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Above: Common Slit-faced Bat (*Nycteris thebaica*) exiting Gatkop Cave, Meletse Bat Research and Conservation Training Centre, Limpopo Province, South Africa.

Inside this issue

Recent literature

Conference

17th International Bat Research Conference, 2016, Durban, South Africa

The following abstracts relate to African bats or are of general interest:

Plenary

Understanding the systematics of a country's bat fauna and its implications for different fields of research: an example from Madagascar

Steve Goodman

In 1995, Randolph Peterson and colleagues published a monograph on the bats of Madagascar, in which they recognized 28 species for the island. This work was based largely on specimens housed in numerous museums around the world and a 1967 field trip to the island. Soon after the publication of the monograph, intensive fieldwork commenced by several different research groups, which included visits to remote and poorly known regions of the island, exploration of numerous cave systems, and the collection of voucher specimens with associated tissues. Over the subsequent nearly 20 years, information on the bat fauna of the island has increased considerably and as of June 2016, 46 species are recognized, 86% being endemic; based on known candidate species, the fauna probably contains about 50 species. In the context of this presentation, the recent history of the exploration of the island's bat fauna is explained, the different techniques used, and the evolution of conceptual frameworks and studies as we learned more about these animals. We also review the importance of solid taxonomy in the interpretation of different ecological and epidemiological studies on the island's chiropteran fauna.

Bats, taxonomy, and a new "Age of Discovery"

Paul Bates, Nancy Simmons, Andrea Cirranello, Malcolm Pearch

For many, the 19th/early 20th centuries would appear to be the great age of taxonomic discovery. It was a time when the pre-eminent museums of the Western world sucked in a treasure trove of exotic specimens for description, classification, and naming. Of the >1350 bat species that are currently recognised, the majority were described between 1830 and 1930. Today, there is a perception that taxonomy – the description, naming and classification of organisms - is a dead science. This is misplaced; the reality is that we are living in a new 'Age of Discovery.' Nearly 200 new bat species have been described since 2000, representing an increase in known diversity of about 1% annually. These discoveries are geographically widespread but not equally distributed. Hot spots include Madagascar (18 species), Southeast Asia (38 species), and especially South America (50 species). In contrast, North America has no new species, Europe has three, and continental Africa, considering its zoogeography, has surprisingly few (25 species). For conservationists, there is an urgent need for taxonomic information relating to patterns of distribution and endemism. It is ironic that heat maps of diversity for continental African bats show that the areas of richest diversity correspond to countries with the lowest numbers of bat biologists and a marked paucity of recent literature. Therefore, today, in an era where bats face threats throughout their range, there are great opportunities for taxonomists. These opportunities are not only for high impact technical research (such as the description of new taxa) but also in simple, low budget projects, such as gathering and synthesising baseline data on national bat faunas. A dual approach emphasizing both taxonomy and local faunal composition will allow us not only to understand bat diversity better but also to prioritise conservation interventions to protect this diversity for future generations.

Tracking African Straw-Coloured Fruit Bats (*Eidolon helvum*) – a migrating ecological keystone species – past, present and future

Dina Dechman

Migrating animals are moving more and more into the focus of scientist and the public because their presence and absence have great consequences for their environment and us. The Straw-colored fruit bat, *Eidolon helvum* is such a species: long distance migrant, keystone ecosystem provider, reservoir and potential vector of human-relevant diseases and intensively hunted for bush meat. At several temporal and spatial scales using state-of-the-art tracking technology we endeavor to reveal the drivers for migration in this species, and closely linked to this, quantify the ecosystem services this species, probably the most numerous mammal of Africa provides at a landscape level. Unfortunately, we are reaching the limits of what we can learn about small long-distance migrants with current technology. Thus, I introduce ICARUS, a global animal tracking system from space, about to be launched in 2017 that will open up many new possibilities.

From sensory perception to foraging decision making - the bat's point of view

Yossi Yovel

Bats are extreme aviators and amazing navigators. Many bat species nightly commute dozens of kilometres in search of food, and some bat species annually migrate over thousands of kilometres. Studying bats in their natural environment has always been extremely challenging because of their small size (mostly <50 gr) and agile nature. In the past four years, we have developed novel miniature technology to GPS-tag small bats, thus opening a new window to document their behaviour in the wild. However, the movement of an animal alone is not sufficient for studying its decision processes. We therefore equipped our miniature GPS devices with an ultrasonic microphone which allows monitoring the sonar and social communication of freely behaving bats. Because echolocating bats rely on sound emission to perceive their environment, on-board recordings enable us to tap into their sensory 'point of view' and to monitor fundamental aspects of their behaviour such as attacks on prey and interactions with conspecifics. This intimate description of behaviour allows us to examine bat decision making under natural conditions. We used this approach to study several systems of which I will focus on three: (1) I will discuss how a social bat species (*Rhinopoma microphyllum*) that searches for ephemeral prey benefits from a collective search in a group. (2) I will compare two *Myotis* bat species that exhibit very different foraging strategies, resulting from the nature of the prey they seek, and (3) I will describe dramatic differences in the foraging behaviour of city vs. country fruitbats (*Rousettus aegyptiacus*). Finally I will also present our current effort to include more on-board sensors for the study of bat neuro-ecology including acceleration, EEG and physiology sensors.

