429 adult females) and an isolated population of *R. aegyptiacus* in the Dakhla Oasis, Egypt (2315 individuals, 529 females). Seasonal dynamics of reproduction in both regions showed similar patterns. Females gave birth during most of the year except in winter months. In both regions, the timing of reproduction had peaks in April–May and August–September, the spring peak was more pronounced. This pattern comports with a seasonal polyestry, a typical reproductive strategy of bats in tropical regions. With this exception, however, polyestry is unknown in bats from temperate regions. In the same areas 240 individuals (43 bats in Cyprus, 131 in Egypt and 66 in Turkey) were followed using the automated radiotracking system, BAARA, manual tracking, and GPS transponders (in total 230,000 fixes). In Egypt and Turkey the vast majority of tracked individuals preferred foraging grounds close to major roosts (as well as preference for their own individually specific feeding sites), while in Cyprus bats visited food sources 20 km from roosts. Low spatial activity was correlated with limited capacity of food resources and regular use of individually specific foraging grounds. While areas with diverse and rich food resources, local spatial activity increased significantly.

Evidence for Ecologically Mediated Perception of Species Specific Signatures in Echolocation Calls of the same Peak Frequency

Anna Bastian and David Jacobs - University of Cape Town, South Africa

Rhinolophus capensis uses peak echolocation frequencies which range from 75 kHz at one end of its coastal distribution in South Africa to 85 kHz at the other end. We tested whether peak frequency was the only acoustic parameter used to discriminate between conspecifics and other species. In habituation-dishabituation playback experiments we exposed 75-kHz and 85-kHz *R. capensis* individuals to a set of acoustic test stimuli each consisting of echolocation calls of the same peak frequency namely *R. capensis* calling at 85 kHz and another species, *R. damarensis*, calling also at 85 kHz. The two test groups differed in their behavioural responses to the test stimuli. The 85-kHz group discriminated between calls from conspecifics (85 kHz) and calls from *R. damarensis*

(85 kHz) despite both stimuli having the same peak frequency. This indicates that other components besides peak frequency may contain species specific signatures. In contrast, the 75-kHz test group did not discriminate 85-kHz *R. capensis* from 85-kHz *R. damarensis*. This group is isolated from other *R. capensis* populations but co-occurs with *R. damarensis* and, in its habitat; 85-kHz calls likely represent another species. Furthermore, the 85-kHz *R. capensis* co-occurs with *R. clivosus*, the juveniles of which use similar echolocation frequencies of about 88 kHz and it has to regularly use other acoustic cues to avoid making recognition errors. We discuss our findings in the context of a multilayer recognition system which is required in the presence of other species using similar frequencies.

Circum-Mediterranean Phylogeography of a Bat Coupled with Past Environmental Niche Modelling: a New Paradigm for the Recolonization of Europe?

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The isolation of populations in the Iberian, the Italian and the Balkan peninsulas during the ice ages define four main paradigms that explain the distribution of intraspecific genetic diversity in Europe, though not without exceptions. In this study we investigated the phylogeography of a wide-spread bat species, the bent-winged bat, *Miniopterus schreibersii* around the Mediterranean basin and the Caucasus. Samples were collected from 28 new locations in 14 countries, and combined with previous data from four countries. We also undertook an environmental niche modeling (ENM) analysis, for predicting the current and past continental distribution of the species during the last glacial maximum (LGM). The genetics results indicate that populations of *M. schreibersii* in Europe went extinct and the continent was repopulated from Anatolia after the end of the LGM. The data show signatures of a gradual geographic expansion, as well as philopatric distributions of individual populations. In the Maghreb region of North Africa, there is evidence for the presence of a new *Miniopterus* species (*Miniopterus maghrebensis*) occurring sympatrically with the nominotypic form, which we describe here for the first time. However, the fossil record in Iberia and the ENM results indicate continuous presence of *Miniopterus* in this peninsula that most probably was related to the Maghrebian lineage during the LGM, but did not persist after the LGM. Combined with similar results from previous studies, we define a new paradigm that involves the recolonization of all of Europe from Anatolia. The study shows how genetics and ENM approaches can complement each other in providing a more detailed picture of intraspecific evolution of species.

Echolocation in Non-echolocating bats

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Since the early days of research on echolocation, the widely held view is that old world fruit bats (Pteropodidae) do not use echolocation and rely on highly sensitive night vision. The only exception was the genus *Rousettus* whose members use a "strange" form of clicking echolocation. The non-echolocation dogma was also the basis for dozens of studies attempting to explain the evolution of echolocation. Here, we challenge this dogma. We conducted a study on the possible use of echolocation in Pteropodidae and found that all genera we tested (*Eonycteris*, *Cynopterus* and *Macroglossus*) do in fact produce short high frequency click-like sounds that are probably used for echolocation. All bats dramatically increased (4 folds) the number of clicks per time unit in darkness compared to a light condition. While emitting these clicks, bats were able to orient in a completely dark room (<10⁻⁴lux), avoiding 1 cm diameter wires and landing on a feeding platform. Moreover, several individual whose eyes were covered produced even more clicks and were still able to perform these tasks. We are currently investigating the sound production mechanism and comparing the clicks to those of the better studied *Rousettus*-genus. We are convinced that more bats from the Pteropodidae family produce echolocation clicks. The use of echolocation by bats formerly believed to be non-echolocators may completely revise our understanding of the evolution of echolocation and of the difficulty of evolving such a trait.

Tracheal Calcification in Birds, Bats, Shrews, and Mice

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Post-natal calcification in the respiratory tract has been associated with mechanical stress imposed by muscles. Respiratory tract calcification is extensive in birds and is suggested to have evolved in response to stresses from vocalization/signing. Little is known about tracheal calcification in bats and how this might relate to flight and/or echolocation. Bats and birds synchronize respiration with wing-stroke to economize flight, resulting in compressive forces imposed by flight muscles on the respiratory tract. We hypothesized that tracheal and primary bronchi calcification will occur in echolocating *Artibeus jamaicensis* but not in nonecholocating *Syconycteris australis* and *Pteropus rodricensis*. We also compare tracheal and bronchial calcification between bats and shrews (*Sorex vagrans*) known to use sonar and the house mouse (*Mus musculus*), not known to produce sonar, to assess phylogenetic aspects. Tracheae were dissected from *A. jamaicensis* (N=4, 1-4 years old), *S. australis* (N=2), *P. rodricensis* (N=1), *S. vagrans* (N=6) (all of unknown age), and *M. musculus* (N=3, 4 months old) and cleared and stained with alcian blue and alizarin red. Tracheae and primary bronchi of *A. jamaicensis* and *P. rodricensis* were heavily calcified. *S. australis* tracheae showed heavy calcification with traces of calcification present in the bronchi. Tracheal calcification was present in some *S. vagrans* (N=3) but not in the bronchi. No calcification was detectable in mouse respiratory tracts. These preliminary data suggest calcification is not solely due to vocalization or solely flight mechanics. More data are needed from a wider range of mammals to assess the role that age possibly plays.

Bats without Borders --The Distribution and Conservation of Cave-dwelling Bats in Southern Africa

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Southern Africa is a subcontinent rich in bat fauna, but limited distribution data hinders ecological and conservation research. Climate change and extensive landuse change are recognised as major threats to bats globally; yet, despite bats being a major taxonomic group in southern Africa we are unable to measure biodiversity change and consequently cannot implement any proactive measures to counter any declines. The overall aim of this project is to determine the distribution of focal cave-dwelling bat species. As a group, cave-dwelling bats are considered to be at higher risk from human impacts, due to their dependency on and 'visibility' in caves. We used Maximum entropy modelling (Maxent) to model habitat suitability in order to determine which ecogeographical variables influence/limit their distributions. Maxent uses presence-only occurrence data, which is particularly important when absence data is hard to obtain. Predictive maps were generated for focal species, using recently validated museum specimen data, and a suite of environmental predictor variables (including geological, physical and climatic data from southern Africa). Relevant variables predicting suitable habitat over this large subcontinent were species-specific, but in general water availability (both temporary and intermittent), seasonal precipitation, vegetation and distance to karst (caves/limestone areas) were the most important factors associated with distribution patterns. This study illustrates how predictive modelling can be used as an important conservation tool to direct field work and inform conservation priority areas for research and monitoring of poorly studied species relatively quickly and at low cost.

Full Night On-board GPS Tracking and Audio Monitoring of Echolocating Bats

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Tracking animals in the wild is a challenging task. Tracking bats is even more demanding due to their small size and high speeds of movement. To overcome these difficulties we have developed a miniature device that includes a Global Positioning System (GPS) and an ultrasonic microphone. Since echolocating bats emit sounds in order to perceive their environment it is possible to infer their activity by recording their vocalizations. Ultrasonic recording also enables monitoring the presence of conspecifics. Our method thus allows full-night tracking of bats while monitoring their behavior. We used the device to track *Rhinopoma mycrophyllum* bats, a social echolocating bat species that is common in northern Israel during the summer. These first full-night recordings of the echolocation of a single bat enable us to probe fundamental questions such as what determines pulse repetition rate and how the presence of conspecifics influences the emission parameters of an individual. Our main interest, however, is to determine the factors influencing foraging success and foraging planning. Preliminary analysis revealed many details on the ecology of these bats such as the duration of their foraging, the distances covered and the number of insects attacked per night. We found a large variability in foraging characteristics and are now analyzing how the: (1) strategy of movement, (2) presence of conspecifics and the (3) past success influence foraging success and future behavior. We expect that further development of this method will open a new window into the cryptic world of echolocating bats.

The Effects of Conspecifics on Echolocation in Bats

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Bats may face any number of challenges to their echolocation systems when flying with conspecifics. These may include jamming, interference, masking, echo ambiguity, and even the acoustic "clutter" created by echoes from the physical bodies of conspecifics. Whilst the Jamming Avoidance Response (JAR) is well documented in the electric fishes, the concept is not coherent when applied to echolocating bats. We investigated the effects of conspecifics on echolocation in *Myotis daubentonii* and *Rhinolophus capensis*. We used multi-microphone array systems to record bats flying alone and in pairs in indoor and outdoor flight rooms and also bats flying freely in the field. From these recordings we reconstructed flight paths and calculated call intensity, among other echolocation call parameters. Calls of *Myotis daubentonii* were shorter in overall duration and wider in bandwidth (steeper sweep rate and lower FM-min) when flying with conspecifics compared to when flying alone. In *Rhinolophus capensis* we found that the terminal FM sweep was longer and wider in bandwidth (same sweep rate, but decreased FM-min) when flying with conspecifics that when flying alone. Our findings show significant changes in the call parameters of two different bats, with very different echolocation systems, when flying with conspecifics.

Are Eocene Megabats Masquerading as Primates?

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The fossil record of megabats (Pteropodidae) is notoriously poor. Analyses of molecular and morphological data indicate that pteropodids diverged from other bats no later than the early Eocene (~50 MYA), yet few pteropodid fossils are known other than late Pleistocene-Holocene records. It is apparent that the highly-derived bunodont dentitions of extant pteropodids evolved from a tribosphenic insectivorous ancestry, making recognition of ancient megabats in the fossil record difficult. Similar dental transitions occurred in primates and may have taken place at about the same time. Some fossil taxa previously recognized as primates could be fruit bats instead. One famous example is *Propotto* from the early Miocene of East Africa, which was originally described as a lorisiform primate but later recognized as a pteropodid instead. *Maunghanhinus*, originally described as a strepsirhine primate from the late Eocene of Thailand, could represent a similar example. Its lower premolars (simple, triangular), molars (flattened trigonids, straight labial cristid obliqua incorporating the hypoconid, low, flat lingual talonid basin) and long, low mandibular body are reminiscent of *Propotto* and potentially reflect attributes expected in early megabat morphology. There is little convincing evidence that *Maunghanhinus* is a primate and it is possible that it is actually an early pteropodid. One possible reason why so few pteropodids fossils have been recovered over a 50 million year time span is that researchers may not have fully considered the potential phylogenetic affinities of some fossils. There is no necessary reason to expect that every small, bunodont, frugivorous Eocene mammal represents a primate.

Tanzanycteris Actually a Hipposiderid?

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Tanzanycteris mannardi is the only known Eocene bat with extremely enlarged inner ears. The holotype is a single partial skeleton from the middle Eocene locality of Mahenge in Tanzania. The preservation is poor and most of the bone is dissolved. However, examination of 2D-microradiographs revealed large cavities inside the skull that reflect the huge size of the former inner ears. This surprising result was recently confirmed by means of micro-CT and new characters were recognized which clearly discriminate the inner ear morphology of *Tanzanycteris* from those of living rhinolophids and the mormoopid *Pteronotus parnellii*. However, inner ears of *Tanzanycteris* do show a very high similarity to hipposiderids, the third group of living bats with enormously enlarged cochleae. Thus, the question arises, whether *Tanzanycteris mannardi* (placed in its own family, Tanzanycteridae, when originally described) is actually an early hipposiderid. We compared *T. mannardi* with fossils with completely preserved skulls from Green River, Messel, and with the exceptional case of Stehlinia from Quercy. We detected by micro-CT some bony remains of the vestibular organ, which serve to establish a cochlear/vestibular size index. This cochlear/vestibular index permits comparisons with less complete specimens than does the cochlear/basicranial width index. This is important because several species from Quercy and elsewhere lack complete skulls but do preserve isolated cochleae and vestibular organs. This measure confirms that *Tanzanycteris mannardi* possessed a highly sophisticated echolocation system with constant frequency sounds and high duty-cycle echolocation and thus was very similar to living hipposiderids.

Molecular Analysis of B- and T-lymphocyte Cell Markers in Different Bat Species

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Chiropteran species are known reservoirs for many emerging viruses and act as natural hosts for diseases with importance for both public and animal health. With expansion of the human population and encroachment of bat habitats, the contact between humans, their livestock and different bat species are becoming more frequent, which facilitates the spill-over of viruses found in bats and the emergence of novel diseases. Despite this epidemiological role, little is known about immunological processes in bats and how their immune system controls viral infections. In order to gather more information about bat immune response we determined the sequences of the four main lymphocyte cell markers (CD3, CD4, CD8 and CD19) of species from three bat families (*Vespertilionidae*, *Phyllostomidae* and *Rousettinae*). Genomic DNA samples of spleens from three bat species (*Myotis myotis*, *Phyllostomus discolor* and *Rousettus aegyptiacus*) were used as a template for Polymerase Chain Reaction (PCR). Forward and reverse primers of CD3, CD4, CD8 and CD19 were designed from closely related sequence data available in GenBank. The obtained bat sequences were compared with other published information and phylogenetic analysis was applied to gain further insights on the evolution of bat immune responses. Our results are also important in order to obtain specific immunological tools for the different bat species.