Papers

Faster, longer, stronger – how bats deal with severe acoustic interference

Eran Amichai, Gaddi Blumrosen, Yossi Yovel

Active-sensing systems such as echolocation provide animals with distinct advantages in dark environments. For social animals, however, like many bat species, active sensing can present problems as well: when many individuals emit bio-sonar calls simultaneously, detecting and recognizing the faint echoes generated by one's own calls amid the general cacophony of the group becomes challenging. This problem is often termed 'jamming' and bats have been hypothesized to solve it by shifting the spectral content of their calls to decrease the overlap with the jamming signals, a response termed jamming avoidance response (JAR). We tested bats' response in situations of extreme interference, mimicking a high density of bats. We played-back bat echolocation calls from multiple speakers, to jam flying *Pipistrellus kuhlii* bats, simulating a naturally occurring situation of many bats flying in proximity. We examined behavioural and echolocation parameters during search phase and target approach. Under severe interference, bats emitted calls of higher intensity and longer duration, and called more often. Slight spectral shifts were observed but they did not decrease the spectral overlap with jamming signals. We also found that pre-existing inter-individual spectral differences could allow self-call recognition. Bats flying within a group may alter their echolocation in response to jamming, and in response to the physical presence of other bats (clutter response), as we have shown in a recent study. In this study we were able to separate the two and investigate the bats' response to acoustic interference per-se. Our results suggest the bats' response was aimed to increase the signal-to-noise ratio and not to avoid spectral overlap.

Conservation of fruit bats: needs of hunters, communities and governments

Daudet Andriafidison

In a recent Global Mammal Assessment, Madagascar's three fruit bats, all endemic, and including *Pteropus rufus* and *Eidolon dupreanum* were listed as Vulnerable, and *Rousettus madagascariensis* as Near Threatened. The threats to these bats are hunting and habitat loss. They are hunted for food, for sport and to protect fruit crops. Hunting is legal, although there is a closed season during the period of gestation and lactation. Fruit bats are mostly hunted to meet the needs of local subsistence. In some parts of Madagascar, they are also hunted for commercial purposes to supply hotels and restaurants. Estimates have shown that the level of hunting of *P. rufus* in western Madagascar is unsustainable. Hunting at roost sites is common, and far more destructive than trapping bats at their feeding sites. *Pteropus rufus* roosts in trees and is therefore highly visible and easily hunted. *Eidolon dupreanum* roosts in rock crevices which often provide protection, but hunters use smoke and nets to catch the bats. *Rousettus madagascariensis* roosts in caves and is hunted in some areas. Even in areas where hunting of *P. rufus* is not a problem, its roosts, which usually occur outside protected areas, are threatened by wildfire, logging and agricultural expansion. In order to conserve Madagascar's fruit bats, we need to know more about their tolerance to disturbance, roosting dynamics, movements, migration and impact of hunting. In addition, it is not clear to what extent they are dependent on intact forest, particularly for feeding sites. Evidence suggests that they prefer to feed near intact forest, but can also live in areas far from forests. The main possibilities for conserving fruit bat roosts involve working with communities, biologists, conservationists and local national authorities and the police.

Deterring pteropodid bats from feeding on commercial fruit in Madagascar without depleting the bat population

Radosoa Andrianaivoarivelo

We compared the effectiveness of methods of deterring *Pteropus rufus* from feeding on commercial fruit in east central and south east Madagascar in 2012-2013 during the litchi harvest. Two of the three methods used, installing plastic flags and ringing bells in the trees, were derived from those used by litchi growers in the south east. We improved and standardized these methods and compared their effectiveness with an organic product made from dried blood and vegetable oil (Plantskydd®) with a taste and odour aimed at deterring mammal feeding. We used 250 fruit groups during our investigation. Fruit group consists of four to 10 panicles grouped in the same space, randomly chosen in the tree as a sample unit. R.Stat was used to analyze the data. The damage by the bats per litchi tree ranged from 440 to 7040 g and two of the three methods reduced the fruit lost to bats: the plastic flags and the organic deterrent. There were significant differences in the damage levels between sites and between our three deterrence methods. However the plastic flags and bell ringing methods were less effective in reducing the bat damage compared to the taste deterrent. The latter was most effective when it had enough time to dry and adhere to fruits after spraying before rain. Its effectiveness was further demonstrated in flight cage experiments during which *Rousettus madagascariensis* avoided litchis treated with Plantskydd®. Results from bat faecal samples revealed no feeding preference but the collected samples contained large numbers of *Ficus* seeds, suggesting they extensively feed on *Ficus* fruits rather than on fruit of economic importance. Apart from fruit ripeness, tree productivity or other phenological factors did not affect the amount of fruit eaten by the bats. Birds were a major cause of fruit loss, even greater than fruit bats.

Trait-based diet analysis of a moth specialist horseshoe bat: novel insights into foraging ecology

Aitor Arrizabalaga-Escudero

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

The evolution of distinct acoustic phonotypes in a species complex with gene flow

Anna Bastian, Nicolas Nesi, Niko Balkenhol, David Jacobs

Rhinolophus simulator and *R. swinnyi* are two horseshoe bat species with partially overlapping distributions in eastern sub-Saharan Africa. The two species are generally similar in morphology and can therefore be easily confused with each other. However, their echolocation peak frequencies are very distinct with *R. simulator* calling at 80.3 kHz and *R. swinnyi* at 103.8 kHz. Contrary to the clear phonotypic distinction between *R. simulator* and *R. swinnyi*, a molecular phylogenetic analysis based on mitochondrial and nuclear data revealed a clade formed by both, 80 kHz *R. swinnyi* and 103-kHz *R. simulator*. More precisely it was found that *R. swinnyi* is polyphyletic; *R. swinnyi* individuals from the central-north populations occur with *R. simulator* individuals in one clade whereas *R. swinnyi* individuals from the southern populations form another, non-sister, clade. This unexpected phylogenetic pattern is incongruent with current taxonomy and the phonotypic pattern. To understand the occurrence of the distinct phonotypes within the same genetic clade, we developed three hypotheses: 1) *R. simulator* and *R. swinnyi* represent one species and the two phonotypes are due to phenotypic plasticity, 2) *R. simulator* and *R. swinnyi* represent one species but in the early process of diversification and the phonotypes are indicators of divergence in a context of gene flow, 3) *R. simulator* and *R. swinnyi* are two species with interspecific hybridisation and the two phonotypes are due to disruptive selection. Our general aim was to understand the processes underlying the observed phenotypic integrity despite genetic similarity by reconstructing the evolutionary history of the *R. simulator-R. swinnyi* clade. We are using an integrative approach which allowed us to analyse and compare patterns of variation in molecular (mitochondrial and nuclear), phenotypic (bioacoustical and morphological) and environmental spatial data. We will report on these analyses with a focus on the landscape genetics approach.

The Dhofar region: a zone of bat endemism in southern Arabia

Petr Benda, Antonin Reiter, Marcel Uhrin

The southern part of the Arabian Peninsula is considered a part of the Afro-tropic region; the bat fauna of this part of the Peninsula, 38 species of ten families in total, represents a regular segment of the African fauna with a minor part of representatives from the South Palaearctic eremic fauna (23.7%) and only few of the Mediterranean fauna (10.5%). A peculiar position shows the bat fauna of the Dhofar region, which is situated on the Yemeni-Omani transition and represents a narrow strip of relatively humid habitats along the shore of the Arabic Sea, isolated from the Palaearctic parts of the Middle East by waste desert areas of the Empty Quarter. The region is typical by the Sudan savannah vegetation with a characteristic phenology influenced by the monsoon cycle of the Indian Ocean, both characters being different in surrounding regions. The bat fauna of the Dhofar region is relatively poor, it comprises of 14 species of nine families. However, a relatively large segment of these species (28.6%) is represented by local endemics. These four bats are members of four families, viz. *Rhinopoma hadramauticum* (Rhinopomatidae), *Asellia arabica* (Hipposideridae), *Triaenops parvus* (Rhinonycteridae), and *Pipistrellus sp.* (Vespertilionidae). Such a large percentage of endemism is not known in other mammalian groups of the Dhofar region and this is the only zone of a significant bat endemism in the Middle East. Most of the Dhofar endemics show close relations to the faunas living to the east of Dhofar; it suggests a big importance of the Empty Quarter desert for the history of the Dhofar biota forming.

Designing a multi-species monitoring network to understand bat distributions in southern Africa

Rachael Cooper-Bohannon, Hugo Rebelo, Francisco Amorim, Gareth Jones, Orly Razgour, Fenton (Woody) Cotterill, Ara Monadjem, Corrie Schoeman, Peter Taylor, Kirsty Park

Despite bats being a major taxonomic group in southern Africa, the lack of distribution and population trend data prevent biodiversity change being measured, thus undermining proactive conservation actions. We combine species distribution models (Maxent) and conservation planning tool (Marxan) to design a multi-species monitoring network that optimises survey efforts for focal bat species in southern Africa across 11 ecoregions. We present three levels of survey effort, surveying 1, 5 or 10% of species distributions. This study presents a platform to design a large-scale bat monitoring network across southern Africa which could be used to improve species distribution data, understanding factors driving those distributions and in future monitor focal bat population trends.

The sound of silence

Angela Curtis, Eugene Marais

Bat researchers increasingly rely on monitoring echolocation signals to deduce activity and community composition for applied ecology, conservation, diversity and other rapid assessments. Despite the known limitations of bat detectors, they still provide a cost effective and reliable approach to determine bat activity and presence especially when used in conjunction with traditional trapping methods. However eyesight, hearing and smell are often overlooked and could contribute significantly to the ability of bats to navigate complex environments and to detect and capture prey. We physically observed and recorded Egyptian slit faced bats, *Nycteris thebaica*, leaving their roost in an abandoned mine in the Namib Naukluft Park in Namibia, with EcoObs Batcorders. The recordings were carried out simultaneously at two small vertical openings in a sealed mineshaft with the microphones placed so the bats had to fly within 50cm of them. During moonlit nights close to full moon, we could observe and count bats leaving the roost and indeed circling and investigating the batrecorders at close range. However, very few calls were recorded. In contrast, during low light conditions when we could not observe departing bats, multiple passes were recorded at the same locations. The results suggest that *Nycteris thebaica*, is less reliant on echolocation for navigation and prey detection on moonlit nights. It may also explain disparate results reported by researchers regarding the so-called ‘lunar phobia’ and the rarity of *Nycteris thebaica* passes in our ongoing monitoring of bat activity in the hyper-arid Namib Desert.