The Pipistrellus Baculum: Individual and Phylogeographic Variation and Cryptic Species Discrimination

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With the discovery of further cryptic bat species, it is vital to find morphological species discriminating characters. *Pipistrellus pipistrellus* and *P. pygmaeus* have been recognized as separate species since 1997, but no reliable morphological species discriminating trait has been found. The baculum (os penis) has long been used successfully in species discrimination. In this study, we demonstrated how to reliably separate the common pipistrelle and the soprano pipistrelle by simple baculum measurements, and individual and phylogeographic variation of the *Pipistrellus* baculum were quantified. The bacula of museum specimens (Národní Muzeum, Prague) of the two species and of *P. hanaki*, which had already been identified by molecular genetic methods, were imaged with high-resolution microCT. Geometric morphometrics was used to quantify and locate variations in baculum shape. Several measurements were taken on the size-calibrated volume images and their value for species discrimination was tested by discriminant analysis with leave-one-out cross validation. *P. pipistrellus* and *P. pygmaeus* specimens can be discriminated by measuring the projected length, height, and width of the baculum. Variation in baculum shape (alone) cannot be used to separate these species. *P. hanaki* cannot be separated from the other two species by baculum shape. Most of the interspecific variation in baculum shape can be found in the proximal third (the base) of the baculum. Most individual variation can be observed in lateral view, especially in the shape of the curve. Quantitative details of morphology are becoming more important to distinguish cryptic species and understand their phylogeographic distributions.

Paleobiogeography of the Mediterranean Fruit Bats: an Unresolvable Issue?

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The abundant population of *Rousettus aegyptiacus* in the E Mediterranean poses a puzzling topic to historical biogeography. The only offshoot of the family Pteropodidae beyond tropics is an enigmatic issue: there is no clear idea on its origin, driving factors and modes of survival under quite unfavorable conditions. The present contribution summarizes the results of a multidisciplinary project intended to answer these questions. Detailed phylogeographic analyses (using both multiple molecular markers and biometric comparisons) demonstrated (a) homogeneity of the populations within the inner Mediterranean (except for Cyprus), (b) distinct subclades in S Arabia, Sinai, Egypt and Cyprus, (c) well marked divergence between the Mediterranean and sub-Saharan populations in some markers (dating the split to ca 1-3 My ago) but (d) a large amount of alleles and haplotypes common to both the clades. The default interpretations suggest the post-Neolithic spread throughout the Mediterranean as the major dispersal event and a source of it in the southern Arabia or sub-Saharan Africa. Yet, such "out-of-Africa-hypothesis" generates the scenarios which contradict both the observed geographic patterns of genetic diversity and the history of requisite contextual factors. A reversed approach supported by fossil remains in the Middle Pleistocene site Qesem, Israel, produces then the scenarios centered with a palaeochoric status of the Mediterranean form and suggesting that it could even become a source population for a spread to Africa. The respective scenario could also resolve the unanswered question on the background factors (including food resources) promoting long-term survival and peripatric diversification events in the region.

Environmental Margin, Island Evolution, and Anthropogenic Impact in Middle Eastern Populations of the Egyptian Fruit Bat

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We present a study of the population genetic architecture and microevolution of the Egyptian fruit bat (*Rousettus aegyptiacus*) at the environmental margins in the Middle East using mitochondrial sequences and nuclear microsatellites. In contrast to the rather homogenous population structure typical of cave-dwelling bats in climax tropical ecosystems, a relatively pronounced population diversification was observed. The evolution of this pattern could be ascribed to the complicated demographic history related to the range margin fragmentation and complex geomorphology of the studied area. Lineages from East Africa and Arabia show divergent positions. Within the northwestern unit, the most marked pattern of the microsatellite dataset is connected with insularity, as demonstrated by the separate status of populations from Saharan oases and Cyprus. These demes also exhibit a reduction in genetic variability, which is presumably connected with founder effects, drift and other factors related to island evolution. Genetic clustering indicates a semipermeability of the desert barriers in the Sahara and Arabian Peninsula and a corridor role of the Nile Valley. The results emphasize the role of the island environment in restricting the gene flow in megabats, which is also corroborated by biogeographic patterns within the family, and suggests the possibility of nascent island speciation. Distribution of subpopulations indicates ecological differentiation. Demographic analyses suggest that the colonization of the region was connected to the spread of agricultural plants; therefore, the peripatric processes described above might be because of or strengthened by anthropogenic changes in the environment and thus show some attributes of biological invasion.

Can an Evolutionary Trade-off Between Bite Force and Detection Range Explain Anomalously High Frequency Echolocation Calls?

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The skulls of animals have to perform many functions. Optimization for one function may mean that another function is not optimized. Such trade-offs may be responsible for one or more functional traits deviating from allometry. Here we investigate whether such a trade-off exists between the masticatory and echolocation functions of bat skulls. Several species of rhinolophids (e.g. *R. clivosus*) deviate from the allometric relationship between body size and peak echolocation frequency. Such deviation may be the result of selection for increased bite force resulting in a decrease in snout length. A decrease in snout length could lead to higher echolocation frequencies and consequent reduction in detection range. If so, there should be a negative relationship between bite force and detection range. We investigated bite force and detection range in several species of rhinolophids throughout southern Africa using bite force measurements, echolocation and skull morphology. Contrary to our prediction there was a positive correlation between bite force and detection range. After controlling for body size neither peak echolocation frequency nor bite force was correlated with rostrum length. Instead nasal capsule volume was a better predictor of peak frequency than nasal capsule length across rhinolophid species. Furthermore, *R. clivosus* has a smaller nasal capsule volume than predicted from its size. Thus the anomalously high peak echolocation frequency of *R. clivosus* cannot be explained by optimization of the masticatory function of the skull. Instead, it appears that selection has acted on nasal capsule volume directly resulting in an increase in echolocation frequency.

Patterns of Social Behaviour of *Rousettus aegyptiacus* in a Captive Breeding Colony

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Components of social behaviour of *Rousettus aegyptiacus* was studied in a captive colony of about 50 marked individuals in the Prague ZOO during 2010-2012 using quantitative post-hoc analyses of video- and audio records taken in a standardized way in weekly intervals, 90 mins prior to beginning of night activity. With few exceptions the adult individuals kept their fixed positions within the cluster throughout whole observation period. The largest variation in position within the cluster was typical for yearlings. In contrast to courtship behaviour and mating, which occurred throughout the year, parturitions were strongly synchronized and appeared within a week (bimodally in September/October and March/April). Couples and mating behavior were regular component but frequencies of them exhibited a clear peak during early lactation. A specific male courtship calls produced through nose appeared just in these periods. Couples were initiated either by males and females (in almost the same percentages). Males claimed females either by violence, protection or gradual allogrooming - the manner of forming couples seems to be dependent on age of the female. In violent approach, allogrooming has never been observed. Mothers' care of juveniles is very long, common roosting and grooming appeared long after weaning. Appearance of specific juvenile calls used in communication between young and adult decreased markedly in the third month after birth, but the last mother-young association was observed five months after birth. Bioacoustic analyses of courtship and juvenile calls are included.

Pathology of Marburg Virus Infection in a Natural Reservoir Host, *Rousettus aegyptiacus*

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Marburgviruses (family Filoviridae) are the causative agents of Marburg hemorrhagic fever (MHF), a significant human disease because of its rapid person-to-person transmission, high case-fatality rate (up to 90%), and lack of specific therapy. Several lines of epidemiologic, ecological, and molecular evidence have shown that the Egyptian fruit bat (*Rousettus aegyptiacus*) is a natural reservoir host of *marburgviruses* in Africa, and have directly linked outbreaks of MHF in humans to spillover from bats. Examination of limited sets of tissues collected during field studies of two large colonies of *R. aegyptiacus* in Uganda suggests that natural infection of bats with *marburgviruses* causes no significant clinical disease; this is consistent with the bat's suspected role as a reservoir host. In 2011, a captive breeding colony of *R. aegyptiacus* bats was established at the Centers for Disease Control and Prevention, Atlanta, GA, USA. Through experimental infection studies under Biosafety Level 4 laboratory conditions, we investigated the clinical and pathologic effects of experimental Marburg virus infection in Egyptian fruit bats. The tissue distribution and specific cell tropism of Marburg viral antigen were characterized using immunohistochemical staining techniques, and compared to findings in naturally-infected bats. These results contribute to the understanding of the pathogenesis of Marburg virus infection in *R. aegyptiacus*, and provide support for our experimental model of this virus-reservoir host system.

Horseshoe Bats Can Use Information in Echoes of Conspecific Calls for Spatial Orientation

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Bats in the wild often echolocate in the presence of other echolocating individuals. It is currently unclear if, in such situations, an individual bat experiences jamming by conspecific sonars or uses the information generated by conspecifics for its own means. We conducted behavioral experiments to address whether horseshoe bats are able to use spatial information in echoes reflected from conspecifics' calls. Greater horseshoe bats (*Rhinolophus ferrumequinum*) were trained to fly laps in a square flight tunnel that was lined with sound-absorbing foam. Pairs of bats were then introduced into the tunnel. When the two bats were passing a corner, a rapidly moving object was triggered using computer-controlled light barriers. The front bat that has already turned the corner can detect the object with its own echolocation calls as it is now directly in front of him. The hind bat that is still approaching the corner can only detect the moving object behind the corner in the echoes of the front bat's calls, since they are less attenuated on the way to the hind bat than the hind bat's own calls. These are attenuated twice by diffraction on the way to the caller, whereas the echoes of front bat's calls diffract only once on the way to the hind bat. The control experiment confirmed that the hind bat reacted to the moving object only when it was ensonified by the front bat's calls. This is the first conclusive evidence that echolocators use information in the echoes of extraneous sonars. Such ability could facilitate sensory cooperation among echolocating bats.

Comparative Genomic and Phylogeographic Analysis of Horseshoe Bats

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Advances in phylogeography suggest taxonomic boundaries may commonly arise and persist in the face of gene flow. Consequently the formation and maintenance of reproductive barriers may involve just a few so-called 'barrier genes' that function in aspects of pre- and/or post-copulatory mate choice. Here we combined phylogenetic and genomic analyses to identify potential barrier genes in horseshoe bats (Rhinolophidae). Rapid diversification in this speciose family might have been further facilitated by their use of constant frequency calls that appear to play a dual role in echolocation and communication. Thus divergent selection on the echolocation call frequency for hunting or habitat-use could also lead to pre-mating isolation. We obtained RNASeq data from nine horseshoe bat taxa and built alignments for ~3000 coding gene sequences. From these we identified candidate barrier genes based on known function, including 85 hearing genes and 270 reproductive genes. To assess whether these genes have contributed to horseshoe bat diversification, we tested for positive selection at each locus across the clade and found 66 genes showing evidence of molecular adaptation, including one linked to hearing. Next, to determine whether candidate barrier genes show reduced gene flow between hybridizing horseshoe bat species, for each locus we compared the relative support of competing phylogenetic hypotheses consistent with and without nuclear introgression. Initial findings revealed numerous genes have resisted introgression, although these did not include the candidate barrier genes identified. These first insights into the genetic basis of bat species barriers highlight the promise of genome approaches for bat research.

Evaporative Water Loss in a Warming World: Respiratory and Cutaneous Partitioning, and Interspecific Variation in Heat Tolerance

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Although evaporative water loss (EWL) in bats has been examined in several contexts, relatively little is known about interspecific variation in maximum cooling capacity and heat tolerance. We measured EWL, body temperature (T_b) and metabolic rates during summer in three species in a hot, semi-arid habitat in northern South Africa. Both *Sauromys petrophilus* (11 g; Molossidae) and *Taphozous mauritanus* (26 g; Emballonuridae) showed typical large increases in EWL as air temperature (T_a) approached T_b , with values of approximately 24 and 15 mg g⁻¹h⁻¹ respectively at $T_a \approx 42$ °C. However, *Nycteris thebaica* (12 g; Nycteridae) appeared to be considerably less heat tolerant and began increasing EWL at a much lower T_a to a maximum of 17 mg g⁻¹h⁻¹ at $T_a \approx 39$ °C. All three species exhibited maximum T_b values among the highest reported for bats. Another relatively unexplored aspect of EWL that is important for predicting performance at high T_a concerns the relative roles of cutaneous and respiratory evaporation. We trained ten *Epomophorus wahlbergi* to wear masks while hanging inside metabolic chambers, and measured EWL partitioning into cutaneous and respiratory components. Respiratory evaporation represented the majority of EWL at $T_a = 10 - 35$ °C, but at higher T_a the cutaneous component increased to around 65 % at $T_a \approx 40$ °C. A better understanding of EWL partitioning and interspecific variation in evaporative cooling capacity is needed to predict responses to more frequent and intense heat waves in hot environments, where extreme heat can cause large-scale mortality.

The Distribution of Bat Species Richness in Sub-Saharan Africa

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Sub-Saharan Africa harbours a high diversity of bat species across a spectacular array of landscapes and habitats. Many of these species face threats from habitat degradation, roost disturbance and over-exploitation as food sources. Understanding the distribution and drivers of species richness may assist with focusing conservation attention, but such studies have yet to be published for sub-Saharan Africa. Our main aim is to map bat species richness across sub-Saharan Africa, and to correlate this with environmental features of the landscape. We achieve this by estimating the potential distribution of 215 species of bat using environmental niche-based models based on 14,145 unique locality records. Neither sampling effort, nor species richness is evenly distributed across the region. Highest species richness is recorded in the Albertine Rift, the northern shores of Lake Victoria in East Africa, and the Upper Guinean forest zone of West Africa. Other areas of high richness include eastern South Africa and southern Mozambique, Zimbabwe, Malawi, coastal Kenya and Tanzania, the Ethiopian rift valley, the Congo basin north of the Congo River and the humid Guinean woodlands north of the rainforest in West Africa. Uniformly species poor areas include the arid zones of south-western Southern Africa, the entire Sahel zone of North Africa, and the Horn of Africa. Species richness was not correlated with sampling effort, altitude or altitudinal roughness. The well-defined richness gradients facilitate further work on the drivers of phylogenetic and functional bat diversity on the African continent.

Geographic Variation in the Echolocation Calls of a Species of Horseshoe Bat, *Rhinolophus simulator*

Gregory Mutumi and David Jacobs - University of Cape Town, South Africa

Geographic variation (GV), as an indicator of incipient speciation has poorly understood underlying processes. Geographic variation in southern African mammals has been little studied despite the region's varied geography which is likely to result in great phenotypic variation as populations become adapted to local habitats. We investigated GV in echolocation calls of an African horseshoe bat, *Rhinolophus simulator* in the context of James' Rule and two other hypotheses (foraging habitat and humidity hypotheses). We measured the morphology and echolocation peak frequency of 89 *R. simulator* individuals across their distribution range. There was little variation in echolocation frequency of *R. simulator* and contrary to James' Rule and the foraging habitat hypotheses, the peak frequency of *R. simulator* was not correlated to body size or vegetation index, respectively. However, the peak frequency at one site was significantly lower than at the other sites and this site also had highest mean annual rainfall and temperature. This suggests that the lower peak frequency evolved at this site because it increased detection range in the more humid conditions (humidity hypothesis) that prevailed here.

Foraging at Wastewater Treatment Works Increases Health Risks in an Urban Adapter, the Banana Bat

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The Banana Bat, *Neoromicia nana*, is an urban adapter that exploits swarms of pollution-tolerant chironomid midges at wastewater treatment works (WWTWs). We have previously shown that although WWTWs are beneficial to *N. nana* in creating an optimal food resource in the short-term, there are also long-term costs, specifically the accumulation of metal pollutants such as cadmium, chromium and nickel in the muscle, liver and kidney of *N. nana*. Here we investigated how foraging at WWTWs versus unpolluted sites, impacts various levels of the physiology of *N. nana*. We used haematocrits to assess haematological differences, hepatosomatic and renalsomatic indices to evaluate relative size differences in detoxification organs, and gonadosomatic indices to evaluate relative size differences in reproductive organs of male bats. We found that haematocrits were significantly higher in *N. nana* foraging at WWTWs indicating that *N. nana* may be compensating for a chronically low oxygen circulation within the body or kidney damage. In addition, hepatosomatic and renalsomatic indices were significantly higher suggesting hypertrophy of the detoxification organs. Finally, the gonadosomatic index of the testes were also significantly larger at WWTWs, suggesting that reproductive potential of males may be compromised, hence warranting further analyses, currently underway in our laboratory. Sub-lethal damage from pollutants is evident in *N. nana* foraging at WWTWs and chronic health problems may ultimately extend to the population level.

Echolocation Divergence in Horseshoe Bats Despite Extensive Gene Flow

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Horseshoe bats (Rhinolophidae) have evolved a unique echolocation system and geographic variation in resting frequencies (RF) across species' distributions is well documented. Whether these patterns are the result of selection, neutral drift or their interaction remains unclear. Here we used ecological parameters together with neutral and functional genetic variation to investigate the evolution of echolocation divergence (ED) in the Cape horseshoe bat, *Rhinolophus capensis*. A clinal pattern of increasing RF from west to east characterises the species distribution (75.7 - 86.5 kHz), which spans several major biomes and a pattern of increasing rainfall. This translates into a habitat gradient from open and sparse (west) to more cluttered habitats (east). Patterns of variation at the mitochondrial control region revealed minimal evidence for population structure ($F_{ST} = 0.38$) but significant asymmetric migration between populations. Genetic distance accounted for <10% of RF variation but mean annual rainfall (a proxy for habitat structure) explained 82%. Thus selection for higher frequencies in more cluttered habitats (foraging habitat hypothesis) appears greater than the homogenizing effect of gene flow in *R. capensis*. This could be the result of variation in the 'hearing gene' Prestin which encodes the mammalian cochlear amplifier and has evolved under strong positive selection in the ancestors of horseshoe bats. However, sequence data from the coding region of Prestin in several *R. capensis* populations revealed highly conserved gene sequences. Therefore, ED can occur despite genetic homogeneity and a lack of functional gene sequence variation. Instead, differences in gene expression/regulation may play a significant role.

The Role of *Pteropus rufus* in Forest Regeneration in Madagascar

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Madagascar has three endangered and endemic species of fruit bats. The largest one, *Pteropus rufus*, is relatively common and distributed widely in the country. So far 110 plant species have been identified in its diet, including 59 (55%) endemic species. This suggests that *P. rufus* has a very diverse diet, which has enabled it to adapt to areas with vastly differing vegetation types, e.g. dry deciduous forest in the south, littoral forest on the coast, and lowland rain forest in the north-east. This study aimed to determine the efficiency of Malagasy bats in promoting forest regeneration by comparing the germination success of seeds from faecal and ejecta pellets with those of ripe fruits. The seeds were exposed to progressively more natural challenges. Treatments were performed in conditions ranging from the laboratory, where sterilized seeds were placed on filter paper in a Petri dish, through differently treated soil and finally, in their natural conditions. Additionally, using high resolution GPS tags, we recorded the movement and foraging patterns of the Madagascar flying fox in a fragmented landscape. Findings will illustrate the role of *P. rufus* in forest regeneration through long distance seed dispersal, habitat preferences and movements across isolated forest fragments. Knowledge about this behaviour in relation to constant disturbance and hunting may help in further conservation actions and assist with the protection of these important Malagasy mammals.

Delimiting Cryptic Species for 'The Bats of Kenya' – the Genus *Miniopterus* (Miniopteridae)

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We are conducting a country-wide survey and inventory of bat species in Kenya, a megadiverse country with more than 100 mostly insectivorous bat species. This work entails characterizing and delimiting a number of cryptic and poorly understood taxa. Among the latter group, the Old World bent-winged bats *Miniopterus* (Miniopteridae) are especially challenging. Since 1999, when only 11

species were known, the number of *Miniopterus* species recognized has more than doubled. Both vocalization calls and analyses of genetic and morphological variation have contributed to this taxonomic proliferation. During surveys in Kenya, we identified at least three species of *Miniopterus* in the field. Through a series of analyses, we (a) present an expanded phylogeny of the genus *Miniopterus* that includes these forms; (b) distinguish the species from each other in vocalization, genetic, and morphological terms; (c) determine their ecological and geographic distributions; and (d) assess the proper names to apply to these forms, through comparisons with the holotypes for both *M. rufus* Sanborn 1936 and *M. africanus* Sanborn 1936.

Ontogeny of Vocal Communication of the Egyptian Fruit Bat and the Role of Learning in its Acquisition

Yosef Prat, Mor Taub, and Yossi Yovel - Tel Aviv University, Israel

Acoustic communication is fundamental in social systems of many animal species. Vocal learning, the competence to learn new vocalizations from auditory inputs, is a key element of complex vocal communication, and has been described mostly in courtship songs of birds and of a few mammals. However, experimental evidence of vocal learning in broader contexts is scarce. The sociality and acoustic abilities of bats present an excellent model for studying the development of vocal communication. We followed the vocal ontogeny of the extremely social and vocal Egyptian fruit bat (*Rousettus aegyptiacus*), from birth to adulthood. Pups were reared in small colonies or in acoustic isolation, and were monitored continuously by audio and video. The captured video enabled identification of speakers and contexts. Computational tools, developed specifically for this task, created a library of dozens of thousands of calls, where each call is associated with its context and speaker. Using this massive annotated lexicon we could follow the ontogeny of vocal communication. We grouped the entire corpus into few clusters, and observed the gradual assimilation of pups' calls into the adult clusters. Furthermore, pups reared in isolation demonstrated delayed vocal development, and their calls differed from the adult repertoire, compared to pups in the same age, which were raised among other bats. These results illuminate the ontogeny of social communication and imply a role for vocal learning in the acquisition of the diverse repertoire of *R. aegyptiacus*. Our data and tools also facilitate the comprehensive description of a rich vocal communication system.

Effects of Climate Change on Bat Distributions: What Do We Know? What Can We Do?

Hugo Rebelo and Gareth Jones - Universidade do Porto, Portugal; University of Bristol, UK

Earth's ecosystems and global biodiversity are facing an escalating decline and in the forthcoming years human-induced climate change (CC) are expected to become one of the major driving forces of such loss. Despite its relevance, and considerable research on other organisms, the potential effect of CC on bats has received little attention. Yet, within this context a considerable research has been devoted on predicting the potential future distributions of bats due to CC. In this talk it will be given an overview on the effects of CC on bat distributions for both temperate and tropical climates and how to develop monitoring networks (MN) that allow a proactive response to the predicted range shifts. Overall, regions currently possessing high species richness are predicted to lose their relevance, especially in the tropics. In temperate climates a general pattern of range shifts towards nowadays cooler regions is predicted. However, there is a higher risk of extinction for species associated to colder climates due to the severe reduction of suitable climatic space throughout the 21st century. Moreover, hibernacula for at least one bat species are also predicted to shift towards cooler latitudes. To validate and detect these potential range shifts the establishment of MN is essential. By sitting monitoring stations in areas sensitive to CC it may be possible to detect species' range shifts whenever they happen. By identifying priority areas for bat conservation and with the establishment of MN it might be possible to react proactively to the potential effects of CC.

Where East (Africa) Meets West: Bat Biodiversity and Biogeography in Southwestern South Sudan

DeeAnn Reeder - Bucknell University, USA

The new country of South Sudan is larger than Kenya, Uganda, and Rwanda combined, is characterized primarily by moist savanna and montane forests, and is historically known to house a variety of bat species. Along the southwest border of South Sudan with Democratic Republic of the Congo and Central African Republic lies a belt of tropical/subtropical forest. The presence of this tropical zone near the Congo Basin ecoregion sets it apart from the rest of South Sudan, and elements of the faunas and floras of West Africa and East Africa overlap here. As noted by Karl Koopman in his seminal work on the bats of Sudan, the diversity of bats that should be found in this region is vast, yet uncharacterized. Fieldwork was conducted in Bangangai Game Reserve, Western Equatoria State in July 2012, with a follow-up trip to Bangangai and Bire Kpatuos Game Reserves in May and June 2013. Classification efforts are still underway, but bats captured thus far include: Pteropodidae (*Epomophorus*, *Micropteropus*, *Hypsignathus*, *Lissonycteris*); Vespertilionidae (*Scotoecus*, *Scotophilus*, *Neoromicia*, *Glauconycteris*, and the new genus *Niumbaha*); Emballonuridae (*Taphozous*); Nycteridae (*Nycteris*); Hipposideridae (*Hipposideros*); and Molossididae (*Chaerophon*). Bats in the families Rhinolophidae and Megadermatidae are expected, but have not been captured to date. I will present my findings from both the 2012 and 2013 field seasons within the context of the unique biogeography of this region.

Cautionary Tales in Reconstructing the Evolutionary History of Island Bats

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Bats represent some of the most dramatic natural dispersal events among mammals, with representative taxa inhabiting most continental and oceanic islands. Within these island systems, commonly-asked phylogeographic questions investigate aspects of the evolutionary history of populations: Where did the island populations disperse from? How many dispersal events occurred and when? What was the direction of dispersal? Questions of conservation relevance may also be of concern in many island systems: To what extent do island populations exchange alleles with source population(s) or with other island populations? How diverse are island populations? Coalescent-based phylogeographic analyses have been applied to answer these questions in several systems. These powerful analyses demand judicious application, as they can be positively misleading when misused. Here, we review some cautionary tales learned from analyses of Hawaiian *Iasiurines*, Caribbean *Pteronotus*, and Malagasy *Triaenops* and *Myzopoda*. These studies demonstrate that model choice is extremely important. The flexibility permitted by approximate Bayesian computation (ABC) approaches makes available a wealth of diverse models, but also demands that researchers think creatively

when considering models to test and that we collect sufficient data to test parameter-rich models. In island systems, it is also important to sample multiple source populations and to consider the possibility that the direction of dispersal might not be easily predicted. These examples illustrate the power of this approach, but also illustrate the need for a thoughtful application of analyses.

Three Tales of Six Bats: Factors Shaping Cryptic Bats Distribution in Iberia

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Cryptic species pose a challenge to conservation by leading to biodiversity underestimations, may conceal threatened taxa within the cryptic complex and also bring the need to redefine what was classified as a single species distribution and environmental requirements. There is evidence that 20% of Iberian bat species harbour cryptic complexes and in this study we analyse the distribution patterns of three cryptic complexes in Iberia: *Plecotus auritus/a. begognae*, *Eptesicus serotinus/isabellinus* and *Myotis mystacinus/alcahoae*. We aimed to determine the distribution patterns of each species in Iberia, the ecological factors limiting these patterns, the identification of contact zones between sister species and the potential overlap between their ecological niches. Species identification was validated genetically by sequencing a fragment of the mtDNA cytochrome *b* gene. Maxent was used to build species distribution models, employing 15 variables relevant for bat occurrence. Most species distributions seem to be shaped by climatic factors and the presence of some linear features such as slopes, however *E. isabellinus* and *M. alcahoae* also showed affinity to the presence of forests. Moreover, niche analyses showed that the niches of *P.a. begognae* and *M. mystacinus* encompassed those of *P. auritus* and *M. alcahoae*, respectively. In the case of *E. serotinus/isabellinus*, both species seem to be competing for similar resources, as their niche overlap is high but their contact zone is restricted to a few locations in central Iberia. Here we show that combining genetic analyses with species distribution modelling provides important insights on the dynamics of the distribution of cryptic species.