Composition of the excreted microbiota of bats: insights from different body habitats across co-roosting insectivorous species

Muriel Dietrich, Teresa Kearney, Ernest Seamark, Wanda Markotter

Despite its importance for disease ecology, the microbiota of bat populations is poorly documented, especially for samples potentially implicated in pathogen transmission such as urine and saliva. Here, we examined the composition and structure of bacterial communities excreted by insectivorous bats, focusing on three body habitats, i.e. saliva, urine and faeces. Urine harbored more diverse bacterial communities than saliva and faeces and bacterial community composition was distinct across body habitats with the majority of phylotypes being body habitat-specific. Within each habitat, interindividual variability was high, but some species-specific patterns were observed in the salivary microbiota in particular. We identified major zoonotic bacteria for which bats are reservoirs, such as *Leptospira, Rickettsia, Bartonella* and *Coxiella*, but also other potential opportunistic pathogenic bacteria in all body habitats. Our results represent a critical baseline for future studies investigating the role of microbiota on infection in bats and the transmission of bat-borne pathogens.

Bat diversity and human-bat interactions in Gorongosa National Park, Mozambique

Jennifer Guyton, **Andrea dos Santos**, Piotr Naskrecki

The bat fauna of Mozambique is poorly known, with very few studies published after the civil war began in the 1970’s. Here, we report on the results of four annual bat diversity surveys in Gorongosa National Park, Mozambique, from 2013-2016, with comments on bat-human interactions and conservation in Gorongosa. As of this writing, 37 bat species have been recorded in Gorongosa National Park, more than half the number known from the entire country. Because Gorongosa contains a diverse suite of habitats with high turnover, including large limestone cave systems, these 37 species are represented among several seemingly distinct communities. Additionally, some of these species seem to have close associations with human communities in the park’s buffer zone, and we will here present preliminary results on a study exploring human-bat affiliations and its implications for conservation and potential zoonoses. These results motivate further study of Gorongosa’s bat community structure, diversity, and disease ecology.

Too hot to sleep? Sleep behaviour and surface body temperature of Wahlberg’s Epauletted Fruit Bat

Colleen Downs

Sleep and factors that affect it have been well documented, however, in light of global climate change the effect of temperature on sleep patterns has only recently gained attention. Consequently we investigated seasonal temperature effects on sleep behaviour and surface body temperature of freeranging Wahlberg’s Epauletted Fruit Bat, *Epomophorus wahlbergi*, at a tree roost. Sleep behaviours of *E. wahlbergi* were recorded. Individuals generally spent more time awake than sleeping. Percentage of each day spent asleep was significantly higher during winter (27.6%), compared with summer (15.6%). Sleep duration decreased with extreme heat as bats spent more time trying to cool. Skin temperatures of *E. wahlbergi* were significantly higher when T_a was ≥35 °C and no bats slept at these high temperatures. Consequently extremely hot days negatively impact roosting fruit bats, as they were forced to be awake to cool themselves. This has implications for these bats given predicted climate change scenarios.

Acoustic sensing from a stable platform, the importance of head and ear movements

Ofri Eitan, Alex Kucherov, Arjan Boonman, Gabor Kosa, Yossi Yovel

Egyptian fruit-bats (*Rousettus aegyptiacus*) rely on echolocation (lingual) not only in caves but also while navigating outside. They regularly use echolocation when flying near trees even in relatively high light levels. The accurate ranging information provided by echolocation is probably important for these bats when landing on branches. In order to maintain this accuracy the bats have to overcome their highly unsteady movement. Flapping flight, characteristic of all bats, results in instances of zero acceleration in between intervals with high acceleration (during the down stroke). From a sensory point of view, this is highly challenging because the sensory reference frame, the head, is constantly oscillating, necessitating a calibration of any spatial measurement. We used a highly advanced tracking system allowing 0.1mm tracking accuracy along with synchronized audio recordings to study head, body and pinnae movements of Egyptian fruit-bats during flight sessions toward a landing platform. Our system enabled accurate reconstruction of the bats’ body movement and ear posture on the exact moment of the emission and arrival of the echo. Using dead specimens and 3D printing we reconstructed the bats’ head related transfer function (HRTF). We found that the bats deal with the noise induced by flapping flight by moving their head in perfect harmony with their ears and body motion, thus compensating for this instability. Bats moved their head such that it pointed directly towards the target at the moment of signal emission and reception, similar to how a gimbal mounted on a moving platform (e.g., a drone) stabilizes the sensor it carries (e.g., a camera). This strategy combined with optimizing SNR via moving the ears to the exact same posture at the moment of echo-reception, allows the bat to assess the angular location of the landing target (and other objects) in an unbiased highly accurate manner.