Bat Malaria – a Focus on Hepatocystis in African Epauletted Fruit Bats

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Bats are known as important reservoir hosts for numerous emerging and highly pathogenic viruses. It is less well known that they also host a diverse set of malaria parasites species (family Haemosporida). To date, eight different genera (out of 14) of *Haemosporida* are described from the chiropterans, with all except two of these genera restricted to bat hosts. *Hepatocystis* is one of the latter genera that in addition to bats, uses rodents, artiodactyls and primates as vertebrate hosts. This genus is distributed in the Old World tropics and features a slightly modified life cycle compared to *Plasmodium* and lacks the parasite stages that are associated with the typical malaria symptoms. We report infections with *Hepatocystis* from West and East African bats, almost exclusively epauletted fruit bats (Pteropodidae), which feature high prevalences. We used a combination of microscopy and molecular methods to characterize the infections. The detected *Hepatocystis* parasites show a remarkable phylogenetic diversity and group with mammalian *Plasmodium* species. Some evidences indicate multiple infections in this host group. We conclude that these infections are almost universal in several African pteropodid bats, indicative of continuous and highly efficient transmission cycles.

Sympatric Horseshoe Bats Differ in Flight Performance in Confined Space

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In south Eastern Europe all five European horseshoe bat species occur sympatrically, and are presumed to compete for insects during periods of low insect abundance. They are known to forage within or close to vegetation, e.g. within woodlands. In this habitat maneuverable flight is essential for effective prey pursuit and avoiding collisions with vegetation. We hypothesized that resource partitioning in these species is effected by differences in their ability to maneuver within dense vegetation and tested 2 - 6 individuals of each species in an obstacle course simulating standardized vegetation. The course comprised three rows of vertical rods with inter-rod distances set from 45 - 10 cm at 5 cm increments, within a flight tunnel. The rods had a diameter of 6 mm ensuring that detection of the obstacles was not a limiting factor. Individuals were presented with each inter-rod distance during six consecutive trials on three separate occasions, and were scored on their success (based on number of touches, falls, rejections and invalid trials). All individuals managed to negotiate inter-obstacle distances of as little as 30 cm. At the smaller spacings, the smallest species, *R. hipposideros*, and one of the middle-sized bats, *R. euryale*, performed best. The largest species, *R. ferrumequinum*, showed the poorest performance. It therefore seems that the size of the different bat species plays an important role for their niche differentiation but other factors seem to be important as well. Therefore our next step will be to compare the performance with the wing morphology of these species.

Species Interactions during Diversification and Community Assembly in *Miniopterus* Bats in Madagascar

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Ecological differentiation may occur rapidly in clades undergoing adaptive radiation. Closely related, ecologically similar species often have adjacent distributions, suggesting competitive exclusion may influence community assembly. To determine whether the 11 endemic *Miniopterus* species in Madagascar could potentially compete with one another for habitat, we used ecological niche modeling to assess similarity of potential habitat use, both for current and last inter-glacial climates. We then used null models to examine dispersion patterns of sympatric species in terms of their phylogenetic relatedness and phenotypic and sensory characters – body size, skull morphology and echolocation - with the goal of understanding whether the assembly of 21 *Miniopterus* ensembles, sampled across Madagascar, was non-random. Of the four sister species pairs, we only found statistical support for ecological similarity between one sister species pair. Similarly, the overlap in potential habitat use was significantly high in < 15% and significantly low in > 65% of all possible species pairs (n = 54 pairs), implying that competition for habitat between most species pairs

is unlikely. In 87% of the observed combinations of sympatric *Miniopterus* species, we found significant signal for over dispersion of phenotypic and sensory characters, or phylogenetic branch length. The most commonly sampled *Miniopterus* ensembles displayed non-random patterns in multiple skull, body size and echolocation characters associated with the trophic niche. Collectively, our results suggest that selective processes associated with the adaptive radiation of *Miniopterus* species in Madagascar favoured bats to diversify first into habitat specialists (e.g., mountain versus lowland) and later into dietary specialists within a given habitat.

Bat Conservation Africa: a Voice for Our Friends in the African Night Sky

Iroko Tanshi - University of Benin, Nigeria; Bat Conservation Africa

Africa is home to 20% of the world's bat species. However, this rich diversity of over 220 species faces increasing threats from habitat destruction, persecution and the bush-meat trade. Meanwhile African bat researchers frequently study in isolation, working with scant resources and limited support. Thus, to date, when viewed from a global perspective, much of Africa appears to be a bat research and conservation void. To meet this challenge, in February, 2013, Bat Conservation Africa was launched in Naivasha, Kenya. With a leadership drawn from the six sub-regions (Central, East, North, Southern, West Africa and Western Indian Ocean Islands), it aims to provide a network for all (students, experts, African or international) interested in Africa's bat fauna. Its model for integrating research, education and conservation involves working in-country to raise capacity, recruit new members, raise public awareness, update national species lists, identify important bat areas, and influence local decision makers to promote pro-bat conservation policies. At a regional level, overarching threats and challenges to bat conservation will be addressed. On a continental scale, the network will develop projects that involve assessments of species status and field based trans-national projects. So far, the network has submitted two grant proposals. Other outputs include members working on collaborative reviews and research papers. Membership has grown steadily since the launch and each week, on e-mail, there is a lively exchange of views on an eclectic range of subjects. Clearly, this budding network will define the future of bat conservation in Africa.

Climate Change, Global Water Stress, and the Conservation of Insectivorous Bats

Daniel Taylor, Trish Badeen, and Mylea Bayless - Bat Conservation International, USA

Climate change is adversely affecting the global distribution and availability of water sources. Due to inherent physiological traits, insectivorous bats—which comprise nearly 70% of all species—may be especially vulnerable as they obtain less metabolic water from their food than non-insectivores, especially in arid and semi-arid environments. Research on myotis bats in a semi-arid region of the United States found that reproductive fitness declined significantly with diminishing surface water. To better understand which species and regions may be most vulnerable, we conducted a global gap analysis to identify where high bat species diversity, endangerment, and water stress intersected. Species data were obtained from the International Union for the Conservation of Nature and water data were obtained from a Nature Conservancy model derived from both physical and anthropogenic parameters such as temperature, precipitation, trends in water use by sector, and population density. Countries and regions with the highest vulnerability included Mexico, the Pacific Coast of Peru and Ecuador, Southern Africa, and Western India. Despite overwhelming evidence of negative climate-induced changes to global water availability and the importance of free water to insectivorous bats, limited research or conservation focus has been directed towards this emerging threat. Bat Conservation International will further refine our analyses and prioritize regions where we can work with local partners to raise awareness about water's importance to bats, support research on bats and water, and promote proven mitigation strategies such as watershed restoration and the incorporation of bat water needs into industrial, agricultural and livestock water management.

Bats as Biocontrol Agents Suppressing Nocturnal Flying Pests in Macadamia Orchards in Limpopo Province, South Africa

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Bats are major predators of crop pests. Regular acoustic transects (using ANABAT bat detector), mist-netting and harp-trapping of bats and dietary analyses of four bat species was conducted on two macadamia farms in the northern Limpopo Province between 2010 and 2013. Based on ANABAT call files recorded over seven months throughout the year, 16 species of bats were recorded of which five common species were recorded across three habitats (macadamia orchards, riparian bush and homesteads). Bat activity peaked during February and May, corresponding with high stinkbug (Hemiptera: Pentatomidae) numbers generally recorded at that time (stinkbugs are the major insect pest of macadamia nuts). Activity during winter was negligible. Faecal pellets and culled prey remains from slit-faced bat (*Nycteris thebiaca*), Angolan free-tailed bat (*Mops condylurus*), African pipistrelle (*Pipistrellus hesperidus*) and yellow house bat (*Scotophilus dinganii*) revealed important components of bugs (Order Hemiptera), higher than recorded in previous studies conducted in natural habitats. Future work will focus on a DNA bar-coding approach to probe the diet of bats. Gene sequences ("Bar-codes") have been obtained for 13 species of stinkbugs collected from the study area. A collaborative project between University of Venda and the Centre of GeoGenetics, Copenhagen (Denmark) will conduct Next Generation Sequencing of bat fecal pellets from day and night roosts in macadamia orchards to establish the detailed insect diet of bat species foraging in macadamia orchards and to determine the frequency of stinkbug prey in the diet of at least six species.

Characterization of Seasonal and Stress-related Immunity in Pteropodid Bats

Megan Vodzak and DeeAnn Reeder - Bucknell University, USA

Bats represent critical species: they are physiologically and ecologically unique and are recognized as significant reservoirs for zoonotic diseases. Yet, little is known about their immune responses and how they vary by sex, species, social processes, and environmental conditions. Maintaining a robust defense system at all times is energetically costly and the relative benefits versus costs of this protection vary with life-history state, seasonal shifts in resource availability, and disease risk. In order to better understand the seasonality of immunity, blood samples from male and female captive fruit bats (*Pteropus vampyrus*, *P. pumilus*, *P. hypomelanus*, and *Rousettus aegyptiacus* (males only)) were collected in March, June, September, and December. Additionally, a subset of male *P. vampyrus* and *R. aegyptiacus* were sampled 3 hours post-handling in December. Total antibody (IgG), cortisol,

corticosterone, testosterone (males only), and complement hemolytic ability were measured in plasma samples. Blood smears were analyzed for total and differential white blood cell counts. Data presented will characterize within and between Pteropodid species differences across seasons and in response to stress. Identifying how and why immune defense varies in this taxonomic group is fundamental to understanding infection dynamics, both within bat communities and between bats and other mammals.

Bat Conservation in Kenya: Challenges and Opportunities

Paul Webala - Karatina University College, Kenya

Public perception of Kenya's wildlife is dominated by charismatic megafauna (e.g. lions and elephants). However, bats hold equal or even greater overall importance by performing vital ecological services that benefit agriculture, forestry, and public health. Comprising of 108+ species and a major part of Kenya's biodiversity, bats play vital ecological roles, influencing forest regeneration through plant pollination and seed dispersal and indirectly affecting all other forest biota. Despite such Kenya's amazing species diversity and valuable ecosystem benefits, bats are severely threatened from the disturbance of crucial roosts, persecution and destruction or fragmentation of their roosting and foraging habitats. Many are known only from type specimens and from habitats that are deteriorating at alarming rates. To minimize or reverse threats facing bats and their habitats, address emerging bat conservation challenges and to demystify some negative beliefs, misinformation and myths about bats, Kenyan representatives at a recent African Bat Conservation Summit in Kenya agreed to establish an active Bat Conservation Network for Kenya, KenBAT, as an NGO to provide a platform for sharing and coordinating bat research and conservation activities in Kenya. Through KenBAT, priorities will be identified for bat conservation (including identifying important bat areas) in Kenya through measures such as mapping key bat roosting sites, identifying local Kenyan species "redlist" for their protection, and robust public outreach and environmental educational programmes. Current key research initiatives are highlighted.

How Malaria Gets Around: the Genetic Structure of a Parasite, Vector, and Host Compared

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Parasites with complex life cycles have two host species shaping their genetic structure, but the traditional view posits that the parasite's structure will be mainly determined by the most mobile host species. Malarial parasites are a prime example of parasites with a complex life cycle, needing both a dipteran and vertebrate host to complete their life cycle. In both hosts they impose selection pressures. Yet, how vertebrate and dipteran host populations shape the parasite's genetics has been little studied. The relative contribution of each host to the parasite's population structure has therefore never been satisfyingly determined. Being the most mobile host, we predict that the vertebrate host will show the most similarities with the structure of the malarial parasite. We compare the genetic structure of all three actors in a parasite-vector-host system: the vertebrate host, the long-fingered bat (*Miniopterus schreibersii*); the vector/dipteran host, the wingless bat fly *Nycteribia schmidlii*, and the malaria parasite *Polychromophilus melanipherus* using traditional microsatellite markers, cytbDNA sequencing and a SNP library obtained by ddRAD sequencing. We found relatively high structure in the bats. In contrast, the haplotype distribution of *P. melanipherus* shows little geographic differentiation. We investigate the role of the dipteran host in generating the observed patterns and conclude that the vertebrate host alone is not affecting the genetic structure of the haemosporidian parasite, but that it is probably the high dispersal rate of the vector that shapes the geographical structure of the parasite populations.

Published Books / Reports

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www.africanbats.org/Documents/ACR/2013/ACR_2013.pdf

GIS shapefile data associated with ACR 2013:

Download zipped Taxa file - www.africanbats.org/Documents/ACR/2013/ACR_2013_taxa.zip [3.6 Mb].

Download zipped country file - www.africanbats.org/Documents/ACR/2013/ACR_2013_country.zip [3.3 Mb].

Published papers

Abumandour, M. M. A. and R. M. A. El-Bakary. 2013. Morphological and scanning electron microscopic studies of the tongue of the Egyptian fruit bat (*Rousettus aegyptiacus*) and their lingual adaptation for its feeding habits. *Veterinary Research Communications* 37(3): 229–238. doi: [10.1007/s11259-013-9567-9](https://doi.org/10.1007/s11259-013-9567-9).

This study was carried out on the tongues of 12 adult normal healthy Egyptian fruit bats of both sexes. The tongue is protrusible, elongated flat with a rounded apex and its wide and thickness increase gradually toward the lingual root. There are four types of lingual papillae; two mechanical and two gustatory. The tongue divided into three parts (anterior, middle and posterior), each part subdivides into three regions; two lateral regions and median region, in addition to the lingual apex to the anterior region. The lingual papillae close to the median region of the tongue were posteriorly directed toward the pharynx, while these present on the lateral regions of the tongue are directed medioposteriorly. There are six subtypes of the filiform papillae; three on the anterior part (small, conical and giant), two on the middle part (cornflower and leaf-like papillae) while the posterior part contain rosette shape filiform papillae, in addition to transitional papillae and conical papillae. Two gustatory papillae represented by; small number of fungiform papillae which scattered among the filiform papillae on lingual apex and two lateral regions of the anterior and middle part of tongue, while the three circumvallate papillae on the posterior part were arranged in a triangle form.

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In 2012, an unprecedented number of four distinct, partially overlapping filovirus-associated viral hemorrhagic fever outbreaks were detected in equatorial Africa. Analysis of complete virus genome sequences confirmed the reemergence of Sudan virus and Marburg virus in Uganda, and the first emergence of Bundibugyo virus in the Democratic Republic of the Congo.

Amichai, E., E. Levin, N. Kronfeld-Schor, U. Roll, and Y. Yom-Tov. 2012 (for 2013). Natural history, physiology and energetic strategies of *Asellia tridens* (Chiroptera). *Mammalian Biology* 78(2): 94–103. doi: [10.1016/j.mambio.2012.06.006](https://doi.org/10.1016/j.mambio.2012.06.006).

We used radio-telemetry, observations and physiological measurements to study the basic biology and energetic strategies of *Asellia tridens* in northern Israel from 2009 to 2010. Between late May and early November, the bats occupied abandoned man-made structures in this area. Parturition occurred between late June and mid-July, and juveniles were independent by late August. *A. tridens* foraged near the roost in a vegetation-rich, cluttered background environment, catching insects flying close to vegetation. Its diet was diverse, with Coleoptera, Heteroptera, Diptera and Lepidoptera being the main diet components. During summer, males and females differed in their foraging patterns and energetic strategies: Lactating females departed for more frequent foraging bouts than males, and maintained euthermia throughout the day, while males became torpid on a daily basis.

Annan, A., H. J. Baldwin, V. M. Corman, S. M. Klose, M. Owusu, E. E. Nkrumah, E. K. Badu, P. Anti, O. Agbenyega, B. Meyer, S. Oppong, Y. A. Sarkodie, E. K. V. Kalko, P.H. C. Lina, E. V. Godlevska, C. Reusken, A. Seebens, F. Gloza-Rausch, P. Vallo, M. Tschapka, C. Drosten and J. F. Drexler. 2013. Human Betacoronavirus 2c EMS/2012-related Viruses in Bats, Ghana and Europe. *Emerging Health Threats Journal* 19(3): 456 – 459. doi: [10.3201/eid1903.121503](https://doi.org/10.3201/eid1903.121503).

We screened fecal specimens of 4,758 bats from Ghana and 272 bats from 4 European countries for betacoronaviruses. Viruses related to the novel human betacoronavirus EMC/2012 were detected in 46 (24.9%) of 185 *Nycteris* bats and 40 (14.7%) of 272 *Pipistrellus* bats. Their genetic relatedness indicated EMC/2012 originated from bats.

Baker, K. S., R. M. Leggett, N. H. Bexfield, M. Alston, G. Daly, S. Todd, M. Tachedjian, C. E.G. Holmes, S. Cramer, L-F Wang, J. L. Heeney, R. Suu-Ire, P. Kellam, A. A. Cunningham, J. L. N. Wood, M. Caccamo, and P.R. Murcia. 2013. Metagenomic study of the viruses of African straw-coloured fruit bats: Detection of a chiropteran poxvirus and isolation of a novel adenovirus. *Virology* 441 (2): 95–106. doi: [10.1016/j.virol.2013.03.014](https://doi.org/10.1016/j.virol.2013.03.014).

Viral emergence as a result of zoonotic transmission constitutes a continuous public health threat. Emerging viruses such as SARS coronavirus, hantaviruses and henipaviruses have wildlife reservoirs. Characterising the viruses of candidate reservoir species in geographical hot spots for viral emergence is a sensible approach to develop tools to predict, prevent, or contain emergence events. Here, we explore the viruses of *Eidolon helvum*, an Old World fruit bat species widely distributed in Africa that lives in close proximity to humans. We identified a great abundance and diversity of novel herpes and papillomaviruses, described the isolation of a novel adenovirus, and detected, for the first time, sequences of a chiropteran poxvirus closely related with *Molluscum contagiosum*. In sum, *E. helvum* display a wide variety of mammalian viruses, some of them genetically similar to known human pathogens, highlighting the possibility of zoonotic transmission.

Chawana, R., N. Patzke, C. Kaswera, E. Gilissen, A. O. Ihunwo, and P. R. Manger. 2013. Adult neurogenesis in eight Megachiropteran species. *Neuroscience* 244:159–72. doi: [10.1016/j.neuroscience.2013.04.020](https://doi.org/10.1016/j.neuroscience.2013.04.020).

The present study evaluated, using immunohistochemical methods, the presence and characteristics of proliferating and newly generated neurons in the brain of eight wild-caught adult Megachiropteran species. For the neurogenic patterns observed, direct homologies are evident in other mammalian species; however, there were several distinctions in the presence or absence of proliferating and immature neurons, and migratory streams that provide important clues regarding the use of the brain in the analysis of Chiropteran phylogenetic affinities. In all eight species studied, numerous Ki-67- and doublecortin (DCX)-immunopositive cells were identified in the subventricular zone (SVZ). These cells migrated to the olfactory bulb through a Primate-like rostral migratory stream (RMS) that is composed of dorsal and ventral substreams which merge before entering the olfactory bulb. Some cells were observed emerging from the RMS coursing caudally and dorsally to the rostral neocortex. In the dentate gyrus of all species, Ki-67- and DCX-expressing cells were observed in the granular cell layer and hilus. Similar to Primates, proliferating cells and immature neurons were identified in the SVZ of the temporal horn of Megachiropterans. These cells migrated to the rostral and caudal piriform cortex through a Primate-like temporal migratory stream. Sparsely distributed Ki-67-immunopositive, but DCX-immunonegative, cells were identified in the tectum, brainstem and cerebellum. The observations from this study add to a number of neural characteristics that phylogenetically align Megachiropterans to Primates.

Davies, K. T. J., P. J. J. Bates, I. Maryanto, J. A. Cotton, and S. J. Rossiter. 2013. The evolution of bat vestibular systems in the face of potential antagonistic selection pressures for flight and echolocation. *PloS one* 8(4): e61998. doi: [10.1371/journal.pone.0061998](https://doi.org/10.1371/journal.pone.0061998).

The vestibular system maintains the body's sense of balance and, therefore, was probably subject to strong selection during

evolutionary transitions in locomotion. Among mammals, bats possess unique traits that place unusual demands on their vestibular systems. First, bats are capable of powered flight, which in birds is associated with enlarged semicircular canals. Second, many bats have enlarged cochleae associated with echolocation, and both cochleae and semicircular canals share a space within the petrosal bone. To determine how bat vestibular systems have evolved in the face of these pressures, we used micro-CT scans to compare canal morphology across species with contrasting flight and echolocation capabilities. We found no increase in canal radius in bats associated with the acquisition of powered flight, but canal radius did correlate with body mass in bat species from the suborder Yangochiroptera, and also in non-echolocating Old World fruit bats from the suborder Yinpterochiroptera. No such trend was seen in members of the Yinpterochiroptera that use laryngeal echolocation, although canal radius was associated with wing-tip roundedness in this group. We also found that the vestibular system scaled with cochlea size, although the relationship differed in species that use constant frequency echolocation. Across all bats, the shape of the anterior and lateral canals was associated with large cochlea size and small body size respectively, suggesting differential spatial constraints on each canal depending on its orientation within the skull. Thus in many echolocating bats, it seems that the combination of small body size and enlarged cochlea together act as a principal force on the vestibular system. The two main groups of echolocating bats displayed different canal morphologies, in terms of size and shape in relation to body mass and cochlear size, thus suggesting independent evolutionary pathways and offering tentative support for multiple acquisitions of echolocation.

Dool, S.E., S. J. Puechmaille, C. Dietz, J. Juste, C. Ibáñez, P. Hulva, S. G. Roué, E. J. Petit, G. Jones, D. Russo, R. Toffoli, A. Viglino, A. Martinoli, S. J. Rossiter and E. C. Teeling. 2013. Phylogeography and postglacial recolonization of Europe by *Rhinolophus hipposideros*: evidence from multiple genetic markers. *Molecular Ecology* 22(15): 4055–4070. doi: [10.1111/mec.12373](https://doi.org/10.1111/mec.12373).

The demographic history of *Rhinolophus hipposideros* (lesser horseshoe bat) was reconstructed across its European, North African and Middle-Eastern distribution prior to, during and following the most recent glaciations by generating and analysing a multimarker data set. This data set consisted of an X-linked nuclear intron (Bgn; 543 bp), mitochondrial DNA (cytb-tRNA-control region; 1630 bp) and eight variable microsatellite loci for up to 373 individuals from 86 localities. Using this data set of diverse markers, it was possible to determine the species' demography at three temporal stages. Nuclear intron data revealed early colonization into Europe from the east, which pre-dates the Quaternary glaciations. The mtDNA data supported multiple glacial refugia across the Mediterranean, the largest of which were found in the Ibero-Maghreb region and an eastern location (Anatolia/Middle East)-that were used by *R. hipposideros* during the most recent glacial cycles. Finally, microsatellites provided the most recent information on these species' movements since the Last Glacial Maximum and suggested that lineages that had diverged into glacial refugia, such as in the Ibero-Maghreb region, have remained isolated. These findings should be used to inform future conservation management strategies for *R. hipposideros* and show the power of using a multimarker data set for phylogeographic studies.

Drexler, J.F., V. M. Corman, M. A. Müller, A. N. Lukashev, A. Gmyl, B. Coutard, A. Adam, D. Ritz, L. M. Leijten, D. van Riel, R. Kallies, S. M. Klose, F. Gloza-Rausch, T. Binger, A. Annan, Y. Adu-Sarkodie, S. Oppong, M. Bourgarel, D. Rupp, B. Hoffmann, M. Schlegel, B. M. Kümmerer, D. H. Krüger, J. Schmidt-Chanasit, A. A. Setién, V. M. Cottontail, T. Hemachudha, S. Wacharapluesadee, K. Osterrieder, R. Bartenschlager, S. Mathee, M. Beer, T. Kuiken, C. Reusken, E. M. Leroy, R. G. Ulrich and C. Drosten. 2013. Evidence for novel hepaciviruses in rodents. *PLoS pathogens* 9(6): e1003438. doi: [10.1371/journal.ppat.1003438](https://doi.org/10.1371/journal.ppat.1003438).

Hepatitis C virus (HCV) is among the most relevant causes of liver cirrhosis and hepatocellular carcinoma. Research is complicated by a lack of accessible small animal models. The systematic investigation of viruses of small mammals could guide efforts to establish such models, while providing insight into viral evolutionary biology. We have assembled the so-far largest collection of small-mammal samples from around the world, qualified to be screened for bloodborne viruses, including sera and organs from 4,770 rodents (41 species); and sera from 2,939 bats (51 species). Three highly divergent rodent hepacivirus clades were detected in 27 (1.8%) of 1,465 European bank voles (*Myodes glareolus*) and 10 (1.9%) of 518 South African four-striped mice (*Rhabdomys pumilio*). Bats showed anti-HCV immunoblot reactivities but no virus detection, although the genetic relatedness suggested by the serologic results should have enabled RNA detection using the broadly reactive PCR assays developed for this study. 210 horses and 858 cats and dogs were tested, yielding further horse-associated hepaciviruses but none in dogs or cats. The rodent viruses were equidistant to HCV, exceeding by far the diversity of HCV and the canine/equine hepaciviruses taken together. Five full genomes were sequenced, representing all viral lineages. Salient genome features and distance criteria supported classification of all viruses as hepaciviruses. Quantitative RT-PCR, RNA in-situ hybridisation, and histopathology suggested hepatic tropism with liver inflammation resembling hepatitis C. Recombinant serology for two distinct hepacivirus lineages in 97 bank voles identified seroprevalence rates of 8.3 and 12.4%, respectively. Antibodies in bank vole sera neither cross-reacted with HCV, nor the heterologous bank vole hepacivirus. Co-occurrence of RNA and antibodies was found in 3 of 57 PCR-positive bank vole sera (5.3%). Our data enable new hypotheses regarding HCV evolution and encourage efforts to develop rodent surrogate models for HCV.

García-Pérez, R., M. Gottschling, G. Wibbelt and I. G. Bravo. 2013. Multiple evolutionary origins of bat papillomaviruses. *Veterinary Microbiology* 165(1-2): 51–60. doi: [10.1016/j.vetmic.2013.01.009](https://doi.org/10.1016/j.vetmic.2013.01.009).

Infection by papillomaviruses (PVs) has been linked to different types of neoplasias, in both human and non-human hosts. Knowledge about PV diversity is essential to reliably infer the evolutionary history of these pathogens and to elucidate the link between infection and disease. We cloned and sequenced the complete genome of a novel PV, EhelPV1, isolated from hair bulbs from a captive straw-colored fruit bat *Eidolon helvum* (Pteropodidae, Chiroptera). We also retrieved partial sequences of the E1 and L1 genes from hair bulbs from a captive Indian flying fox *Pteropus giganteus* (Pteropodidae, Chiroptera). The detected virus (PgigPV1) presumably corresponded to a novel type as well. Maximum likelihood phylogenetic analyses were conducted using a representative collection of 132 PVs. EhelPV1 belonged to the Lambda+Mu-PV crown group and was most closely related to another bat PV, MschPV2. Both fragments of PgigPV1 were placed alongside with EhelPV1. The novel PVs were phylogenetically distant from other previously

described bat PVs, namely MrPV1, MschPV1 and RaPV1. We have further characterized the sequence patterns of the E2-binding sites occurring in the upstream regulatory region of Lambda+Mu-PVs. Common fingerprints within this region are shared by certain PVs. However, there is not a sharp correspondence between the repertoire of transcription factor binding sites in the viral regulatory region and host range, tissue tropism or viral life style. Our results reinforce the hypothesis that PVs have undergone an initial radiation prior to the divergence of the mammalian hosts, giving rise to the present-day PV crown groups.

Geldenhuys, M., J. Weyer, L. H. Nel and W. Markotter. 2013. Coronaviruses in South African bats. *Vector-Borne and Zoonotic Diseases* 13(7): 516–519. doi: [10.1089/vbz.2012.1101](https://doi.org/10.1089/vbz.2012.1101).

Recent studies in several African countries have provided the first evidence for the presence of coronaviruses in African bats. Here we describe, for the first time, the detection of RNA of 3 unique coronavirus species in the tissues of South African bats.

Hoffmann, M., M. A. Müller, J. F. Drexler, J. Glende, M. Erdt, T. Gützkow, C. Losemann, T. Binger, H. Deng, C. Schwegmann-Weßels, K.-H. Esser, C. Drosten and G. Herrler. 2013. Differential sensitivity of bat cells to infection by enveloped RNA viruses: coronaviruses, paramyxoviruses, filoviruses, and influenza viruses. *PLoS one* 8(8): e72942. doi: [10.1371/journal.pone.0072942](https://doi.org/10.1371/journal.pone.0072942).