How we study bat migration and why it’s important for conservation

Winifred Frick, Erin Baerwald, Yossi Yovel, Liam McGuire, Rodrigo Medellin

How bats move across landscapes shapes aspects of life history, determines habitat requirements, and impacts vulnerability to global change. Studying migratory behavior of bats has long been thwarted by the limitations of technologies capable of tracking long-distance movements of small-bodied animals that fly and the elusive nature of some migratory species. Early studies of bat migration relied on banding, but this method is unsuitable for species that do not tolerate bands or have low recapture rates. Indirect measures of seasonal or long-distance movements, such as molecular genetics or stable isotopes, are alternative methods which can provide valuable information about connectivity of populations over coarse spatial scales, but are limited in terms of providing detailed information about migratory routes or behaviors. Recent technological advances, such as miniaturized geo-locating devices and radio telemetry networks, provide new opportunities to study seasonal bat movements over long distances. Researchers now have several options to study bat migration, but choosing the best method will depend on the research questions of interest, the autecology of the species under investigation, and the budgetary and logistical constraints of the study. In this synthesis, we review past, current, and future approaches to studying bat migration and emphasize how new methods can be used to answer both applied and basic ecological questions about bat migration. Leveraging new ways to study bat migration, including identifying migratory routes, stopover habitats, and specific migratory behaviors will be key to assessing conservation risk for migratory bats in the Anthropocene.

The faecal virome of the *Neoromicia* genus from South Africa

Marike Geldenhuys, Marinda Mortlock, Jaqueline Weyer, Oliver Bezuidt, Ernest Seamark, Teresa Kearney, Cheryl Gleasner, Tracy Erkkila, Helen Cui, Wanda Markotter

Global viral surveillance and the advent of next generation sequencing (NGS) for bat virome determination has identified various bat taxa as the natural hosts for a significant diversity of viruses. In Africa, the *Neoromicia* genus is of great interest to study in terms of its potential as a viral reservoir. Several of the species within the genus are highly abundant, and often roost underneath the bark of trees, roofs or in the cracks of walls, implicating a potential close contact to humans. The genus had also previously been identified as the host for several novel viruses from the Hantavirus and Alphacoronavirus genera as well as the Paramyxoviridae family. Of special significance is the detection of a Betacoronavirus related to the Middle East respiratory syndrome coronavirus (MERS-CoV). Though this MERS-related CoV showed significant similarity to human MERS, it was still too divergent to be the considered the direct progenitor of the human MERS outbreaks. Since this bat genus is circulating viruses of public health interest, we aimed to determine the diversity of its faecal virome using NGS. A total of 64 faecal or rectal specimens of *Neoromicia* species collected throughout South Africa since 2007 were analysed; after sample processing with an approach targeted toward viral particle enrichment the library was sequenced using Illumina's NextSeq500. Several viral families were confirmed to be present, many of which have not previously been reported from Southern African bats, including the Adenoviridae, Herpesviridae, Papillomaviridae, Picornaviridae and Polyomaviridae families. In addition to Alphacoronavirus sequences, several Betacoronavirus MERS-related sequences were also detected. This initial investigation into the faecal virome allows us to not only identify multiple viral families that are being shed into the environment, potentially infecting other species, but also aids in formulating further studies in determining the potential public health impact of the detected viruses.

Paleogene diversity in North Africa and the origins of African bats

Gregg Gunnell, Nancy Simmons , Erik Seiffert

African Paleogene bats are rare. Except for single specimens from the middle Eocene of Tanzania and the Oligocene of Kenya (undescribed), all Paleogene bats discovered to date are from North Africa. Archaic bats (those which do not belong to any extant family) have been found in the middle early Eocene of Algeria, the late early Eocene of Tunisia, and the early middle Eocene of Morocco. While it is not possible to assign most of these specimens to specific families, all share basic features with European archaic bats and none represent extant families. All other North African Paleogene bats belong to either the endemic Philisidae (probable sister taxon to Vespertilionidae and represented in all localities) or to extant bat families. The extant families known from North African Paleogene sites include Vespertilionidae, Emballonuridae, Nycteridae, and Hipposideridae – all more or less ubiquitous across most of the Old World in the past but today unknown from Europe except for Vespertilionidae. The lone exception to this general African Paleogene pattern is the bat assemblage from the Fayum in Egypt (late Eocene, Priabonian through early Oligocene, Rupelian). In addition to the families documented from elsewhere, the Fayum record also includes fossils representing at least one unique archaic family (undescribed) as well as the only Paleogene African records of Rhinopomatidae, Megadermatidae, and Myzopodidae. Of these, myzopodids are known only known from Madagascar, while rhinopomatids and megadermatids are mostly known from Africa, Oceanic Southeast Asia and, in the latter case, from Australia as well. These Paleogene distribution patterns suggest that immigration corridors shifted from Eurasia to southern Asia (circum-Tethys) and Australia during the period from the middle to late Eocene, perhaps in response to global cooling that began in the later Eocene.

2D-radiography and 3D-tomography studies of the cochlea in extant and extinct bats

Joerg Habersetzer, Gregg Gunnell, Nancy Simmons

Echolocation capabilities of bats are correlated with cochlear (inner ear) morphology allowing reconstruction of the habits of extinct bats. Doppler shift compensation and sophisticated use of long CF-FM calls (high duty-cycle echolocation) is associated with inflated cochlea size relative to the basicranial width of the skull. Previous studies, in which cochlear size was measured from 2D-microradiographs, had resolution of about 40µm. In this study, accuracy was increased to 12µm in digital 2D-microradiographs. We compared relative cochlear sizes in nearly half of all extant bat species as well as middle Eocene fossil bats (from the Messel pit in Germany) and *Tanzanycteris mannardi* (from Mahenge in Africa). The same bat specimens were scanned by 3D-µCT at 12µm or higher resolution in order to evaluate different methodological approaches. We found a very high correlation of size measurements in both 2D and 3D datasets, indicating that earlier, less precise measurements were nonetheless obtained from significant morphological landmarks. *Tanzanycteris* was found to be similar to a broad spectrum of hipposiderid bats of similar skull sizes – all of these taxa have extremely enlarged cochleae which clearly sets them apart even from rhinolophid and mormoopid bats that also use high duty-cycle echolocation and have relatively large cochleae.

Eocene fossil bats from Messel have much smaller cochleae, indicating that they were most likely low duty-cycle echolocators. *Tanzanycteris* represents the only known Eocene bat likely to have had an echolocation system like that of hipposiderids, which is thought to be specialized for prey detection in cluttered environments. *Tanzanycteris* was originally placed in a separate monotypic family but given that hipposiderids are also now known from early middle Eocene localities in North Africa, it now appears more likely that it should either be included within Hipposideridae or treated as a sister group of that family.

Long-term social-foraging bonds in bats: combining captive experiments and GPS tracking

Lee Harten, Yossi Yovel

Social foraging theory suggests that group living animals gain from persistent social bonds, allowing both increased tolerance in competitive foraging and information sharing. Bats are among the most social mammals, often living together in colonies of thousands of individuals for dozens of years. However, very little is known about how social interactions facilitate foraging information transfer. We studied two captive bat colonies for over a year observing thousands of social foraging interactions. Individuals in the colonies used one of two alternative foraging strategies, either producing food themselves or scrounging it directly from other individuals. We show that scrounging bats intentionally select whom to interact with when socially foraging, thus generating long-lasting non-random social bonds. We sought out to test whether these long-term producer-scrounger bonds observed in captivity, effect foraging decisions in the wild. Our unique wild in-house fruitbat colony allows us to test such questions. The colony currently consists of ca. 60 individuals representing a small natural colony. The bats roost in our facility but they fly out to forage freely in the wild. This facility enables monitoring an entire colony around the clock. Using automatic video processing, RFID technology, we can track all interactions between individuals when they are in the roost, and our miniature GPS devices enable to follow the bats when they forage outside. In combination this data will allow us to explore whether producer-scrounger bonds are maintained outside the colony and how such bonds are formed, namely, how do scroungers select their preferred producers?

Maternal antibody and the persistence of Lagos bat virus in populations of the African Straw-Coloured Fruit Bat

David Hayman

Bats host important emerging infectious diseases, including Ebola and rabies viruses that differ in their pathogenicity in bats. The study objective is to understand viral and host traits leading to infection persistence within a population of common African fruit bats, *Eidolon* *helvum*, using a Lyssavirus, Lagos bat virus (LBV) as a model, and compare these to previous work on filoviruses in other bat species. Maternally-derived antibody (MDA) titres against LBV were measured through captive studies and anti-LBV antibody decay rates estimated. These data are incorporated into a mechanistic model to determine how host traits, including MDA, colony size, and seasonal birthing, and viral traits, including long incubation periods, interact to allow LBV persistence within bat populations, despite LBV infection being fatal. These studies showed that MDA decays rapidly, but infection related antibody more slowly. Unobserved parameters were estimated and suggest a small proportion of bats die of disease. Pathogen persistence is sensitive to this proportion, along with MDA duration and infection incubation period. These results are consistent with field data with seroprevalence plateauing around 30-40% and very low infection prevalence, with an estimated 1 in 8,300 (0.012%) individuals infected at any one time. These dynamics are different to field observations and model predictions for filoviruses. These results suggest the risk of human infection through spillover for LBV is low and possibly simply correlated with human-bat contact rates.

Can survival analyses detect hunting pressure in a highly connected species? Lessons from Straw-Coloured Fruit Bats

David Hayman, Alison Peel

Animal behaviour, social structure and population dynamics affect community structure, interspecific interactions, and a species' resilience to harvesting. Building on new life history information for the straw-coloured fruit bat (*Eidolon helvum*) from multiple localities across Africa, we use survival analyses based on tooth-cementum annuli data to test alternative hypotheses relating to hunting pressure, demography and population connectivity. The estimated annual survival probability across Africa was high (≥0.64), but was greatest in colonies with the highest proportion of males. This difference in sex survival, along with age and sex capture biases and out of phase breeding across the species' distribution, leads us to hypothesize that *E. helvum* has a complex social structure. We found no evidence for additive mortality in heavily hunted populations, with most colonies having high survival with constant risk of mortality despite different hunting pressure. Given *E. helvum*'s slow life history strategy, similar survival patterns and rate among colonies suggest that local movement and regional migration may compensate for local excess hunting, but these were also not clearly detected. Our studies suggest that spatio-temporal data are necessary to appropriately assess the population dynamics and conservation status of this and other species with similar traits. These results will be put in context of recent findings regarding the causes of mass mortality events in bats globally.

Going batty - Are the brains of bats foraging at wastewater treatment plants affected by toxicants?