Bats (Chiroptera) host major human pathogenic viruses including corona-, paramyxo, rhabdo- and filoviruses. We analyzed six different cell lines from either Yinpterochiroptera (including African flying foxes and a rhinolophid bat) or Yangochiroptera (genera *Carollia* and *Tadarida*) for susceptibility to infection by different enveloped RNA viruses. None of the cells were sensitive to infection by transmissible gastroenteritis virus (TGEV), a porcine coronavirus, or to infection mediated by the Spike (S) protein of SARS-coronavirus (SARS-CoV) incorporated into pseudotypes based on vesicular stomatitis virus (VSV). The resistance to infection was overcome if cells were transfected to express the respective cellular receptor, porcine aminopeptidase N for TGEV or angiotensin-converting enzyme 2 for SARS-CoV. VSV pseudotypes containing the S proteins of two bat SARS-related CoV (Bg08 and Rp3) were unable to infect any of the six tested bat cell lines. By contrast, viral pseudotypes containing the surface protein GP of Marburg virus from the family Filoviridae infected all six cell lines though at different efficiency. Notably, all cells were sensitive to infection by two paramyxoviruses (Sendai virus and bovine respiratory syncytial virus) and three influenza viruses from different subtypes. These results indicate that bat cells are more resistant to infection by coronaviruses than to infection by paramyxoviruses, filoviruses and influenza viruses. Furthermore, these results show a receptor-dependent restriction of the infection of bat cells by CoV. The implications for the isolation of coronaviruses from bats are discussed.

Juste, J., P. Benda, J. L. Garcia-Mudarra and C. Ibáñez. 2013. Phylogeny and systematics of Old World serotine bats (genus *Eptesicus*, Vespertilionidae, Chiroptera): an integrative approach. *Zoologica Scripta* 42(5): 441–457. doi: [10.1111/zsc.12020](https://doi.org/10.1111/zsc.12020).

Integrative taxonomy aims to document biodiversity by incorporating all useful characters to increase confidence in hypotheses about phylogenetic relationships. In this study, we combine data obtained independently from morphology, two maternally inherited mtDNA genes and two biparentally inherited nuDNA genes to make phylogenetic and taxonomic hypotheses about the Palaearctic members of the bat genus *Eptesicus* (Vespertilionidae). This genus is distributed worldwide (except for Antarctica) and is highly diversified, presenting one of the most entangled taxonomic puzzles among all mammals. Our results support restoring the genus *Rhyneptesicus* and separating *E. isabellinus* and *E. pachyomus* from *E. serotinus* and *E. ognevi* and *E. anatolicus* from *E. bottae*. Differences in the phylogenetic hypotheses from mtDNA and nuDNA data suggest the occurrence within *E. serotinus* of evolutionary processes such as mtDNA capture and secondary contacts between partially differentiated ecomorphs. These two evolutionary processes deserve more in-depth studies within the group.

Kgaladi, J., L. H. Nel and W. Markotter. 2010. Comparison of pathogenic domains of rabies and African rabies-related lyssaviruses and pathogenicity observed in mice. *Onderstepoort Journal of Veterinary Research*, 80(1, Art. #511): 1-13. doi: [10.4102/ojvr.v80i1.511](https://doi.org/10.4102/ojvr.v80i1.511).

Several lyssavirus species occur in Africa (Rabies virus, Lagos bat virus, Mokola virus, Duvenhage virus, Shimoni bat virus and Ikoma lyssavirus), displaying a high sequence diversity between isolates belonging to the same species. There is limited information about comparative pathogenesis of these African lyssaviruses and this precludes authoritative opinion on the potential public and veterinary health impact. In this study, an analysis of representative African lyssaviruses attempted to correlate viral genomic sequence similarities and differences with the corresponding pathogenic profiles observed in mice. The study demonstrated that the virus isolates evaluated could be lethal to mice when introduced intramuscularly and that different isolates of the same lyssavirus species differ in their virulence. Using real-time polymerase chain reaction (PCR), viral RNA was detected in brain tissue, but no viral RNA was detected in the salivary glands or blood of mice that succumbed to infection. Comparison of known pathogenic domains indicated that pathogenicity is likely to be dependent on multiple domains. Cumulatively, our results re-emphasised the realisation that the pathogenicity of a lyssavirus species cannot be deduced based on studies of only a single isolate of the species or a single pathogenic domain.

Koubínová, D., N. Irwin, P. Hulva, P. Koubek, and J. Zima. 2013. Hidden diversity in Senegalese bats and associated findings in the systematics of the family Vespertilionidae. *Frontiers in Zoology* 10(1): 1–48. doi: [10.1186/1742-9994-10-48](https://doi.org/10.1186/1742-9994-10-48).

INTRODUCTION: The Vespertilionidae is the largest family of bats, characterized by high occurrence of morphologically convergent groups, which impedes the study of their evolutionary history. The situation is even more complicated in the tropics, where certain regions remain under-sampled.

RESULTS: Two hundred and thirteen vespertilionid bats from Senegal (West Africa) were studied with the use of non-differentially

stained karyotypes and multi-locus sequence data analysed with maximum likelihood and Bayesian methods. These bats were identified as 10 different taxa, five of which were distinctive from their nominate species (*Pipistrellus hesperidus*, *Nycticeinops schlieffenii*, *Scotoecus hirundo*, *Neoromicia nana* and *N. somalica*), based on both karyotypes and molecular data. These five cryptic taxa are unrelated, suggesting that these West African populations have long been isolated from other African regions. Additionally, we phylogenetically analysed 166 vespertilionid taxa from localities worldwide using GenBank data (some 80% of the genera of the family) and 14 representatives of closely related groups, together with our Senegalese specimens. The systematic position of several taxa differed from previous studies and the tribes Pipistrellini and Vespertilionini were redefined. The African *Pipistrellus rueppellii* was basal to the *Pipistrellus/Nyctalus* clade and the Oriental species *Glischropus tylopus* was basal to the East Asian pipistrelles within the tribe Pipistrellini. The African genus *Neoromicia* was confirmed to be diphyletic. Based on GenBank data, *Eptesicus* was polyphyletic, with the Asian *E. nasutus* and *E. dimissus* both supported as phylogenetically distinct from the *Eptesicus* clade. The subfamily Scotophilinae was confirmed as one of the basal branches of Vespertilionidae.

CONCLUSIONS: New taxa and new systematic arrangements show that there is still much to resolve in the vespertilionids and that West Africa is a biogeographic hotspot with more diversity to be discovered.

Lima, L., O. Espinosa-Álvarez, P. B. Hamilton, L. Neves, C. S. A. Takata, M. Campaner, M. Attias, W. de Souza, E. P. Camargo and M. M. G. Teixeira. 2013. *Trypanosoma livingstonei*: a new species from African bats supports the bat seeding hypothesis for the *Trypanosoma cruzi* clade. *Parasites & Vectors* 6(221): 1–17. doi: [10.1186/1756-3305-6-221](https://doi.org/10.1186/1756-3305-6-221).

BACKGROUND: Bat trypanosomes have been implicated in the evolutionary history of the *T. cruzi* clade, which comprises species from a wide geographic and host range in South America, Africa and Europe, including bat-restricted species and the generalist agents of human American trypanosomiasis *T. cruzi* and *T. rangeli*.

METHODS: Trypanosomes from bats (*Rhinolophus landeri* and *Hipposideros caffer*) captured in Mozambique, southeast Africa, were isolated by hemoculture. Barcoding was carried out through the V7V8 region of Small Subunit (SSU) rRNA and Fluorescent Fragment Length barcoding (FFLB). Phylogenetic inferences were based on SSU rRNA, glyceraldehyde phosphate dehydrogenase (gGAPDH) and Spliced Leader (SL) genes. Morphological characterization included light, scanning and transmission electron microscopy.

RESULTS: New trypanosomes from bats clustered together forming a clade basal to a larger assemblage called the *T. cruzi* clade. Barcoding, phylogenetic analyses and genetic distances based on SSU rRNA and gGAPDH supported these trypanosomes as a new species, which we named *Trypanosoma livingstonei* n. sp. The large and highly polymorphic SL gene repeats of this species showed a copy of the 5S ribosomal RNA into the intergenic region. Unique morphological (large and broad blood trypomastigotes compatible to species of the subgenus *Megatrypanum* and cultures showing highly pleomorphic epimastigotes and long and slender trypomastigotes) and ultrastructural (cytostome and reservosomes) features and growth behaviour (when co-cultivated with HeLa cells at 37°C differentiated into trypomastigotes resembling the blood forms and do not invaded the cells) complemented the description of this species.

CONCLUSION: Phylogenetic inferences supported the hypothesis that *Trypanosoma livingstonei* n. sp. diverged from a common ancestral bat trypanosome that evolved exclusively in Chiroptera or switched at independent opportunities to mammals of several orders forming the clade *T. cruzi*, hence, providing further support for the bat seeding hypothesis to explain the origin of *T. cruzi* and *T. rangeli*.

Liu, Y., W. Metzner and J. Feng. 2013. Vocalization during copulation behavior in greater horseshoe bats, *Rhinolophus ferrumequinum*. *Chinese Science Bulletin* 58(18): 2179–2184. doi: [10.1007/s11434-013-5793-3](https://doi.org/10.1007/s11434-013-5793-3).

Vocal communication plays an important role for individual recognition and male-female interaction during mating in greater horseshoe bats, especially in respect to mate fidelity, which ensures that the bats can maintain a stable social organization. Few studies, however, have addressed the calling behavior during copulating in bats. Here, we initially report the copulation vocalizations and behaviors of both male and female greater horseshoe bats. During copulation, the male assumed a dorsal position and arched his back, arming around the female using his feet and thumbs. The male repeatedly produced very short constant frequency (SCF) syllables with high intensity and repetition rate (male 1: 16.48±4.8 ms, male 2: 17.79±4.03 ms) when he tried to insert the penis into the female, and then long syllables (male 1: 42.08±12.67 ms, male 2: 43.02±11.44 ms) after penile insertion. The female bats sometime refused the male bats in the early phase of copulations as emitting noise bursts and broad-band vocalizations, but kept silence during actual copulation. We also found that the SCF copulation calls of one male remained stable peak frequencies on different copulation days although its echolocation call frequency varied each day. Moreover, different male individuals maintained their own “private frequency” in the SCF copulation calls. Therefore, we predicted that the SCF copulation calls may serve as an indicator for female greater horseshoe bats to recognize the mating males in order to maintain mate fidelity because horseshoe bats exhibit sexual segregation before mating. Our results stipulate further studies on mating system and copulation strategies in polygynous bats. Such work may also aid in promoting the preservation of greater horseshoe bats.

Lučan, R. K., and M. Šálek. 2013. Observation of successful mobbing of an insectivorous bat, *Taphozous nudiventris* (Emballonuridae), on an avian predator, *Tyto alba* (Tytonidae). *Mammalia* 77(2): 235–236. doi: [10.1515/mammalia-2012-0067](https://doi.org/10.1515/mammalia-2012-0067).

Mobbing in animals is an aggressive behaviour performed cooperatively towards a potential predator. In bats, the existence of mobbing is based on both intra- and interspecific behavioural responses of freely flying individuals to distress calls emitted by live bats or playbaked by researchers. In this note, we describe the mobbing behaviour of free-living naked-bellied tomb bats *Taphozous nudiventris* on the barn owl *Tyto alba* as the first direct observation of mobbing by a bat on its potential avian predator.

Miková, E., K. Varcholová, S. Boldogh and M. Uhrin. 2013. Winter diet analysis in *Rhinolophus euryale* (Chiroptera). *Central European Journal of Biology* 8(9): 848–853. doi: [10.2478/s11535-013-0199-9](https://doi.org/10.2478/s11535-013-0199-9).

We investigated the winter food of Mediterranean horseshoe bats (*Rhinolophus euryale*) in four winter cave roosts in southern Slovakia and northern Hungary and investigated the relationship between food and ambient temperature. The bats were active during the whole winter period and they produced excrement throughout the entire hibernation period, even when outside temperatures dropped below zero. The guano was in two forms, containing (1) prey items and (2) non-prey items. The identifiable items belonged to lepidopteran species, but only one was identified, on the basis of the genital fragments, the moth *Colotois pennaria*, which was the main prey species in autumn and early winter. Our results shed light on the extraordinarily high level of activity in this bat species during winter hibernation, which in temperate regions is a strategy that enables bats to survive when prey is reduced or absent. In *R. euryale*, the torpor in the course of hibernation is not continuous and our results help to explain how energy losses caused by bat movements are covered.

Naidoo, T., M. C. Schoeman, P. J. Taylor, S. M. Goodman and J. M. Lamb. 2013a. Stable Pleistocene-era populations of *Chaerephon pumilus* (Chiroptera: Molossidae) in southeastern Africa do not use different echolocation calls. *African Zoology* 48(1): 125–142. doi: [10.3377/004.048.0112](https://doi.org/10.3377/004.048.0112).

Our extension of the phylogenetic study of Taylor *et al.* (2009) on a larger, more geographically representative sample confirmed their finding of genetically distinct sympatric lineages of bats currently referred to as *Chaerephon pumilus sensu lato* (*s.l.*) (family Molossidae) in south-eastern Africa. *Chaerephon pumilus s.l.* comprised two cytochrome *b* lineages separated by a mean genetic distance of 0.7% (0.1–1.4%), consistent with intraspecific variability. The *C. pumilus s.l.* clade was paraphyletic, containing a nested *C. leucogaster* (Madagascar) clade. As well as the expected four mitochondrial control region lineages, we identified a new strongly-supported clade from the Durban area. Indices of diversity and neutrality, combined with a ragged multimodal mismatch distribution, are inconsistent with demographic expansion of a single *C. pumilus s.l.* population in southeastern Africa, and suggest that the control region lineages are stable units at demographic equilibrium. Dating analyses suggest that these lineages were established during the late Pleistocene, between 60 000 and 13 000 years ago. We found no evidence to support our hypothesis that the sympatric genetic lineages of *C. pumilus s.l.* are associated with distinct sonotypes, as discriminant function analysis based on four echolocation parameters could not discriminate between the four clades. We hypothesise that the different genetic lineages may be distinguished by differences in social communication and behaviour.