Kate Hill, Corrie Schoeman, Dalene Vosloo

Neoromicia nana bats exploit the abundance of pollutant tolerant chironomid midges breeding at wastewater treatment works (WWTW) and accumulate metals such as Fe, Cu and Zn in their livers and kidneys. If these metals persist in their circulation systems, and cross the blood brain barrier (BBB) they can have adverse effects on critical functions such as coordination and echolocation. This study aimed to 1) analyse trace metal levels in brain and hair samples (as a proxy of circulating metals) to determine if excess metals pass through the BBB via the circulatory system; and 2) measure biomarkers of protection (antioxidant capacity), neuron function (acetylcholinesterase activity), cell viability (caspase 3 activity), DNA damage (DNA fragmentation) and lipid damage (lipid peroxidation) of *N. nana* foraging at WWTW and reference sites. We found no evidence of higher metal accumulation in hair or brain tissue of WWTW bats compared to those from reference sites. Furthermore, we found no evidence of lipid peroxidation and no significant differences in apoptosis, acetylcholinesterase activity or DNA damage between the brains of WWTW bats and those of reference site bats. Although we previously reported high Fe, Cu and Zn levels in the liver and kidneys of WWTW bats, the lack of metal accumulation in hair and brain tissue suggests that metal binding proteins in these organs are sufficient to prevent accumulation of metals in other tissues. Whether this holds true for metals accrued from exposure routes other than food remains to be tested.

Ecological adaptations and human induced differentiation reversal in a bat of tropical origin at the humid-arid transition zone

Pavel Hulva, Tereza Střibna, Dušan Romportl, Simone Santoro, Ivan Horaček, Asaf Tsoar, Ran Nathan, David Shohami, Alejandro Centeno-Cuadros

The phenomenon of ecotypes in seldom studied in flying vertebrates and especially in bats. In highly mobile animals, adaptive component of evolution could be manifested by association of particular phylogeographic lineages with specific environments. In the present study, we describe the contact zone between Mediterranean and Arabian lineage of the Egyptian fruit bat in the Middle East, mirroring abrupt transition between humid and arid biomes. Behavioral factors and migration of ex-situ evolved lineages rather than in-situ selection is presumably the crucial factor generating above mentioned patterns at microgeographic scale in bats. Therefore, we focused to detailed analysis of gene flow patterns within the study area. We integrated data from movement ecology, species distribution modelling and landscape genetic studies within the framework of circuit theory to verify ecotype status of both populations. Moreover, as stepping stone dispersal could be especially important in crossing desert regions, we focused also to anthropogenic factors presumably facilitating gene flow in respective habitats. In conclusion, we suggest that landscape modifications linked to establishment of human settlements are recently causing differentiation reversal of lineages, that were isolated in the past.

Discovery, diversity and ecology of novel coronaviruses in South African bats

Ndapewa Ithete, Nadine Sampson, Leigh Richards, Samantha Stoffberg, Corrie Schoeman, Wolfgang Preiser

Bats are believed to be reservoir hosts for mammalian alpha- and betacoronaviruses (CoV). Following the emergence of SARS and the subsequent identification of *Rhinolophus sinicus* as the likely ancestral SARS-CoV source, a wide diversity of bat CoV has been described worldwide.

We aim to better understand CoV diversity in South African bats through close transdisciplinary collaborations with ecologists and zoologists. In addition to general "opportunistic" surveillance, we are conducting species-specific investigations concentrating on *Neoromicia capensis* and *Rhinolophus* spp. including longitudinal studies of bat colonies to determine shedding patterns and diversity of viruses present.

Since 2011, 24 different bat species have been sampled along rainfall and altitudinal gradients across different biomes; namely Fynbos, Forest, Nama Karoo, Grassland, and Savanna. Sample types include faecal pellets, saliva and urine swabs, and when voucher specimens are sacrificed for museum collections, blood and organs. We contributed 12 of 15 bat α-CoV sequences reported from South Africa, along with one β-CoV sequence from *N. capensis*, named NeoCoV. Phylogenetic inference shows that NeoCoV belongs to the same viral species as the recently emerged MERS-CoV, responsible for the ongoing outbreak in the Arabian Peninsula.

Using Pan-CoV PCR assays targeting conserved regions of the RNA-dependent RNA polymerase (RdRp) gene, additional viral sequences have been identified in various bat species including *N. capensis*, *R. clivosus*, *Pipistrellus hesperidus*, and *Miniopterus natalensis*. The majority of sequences identified are α-CoVs with ~20% prevalence for *N. capensis*. Of particular interest is the detection of β-CoV sequences closely related to Neo-CoV in *P. hesperidus*. Preliminary analysis of partial RdRp, nucleocapsid and spike gene fragments suggest that these viruses share a common ancestor with Neo-CoV. Screening and virus characterisation efforts are ongoing. By employing an interdisciplinary approach to the investigation of virus-host ecology, we hope to achieve a better understanding of CoVs in South African bats.