Naidoo, S., D. Vosloo and M. C. Schoeman. 2013b. Foraging at wastewater treatment works increases the potential for metal accumulation in an urban adapter, the banana bat (*Neoromicia nana*). *African Zoology* 48(1): 39–55. doi: [10.3377/004.048.0111](https://doi.org/10.3377/004.048.0111).

Wastewater treatment works (WWTWs) are known to provide profitable foraging areas for insectivorous bats in Europe and the New World because of their association with high abundance of pollution-tolerant midges (Diptera). However, bats that feed on these insects may also accumulate metal pollutants such as cadmium and copper in their tissues, with acute or chronic effects on their health. Using a time expansion bat detector, the activity (number of passes and feeding buzzes) of *Neoromicia nana* (family Vespertilionidae) was quantified at three WWTW points – upstream, the point of wastewater effluent discharge, and downstream – along three urban rivers in South Africa. In addition, metal concentrations in the kidney, liver and muscle tissue of *N. nana* caught at the sites were quantified. The diversity of aerial insects, sampled over the same period as the bat surveys, was measured using a black light trap and sweep-netting. Relative abundance and feeding activity of *N. nana* were higher at wastewater-polluted sites than at upstream sites. The most abundant insect order at wastewater-polluted sites and in the diet of resident bats was Diptera. Essential metals (copper, zinc and iron) were detected in all *N. nana* tissue samples, but the toxic metals cadmium, chromium and nickel were mostly present in tissue of bats at wastewater-polluted sites. Thus, although WWTWs provide an optimal food resource to bats in the short-term, it may pose serious long-term health risks for these top predators.

Nakamura, S., S. Settai, H. Hayashidani, T. Urabe, S. Namai, and Y. Une. 2012 (for 2013). Outbreak of Yersiniosis in Egyptian Rousette Bats (*Rousettus aegyptiacus*) Caused by *Yersinia pseudotuberculosis* Serotype 4b. *Journal of Comparative Pathology* 148(4): 410–413. doi: [10.1016/j.jcpa.2012.07.007](https://doi.org/10.1016/j.jcpa.2012.07.007).

This report describes an outbreak of yersiniosis in Egyptian rousette bats (*Rousettus aegyptiacus*) caused by *Yersinia pseudotuberculosis* serotype 4b. Twelve of 61 bats died between November and December 2008 or in May 2009. The bats often displayed multiple yellow-white nodules in the spleen and liver. Microscopically, these consisted of focal necrosis accompanied by inflammatory cell infiltration and colonies of gram-negative bacilli. The bacterial colonies were identified immunohistochemically as *Y. pseudotuberculosis* O4 and *Y. pseudotuberculosis* serotype 4b was identified by bacteriological examination. Polymerase chain reaction demonstrated that the isolate harboured the virulence genes *virF*, *inv* and *ypmA*. YPMa is as a superantigenic toxin that is associated with acute systemic infection in man and may contribute to the virulence of *Y. pseudotuberculosis* in bats.

Quan, P.-L., C. Firth, J. M. Conte, S. H. Williams, C. M. Zambrana-Torrel, S. J. Anthony, J. A. Ellison, A. T. Gilbert, I. V. Kuzmin, M. Niezgoda, M. O. V. Osinubi, S. Recuenco, W. Markotter, R. F. Breiman, L. Kalemba, J. Malekani; K. A. Lindblade, M. K. Rostal, R. Ojeda-Flores, G. Suzan, L. B. Davis, D. M. Blau, A. B. Ogunkoya, D. A. Alvarez Castillo, D. Moran, S. Ngam, D. Akaike, B. Agwanda, T. Briese, J. H. Epstein, P. Daszak, C. E. Rupprecht, E. C. Holmes, and W. I. Lipkin. 2013. Bats are a major natural reservoir for hepaciviruses and pegiviruses. *PNAS* 110(20): 8194 – 8199. doi: [10.1073/pnas.1303037110](https://doi.org/10.1073/pnas.1303037110).

Although there are over 1,150 bat species worldwide, the diversity of viruses harbored by bats has only recently come into focus as a result of expanded wildlife surveillance. Such surveys are of importance in determining the potential for novel viruses to emerge in humans, and for optimal management of bats and their habitats. To enhance our knowledge of the viral diversity present in bats, we

initially surveyed 415 sera from African and Central American bats. Unbiased high-throughput sequencing revealed the presence of a highly diverse group of bat-derived viruses related to hepaciviruses and pegiviruses within the family Flaviviridae. Subsequent PCR screening of 1,258 bat specimens collected worldwide indicated the presence of these viruses also in North America and Asia. A total of 83 bat-derived viruses were identified, representing an infection rate of nearly 5%. Evolutionary analyses revealed that all known hepaciviruses and pegiviruses, including those previously documented in humans and other primates, fall within the phylogenetic diversity of the bat-derived viruses described here. The prevalence, unprecedented viral biodiversity, phylogenetic divergence, and worldwide distribution of the bat-derived viruses suggest that bats are a major and ancient natural reservoir for both hepaciviruses and pegiviruses and provide insights into the evolutionary history of hepatitis C virus and the human GB viruses.

Rainho, A. and J. M. Palmeirim. 2013. Prioritizing conservation areas around multispecies bat colonies using spatial modeling. *Animal Conservation* 16(4): 438–448. <http://doi.wiley.com/10.1111/acv.12013>.

Bats and other vertebrates form large colonies concentrating key populations of multiple endangered species. Their foraging ranges are of critical importance for the colony but can be too vast to preserve in full extent. We evaluated an approach to prioritize areas within this range that conciliates the distinct needs of various species. Our model colony was a large cave-bat nursery harboring *Rhinolophus mehelyi*, *Myotis myotis* and *Miniopterus schreibersii* located in Southern Portugal. With radio-tracking data of foraging bats and spatially explicit modeling, we generated habitat suitability maps for each species. Models incorporated both habitat variables and distance to the roost. The resulting maps were then used separately or in combinations to identify the areas with greatest multispecies conservation value. The best results were obtained by combining individual suitabilities in a single value, weighting each species by its threat risk. Although the overall range of the colony was very extensive, this approach identified the areas that had most multispecies value; more than half of the foraging sites are included in the best 13% of the range, and adding the next best 12% includes almost all sites of the most threatened study species, *R. mehelyi*. The efficiency of the prioritization can be evaluated not only for the species ensemble, but also for individual species. The concentration of most multispecies conservation value in a small area is partly due to the importance of distance to roost as a determinant of foraging habitat selection in all species, so this factor is essential in suitability models used for prioritization. This prioritization process successfully minimizes the amount of land required for protection, while maximizing the quality of the habitat to protect. Such prioritizations should spur the preservation of foraging areas of large multispecies colonies, thus improving the chances of survival of populations of great conservation value.

Reiter, G., E. Pölzer, H. Mixanig, F. Bontadina and U. Hüttmeir. 2013. Impact of landscape fragmentation on a specialised woodland bat, *Rhinolophus hipposideros*. *Mammalian Biology - Zeitschrift für Säugetierkunde* 78(4): 283–289. doi: [10.1016/j.mambio.2012.11.003](http://dx.doi.org/10.1016/j.mambio.2012.11.003).

For habitat specialists, fragmentation has major consequences as it means less suitable habitat for the species to live in. In a fragmented landscape, we would expect larger, but spatially more clustered, foraging ranges. We studied the impact of landscape fragmentation on the foraging range and habitat exploitation of a specialised forest bat by radiotracking 16 female lesser horseshoe bats *Rhinolophus hipposideros* in a landscape with connected woodland structures and in a highly fragmented landscape in Carinthia, Austria. Contrary to our expectations, spatial foraging behaviour was not influenced by fragmentation. No differences in the behaviour of the bats between the sites were evident for the foraging ranges (minimum convex polygon, MCP), the core foraging areas (50% kernel), nor the mean or the maximum distances from the roost. However, in the highly fragmented landscape, the foraging activity of individuals was spatially more clustered and the overall MCP of all bats of a colony was greater compared to the less fragmented landscape. Woodland was the most important foraging habitat for the lesser horseshoe bats at both study sites. Habitat selection at the individual MCPs was evident only at the site with low fragmentation. However, in the core foraging areas, woodland was significantly selected over all other habitat types at both study sites. We conclude that (1) conservation measures for colonies of lesser horseshoe bats should be undertaken within 2.5 km of the nursery roost, (2) woodland is the key foraging habitat particularly in the vicinity of the roost, and (3) any loss of woodland near the colonial roosts are likely to negatively influence the colony, since these bats do not seem to be able to adapt their spatial foraging behaviour in a degraded landscape. The inflexible spatial behaviour of this specialised bat highlights the need to compensate for any habitat loss within the foraging range of a bat colony.

Ruedi, M., B. Stadelmann, Y. Gager, E. J. P. Douzery, C. M. Francis, L. Lin, A. Guillén-Servent and A. Cibois. 2013. Molecular phylogenetic reconstructions identify East Asia as the cradle for the evolution of the cosmopolitan genus *Myotis* (Mammalia, Chiroptera). *Molecular Phylogenetics and Evolution* 69: 437–449. doi: [10.1016/j.ympev.2013.08.011](http://dx.doi.org/10.1016/j.ympev.2013.08.011).

Sequences of the mitochondrial cytochrome *b* (1140 bp) and nuclear Rag 2 (1148 bp) genes were used to assess the evolutionary history of the cosmopolitan bat genus *Myotis*, based on a worldwide sampling of over 88 named species plus 7 species with uncertain nomenclature. Phylogenetic reconstructions of this comprehensive taxon sampling show that most radiation of species occurred independently within each biogeographic region. Our molecular study supports an early divergence of species from the New World, where all Nearctic and Neotropical species plus a lineage from the Palaeartic constitute a monophyletic clade, sister to the remaining Old World taxa. The major Old World clade includes all remaining Eurasian taxa, most Oriental species, one Oceanian, and all Ethiopian species. Another lineage, including *M. latirostris* from Taiwan, appears at the base of these two major biogeographic clades and, because it bears nyctalodont molars, could be considered as a distinct genus. However, this molar configuration is also found in crown-group species, indicating that these dental characters are variable in the genus *Myotis* and may confound interpretation of the fossil record. Molecular datings suggest an origin of all recent *Myotis* in the early Miocene (about 21 MYA with 95% highest posterior density interval 23–20 MYA). This period was characterized by a global climatic cooling that reduced the availability of tropical habitats and favoured the development of more temperate vegetation. This sharp climatic change might have triggered the evolution of *Myotis* in the Northern continents, because *Myotis* ancestors seem to have been well adapted and successful in such temperate habitats. Ancestral area reconstructions based on the molecular phylogeny suggest that the eastern portion of the Asian continent was an important center of origin for the early diversification of all *Myotis* lineages, and involved

relatively few subsequent transcontinental range expansions.

Seltzer, C.E., H. J. Ndangalasi and N. J. Cordeiro. 2013. Seed Dispersal in the Dark: Shedding Light on the Role of Fruit Bats in Africa. *Biotropica* 45(4): 450–456. doi: [10.1111/btp.12029](https://doi.org/10.1111/btp.12029).

In spite of their recognized importance as seed dispersers in other parts of the tropics, seed dispersal by fruit bats has received scant research attention in Africa. To evaluate the role of African fruit bats in seed dispersal, we studied fruits and seeds below 480 bat feeding roosts in the East Usambara Mountains of Tanzania. We compared these findings to those reported in other African localities to place our results in a broader context. We found 49 plant species dispersed by bats: 28 species, 18 genera, and one family are novel reports of bat dispersal in Africa. Approximately 20 percent of the submontane tree flora of the East Usambaras is bat-dispersed, including both widespread and endemic trees. African fruit bats are important seed dispersers at our study site because they move seeds of dozens of species tens or hundreds of meters, even seeds that are too large to ingest (greater than 5 mm in length). Fruit bats are likely important seed dispersers in other Afrotropical forests, as bats elsewhere in Africa are known to consume 20 genera and 16 species of plants reported here. Insights from studying remains under bat feeding roosts offer a simple method to further document and substantially increase our understanding of the role of African fruit bats in seed dispersal.

Sharifi, M. and S. Vaissi. 2013. Postnatal growth in the Long-fingered Bat, *Miniopterus schreibersii pallidus*, in Iran (Chiroptera: Miniopteridae). *Zoology in the Middle East* 59(1): 1–5. doi: [10.1080/09397140.2013.795053](https://doi.org/10.1080/09397140.2013.795053).

This study describes the postnatal development of body mass, forearm length and epiphyseal phalangeal gap in a free ranging population of the Long-fingered Bat, *Miniopterus schreibersii pallidus* Thomas, 1907, in a maternity roost in the Mahidasht cave in western Iran. The pups at birth had a mean body mass of 3.74 ± 0.09 g and forearm length of 24.3 ± 0.31 mm. The length of forearm and body mass increased linearly during first two weeks, and thereafter maintained an apparent stability. The epiphyseal gap of the fourth metacarpal phalangeal joint increased until the thirteenth day, then decreased linearly until the 70th day and thereafter fused. The rate of body mass gain and forearm growth during the first 13 days was 0.54 g/day and 1.39 mm/day, respectively. Initiation of flight occurred three weeks after birth. A method of estimating age was derived from the values of the forearm length and the total gap of the fourth metacarpal-phalangeal joint during the pre-flight and post-flight periods.

Sharifi, M., S. Vaissi, H. Javanbakht and V. Akmal. 2012. Postnatal Growth and Wing Development in Kuhl's Pipistrelle *Pipistrellus kuhlii* (Chiroptera: Vespertilionidae) in captivity. *Zoological Studies* 51(8): 1235–1247. <http://zoolstud.sinica.edu.tw/Journals/51.8/1235.pdf>

Postnatal growth of the body mass, forearm, and epiphyseal phalangeal gap, and changes in wing morphology including the wingspan, wing area, handwing length, handwing area, armwing length, armwing area, aspect ratio, and wing loading were studied in 12 Kuhl's pipistrelles, *Pipistrellus kuhlii*, which were born and reared in a flight cage. The pups at birth had a mean \pm S.E. of 1.04 ± 0.08 g of body mass and forearm length of 11.48 ± 0.45 mm. At 60 d, the mean body mass had reached 87.56% of the adult postpartum mass (5.47 ± 0.07 g), and the mean forearm length was 89.46% of the adult length (35.97 ± 0.86 mm). Rates of body mass gain and forearm growth during the 1st 23 d were 0.10 ± 0.10 g/d and 0.64 ± 0.61 mm/d, respectively. The wingspan and wing area increased linearly until 33 d of age, at which time, young bats exhibited clumsy flight with gentle turns. Analysis of changes occurring in the wing morphology indicated that 7 wing characteristics exhibited rapid growth rates in the “pre-flight” period and secondary slower growth rates in the “post-flight” period. Wingspan, handwing length and area, armwing length and area, and total wing area increased linearly until the age of the 1st flight, after which growth rates significantly declined (all $p < 0.000$). Wing loading decreased linearly (-0.80 N/m²/d) until 41 d of age and thereafter increased to a maximum of 25 N/m² at 88 d of age. The aspect ratio showed a high degree of scatter in the early stages of life, which decreased in the latter period of growth. Additionally, linear regression equations, confidence intervals, and prediction intervals were used for age estimations based on data available for the forearm, body mass, total gap of the 4th metacarpal-phalangeal joint, armwing length, handwing length, and wingspan.

Shen, B., T. Fang, M. Dai, G. Jones and S. Zhang. 2013. Independent losses of visual perception genes *Gja10* and *Rbp3* in echolocating bats (Order: Chiroptera). *PloS one* 8(7): e68867. doi: [10.1371/journal.pone.0068867](https://doi.org/10.1371/journal.pone.0068867).

A trade-off between the sensory modalities of vision and hearing is likely to have occurred in echolocating bats as the sophisticated mechanism of laryngeal echolocation requires considerable neural processing and has reduced the reliance of echolocating bats on vision for perceiving the environment. If such a trade-off exists, it is reasonable to hypothesize that some genes involved in visual function may have undergone relaxed selection or even functional loss in echolocating bats. The Gap junction protein, alpha 10 (*Gja10*, encoded by *Gja10* gene) is expressed abundantly in mammalian retinal horizontal cells and plays an important role in horizontal cell coupling. The interphotoreceptor retinoid-binding protein (*Irbp*, encoded by the *Rbp3* gene) is mainly expressed in interphotoreceptor matrix and is known to be critical for normal functioning of the visual cycle. We sequenced *Gja10* and *Rbp3* genes in a taxonomically wide range of bats with divergent auditory characteristics (35 and 18 species for *Gja10* and *Rbp3*, respectively). Both genes have become pseudogenes in species from the families Hipposideridae and Rhinolophidae that emit constant frequency echolocation calls with Doppler shift compensation at high-duty-cycles (the most sophisticated form of biosonar known), and in some bat species that emit echolocation calls at low-duty-cycles. Our study thus provides further evidence for the hypothesis that a trade-off occurs at the genetic level between vision and echolocation in bats.

Sherwin, H. A., W. I. Montgomery, and M. G. Lundy. 2012 (for 2013). The impact and implications of climate change for bats. *Mammal Review* 43(3): 171 – 182. doi: [10.1111/j.1365-2907.2012.00214.x](https://doi.org/10.1111/j.1365-2907.2012.00214.x).

1. Climate influences the biogeography of bats, their access to food, timing of hibernation, reproduction and development, frequency and duration of torpor and rate of energy expenditure. 2. Empirical data on the impact of climate change on bats are a cause for concern as current increases in global temperature are one fifth, or less, of those expected over the next century. 3. We review

observed impacts of climate change on bats and identify risk factors allowing species-specific predictions. 4. The impact on species is reviewed in relation to six aspects, namely foraging, roosting, reproduction, biogeography, extreme weather events and indirect effects of climate change. For some aspects of species' ecology, there are insufficient data available to make accurate assessment of impacts. 5. We identify seven risk factors encompassing three broad aspects: biogeography - small range size, high latitude or high altitude range and a range occupying a geographic area likely to become water stressed; foraging niche - frugivory and species restricted to aerial hawking; dispersal ability - species with restricted dispersal behaviour. 6. We use the European and north-west African bats as a case study to assess the relative risk of climate change to individual species. Risk scores are compared with existing International Union for Conservation of Nature conservation assessments providing further insight into the conservation outlook for individual species. 7. We provide a base for Chiroptera to be incorporated into future frameworks of risk assessment and identify areas that require further research.

Shi, Z. 2013. Emerging infectious diseases associated with bat viruses. *Science China. Life Sciences* 56(8): 678–82. doi: [10.1007/s11427-013-4517-x](https://doi.org/10.1007/s11427-013-4517-x).

Bats play important roles as pollen disseminators and pest predators. However, recent interest has focused on their role as natural reservoirs of pathogens associated with emerging infectious diseases. Prior to the outbreak of severe acute respiratory syndrome (SARS), about 60 bat virus species had been reported. The number of identified bat viruses has dramatically increased since the initial SARS outbreak, and most are putative novel virus species or genotypes. Serious infectious diseases caused by previously identified bat viruses continue to emerge throughout in Asia, Australia, Africa and America. Intriguingly, bats infected by these different viruses seldom display clinical symptoms of illness. The pathogenesis and potential threat of bat-borne viruses to public health remains largely unknown. This review provides a brief overview of bat viruses associated with emerging human infectious diseases.

Sirami, C., D. S. Jacobs and G. S. Cumming. 2013. Artificial wetlands and surrounding habitats provide important foraging habitat for bats in agricultural landscapes in the Western Cape, South Africa. *Biological Conservation* 164: 30–38. doi: [10.1016/j.biocon.2013.04.017](https://doi.org/10.1016/j.biocon.2013.04.017).

Agriculture and related habitat modification have been identified as globally important drivers of species loss. Habitat modification resulting from agriculture can, however, have both positive and negative consequences for animal species. The ecological trade-offs involved in agricultural development have often not been explored sufficiently well to identify mutually beneficial solutions. Bats, for example, have been strongly impacted by agriculture intensification, mainly through the destruction of forests and natural wetlands. However, artificial wetlands created primarily for irrigation in agricultural landscapes may provide foraging habitats for bats and thus contribute to both the conservation of bat species and the regulation of insect pest species. We studied the influence of artificial wetlands on bat communities in agricultural landscapes in South Africa. We used mixed models to assess spatial variations in species richness, total bat activity, and species activity across 30 landscapes. Each study site was centred on a 'focal wetland' and surrounded by various habitat categories: open habitat, vineyards, orchards and trees. Our results show a crucial role of wetlands for all bat species as well as a significant influence of wetland size and water cover on bat activity. However, we observed no significant difference in species richness and only small differences in activity levels between the 'focal wetland' and the surrounding habitats. The present study contributes to the body of literature suggesting that farm dams may act as biodiversity hot-spots when properly managed. More generally, our analysis suggests that an in-depth understanding of the trade-offs between agricultural production and ecosystem integrity is important for finding mutually beneficial outcomes.

Taylor, P. J., S. Sowler, M. C. Schoeman, and A. Monadjem. 2013. Diversity of bats in the Soutpansberg and Blouberg Mountains of northern South Africa: complementarity of acoustic and non-acoustic survey methods. *South African Journal of Wildlife Research* 43(1): 12-26. doi: [10.3957/056.043.0117](https://doi.org/10.3957/056.043.0117).

We surveyed bats at 30 localities in the Soutpansberg and Blouberg Mountains within the newly proclaimed Vhembe Biosphere Reserve (VBR) of northern South Africa, based on ANABAT acoustic recordings (63 nights) conducted in parallel with captures of 260 individuals from harp traps (29 trap-nights) and mist nets (54 trap-nights), and searches of ten day-roosts and two night-roosts. Twenty-four species of bats were captured, or positively identified from roosts, out of 44 species previously recorded for the VBR. For those species captured during the study and one additional commonly recorded species, *Chaerephon ansorgei*, which was not captured, we compiled a library of ANABAT call parameters for reference calls, based on released bats or bats emerging from known-species roosts. Reference calls were obtained from the study area where possible, or from the closest possible site in the savanna region of southeastern Africa. Using principal component analysis and plots of frequency histograms of selected parameters, we investigated the extent to which reference calls of different species could be distinguished on call parameters. Complete separation was obtained for most species but certain species-pairs or trios showed overlap, particularly amongst molossid bats. Accurate identification of unknown calls was complicated by natural intraspecific variation in echolocation call structure due to habitat and behaviour in our species-rich study area. We advocate a conservative approach whereby species-pairs or groups with overlapping calls are treated as single 'species'. Such underestimation can be partly corrected using rarefaction approaches, as illustrated by data collected from Blouberg Nature Reserve. Particularly when surveying bats in species-rich areas such as the eastern savannas of southern Africa, both acoustic and capture-based surveys are necessary to accurately estimate true species richness. From our capture data and roost searches, we recorded nine to 14 species at four west-east, grouped localities defined by this study. Adding acoustic data using a conservative approach to classify overlapping species-pairs or trios, we obtained minimum richness estimates of 15 to 21 species, values which were close to those predicted by a recent macro-ecological model. We found no evidence for a west-east increase in richness with increasing precipitation as predicted by coarse-scale macroecological predictions.

Thomas, A. J., and D. S. Jacobs. 2013. Factors influencing the emergence times of sympatric insectivorous bat species. *Acta Chiropterologica* 15(1): 121–132. doi: [10.3161/150811013X667920](https://doi.org/10.3161/150811013X667920).

The onset of activity in animals restricted to being active for only part of the day is one of the most fundamental aspects of their biology because it marks the beginning of activities that they need to do to survive and reproduce. Initiation of activity is subject to several factors including presence/absence of predators and the vagaries of environmental conditions at the time of emergence. We tested if the emergence times amongst seven species of sympatric insectivorous bats were explained by predation risk, insect activity and weather conditions. We measured bat emergence times by recording echolocation calls. Peak emergence was correlated with body size, time of sunset, foraging strategy and diet, factors associated with risk of predation. Larger, faster flying bat species emerged earlier than smaller, slower flying species suggesting the former relied on flight speed to avoid predation. Clutter foragers emerged earlier than clutter-edge and open foragers, suggesting that vegetative cover is important for bats trying to avoid predation. Bats feeding on Lepidoptera emerged earlier than bats feeding on Diptera. However, insect peak activity was highly variable and did not differ between orders or time of season. Emergence time was not correlated with any of the weather variables we measured. These results suggest that predation influences fundamental aspects of the biology and ecology of insectivorous bats by determining when it is safe to become active.

Toussaint, D.C., R. M. Brigham and A. E. McKechnie. 2013. Thermoregulation in free-ranging *Nycteris thebaica* (Nycteridae) during winter: No evidence of torpor. *Mammalian Biology - Zeitschrift für Säugetierkunde* 78(5): 365–368. doi: [10.1016/j.mambio.2012.10.001](https://doi.org/10.1016/j.mambio.2012.10.001).

Bats are among the most heterothermic mammals, with nearly all species investigated under free-ranging conditions to date exhibiting some degree of daily torpor and/or hibernation. We investigated thermoregulation during late winter by seven *Nycteris thebaica* in a warm, semi-arid habitat in northern South Africa, using temperature-sensitive transmitters to measure skin temperature (T_{skin}). Unexpectedly, we found no evidence for any expression of daily torpor or hibernation based on a total of 86 days of data from 7 bats (one male and six females), despite air temperatures as low as $\sim 10^{\circ}\text{C}$. Instead, daytime T_{skin} was distributed unimodally with most values in the $33\text{--}35^{\circ}\text{C}$ range, and a minimum T_{skin} of 28.4°C at a roost temperature of 24.6°C . There are several possible reasons why *N. thebaica* may avoid torpor, including predation in roosts, and the long nightly foraging periods of this species compared to many others.

Notice Board

Conferences



1ST INTERNATIONAL CONFERENCE ON THE BIODIVERSITY OF THE CONGO BASIN

To be held at: Kisangani, DR Congo. 6 - 10 June 2014.

To help us plan this event, we kindly request you to indicate your interest and willingness to participate at this conference by sending an e-mail with your contact details to info@congebiodiv.org.

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17TH INTERNATIONAL BAT RESEARCH CONFERENCE

To be held in: Durban, South Africa, 2016

Call for contributions

African Bat Conservation News is divided into two main parts: peer reviewed and non peer reviewed articles.

The non peer reviewed part is further subdivided into a two sections:

Research and Conservation - which aims to promote projects, organizations and individuals working on bat related research, conservation and/or education within Africa and its surrounding islands. Updates on projects and activities are also encouraged.

Observations, Discussions and Updates - This section is used to inform and allow readers to comment on various issues of a thematic nature. It is also used to capture information (e.g. Observations) which may not have enough information to make the scientific contribution section (these observations will be moderated by the editorial board).

The scientific contribution part of African Bat Conservation News is peer reviewed and publishes brief notes concerning the biology of bats, new geographical distributions (preferably at least 100 km from the nearest previously published record), sparsely annotated species lists resulting from local surveys, roost counts, and echolocation of bat species occurring on the African continent and adjacent regions, including the Arabian peninsula, Madagascar, and other surrounding islands in the Indian and Atlantic oceans and those islands just off Africa within the Mediterranean and Red Seas.

Two additional sections are also included in the newsletter - Recent literature - this includes abstracts from recent conferences and recently published works. If you are involved in a conference or have published a paper and wish to have it included in this section please send a copy of the PDF of the paper to the Editor or Scientific Editor.

Notice Board - includes information on future planned conferences, workshops or training opportunities. If you are an organizer of such an event and wish it to be promoted in ABCN then please send the information to the Editor.

African Bat Conservation News Project Cycle

Issues will be published Quarterly (January, April, July, October).

Deadlines for scientific contributions (1 November, 1 February, 1 May, 1 August).

Deadlines for non-scientific contributions (1 December, 1 March, 1 June, 1 September).

Non scientific contributions should be sent to the Editor while scientific contributions should be sent to the Scientific Editor.

Notes to authors are available at www.africanbats.org or download PDF.

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