Convergence and divergence in African horseshoe bats: patterns and process

David Jacobs

Several processes may lead to phenotypic convergence among distantly related lineages including adaptation to similar habitats, neutral evolutionary process such as drift or shared biological constraints that limit the phenotypic variants produced. In contrast, adaptation to different habitats or neutral evolutionary processes acting on small isolated populations of closely related species could result in phenotypic divergence. We investigated convergence and divergence in African horseshoe bats (Rhinolophidae) using several phenotypic features associated with body size, food acquisition and echolocation behaviour. Convergence was evident between distantly related species pairs. There was pronounced convergence between *R. damarensis* and *R. darlingi*, between *R. hildebrandtii* and *R. mossambicus* and between *R. simulator* and *R. blasii*. The resting frequencies (RF) of *R.* cf.*fumigatus* and *R. fumigatus* also converged but not their body sizes. Thus there is convergence in species that have overlapping distributions (*R. hildebrandtii* and *R. mossambicus*; *R. simulator* and *R. blasii*) suggesting that adaptation to similar habitats may be the cause of the divergence. However, there is also convergence in species with disjunct distributions (*R. damarensis* and *R. darlingi*; *R.*cf. *fumigatus* and *R. fumigatus*) suggesting that neutral evolutionary processes such as drift may be responsible. Phenotypic divergence was also evident. It was particularly pronounced in the *fumigatus* group. Close relatives of *R. damarensis* and *R. darlingi*, including *R. eloquens*, *R. fumigatus*, *R. cf. fumigatus*, *R. hildebrandtii* and *R. mossambicus*, have diverged appreciably from the phenotype of both the ancestral character state and *R. damarensis* and *R. darlingi*. Furthermore, there was a pronounced repeated pattern of divergence in RFs amongst pairs of sibling species where one member of the pair retained the ancestral frequency and the other member of the pair diverged appreciably with RFs >100 kHz. This suggests that RF may play an integral role in lineage diversification in this family.

Novel RNA viruses isolated from wingless bat flies parasitizing Egyptian Fruit Bats in South Africa

Petrus Jansen van Vuren, M Wiley, Gustav Palacios, Nadia Storm, Stewart McCulloch, Wanda Markotter, M Birkhead, Allan Kemp, Janusz Paweska

The role of fruit bat ectoparasites in transmission of pathogens has not been extensively studied. The number of pathogens detected in bats is increasing on a regular basis but the true public and veterinary health impact of this is yet to be understood. The mechanisms of transmission are also not yet elucidated. We have collected ectoparasites (family Nycteribiidae) from Egyptian fruit bats (*Rousettus aegyptiacus*) as part of ongoing surveillance for bat-borne zoonotic pathogens. Homogenates were subjected to three blind passages on Vero cells. Supernatant from cell cultures showing cytopathic effects were subjected to transmission electron microscopy and sequence independent DNA amplification followed by next generation sequencing for identification. Two isolates of a novel dsRNA virus in the *Orthoreovirus* genus (Reoviridae) and eleven isolates of a novel -ssRNA virus in the *Orthobunyavirus* genus (Bunyaviridae) were identified from cultured ectoparasite pools. Full genome sequence data suggest that this orthoreovirus represents a new species in the genus and is likely the first member thereof to be isolated from arthropods. Full genome sequence data of the orthobunyavirus isolates indicate that it is sufficiently divergent from other viruses in the genus to represent a novel virus, with its closest relatives isolated from bats and with possible implication in human disease. The isolation, identification and characterization of these novel viruses expand the diversity of known bat-associated viruses, yet further investigation is required to establish their true zoonotic potential.

Metagenomic analysis of the microbiomes of bats in Sierra Leone reveals novel viruses and bacterial human pathogens

Randi Jensen, Thomas Hansen, Sarah Mollerup, Kristine Bohmann, Shapiro Theresa, Tobias Frøslev, Lars Nielsen, Eske Willerslev, Ara Monadjem, Lasse Vinner, Anders Hansen

Zoonotic diseases are an increasing global threat to human health and account for more than 60% of all emerging diseases. Of these more than 70% emerge from wildlife. Tropical Africa is considered a hotspot for emerging infectious diseases and spreading of zoonotic diseases. Bats are known to carry pathogens that have been transmitted to humans making them likely candidates for future outbreaks or epidemics. We applied high-throughput sequencing to 14 faecal samples collected in Sierra Leone from 9 species of bats to compare the bacterial and viral community. We identified the genomes of two new papilloma viruses closely related to other bat papillomavirus genomes, and one new coronavirus genome, closely related to the Human coronavirus 229E. The most abundant identified bacteria are known to be commensal to the hosts, however we also detected a number of microbial pathogens that may cause diseases in humans. For example pathogenic *Rickettsia* species, which can easily spread to humans. Furthermore, we showed presence of *Klebsiella* and *Clostridium* species, which are potentially pathogenic to humans. Our findings accentuate the importance of monitoring bats and other small mammals for potential pathogenic bacteria and viruses to better understand zoonotic transmission. Following the identifications of pathogenic bacteria and novel viruses in this study, we suggest monitoring of bats for *Rickettsia* species and coronaviruses in human populated areas of tropical Africa to improve prediction and thereby perhaps preventing future emerging infectious diseases.

Evidence of cryptic species from investigations of cranio-dental, baculum and cochlea morphologies of southern African horseshoe bat species (*Rhinolophus*)

Teresa Kearney, Ernest Seamark, Catherine Nobrega, Glynis Cron, Jakobus Hoffman,Frikkie de Beer

Cranio-dental and baculum morphologies were investigated in addition to using currently available keys for the identification of new voucher specimens of horseshoe bats (*Rhinolophus*) from southern Africa at the Ditsong National Museum of Natural History (formerly Transvaal Museum). The identification of different baculum morphologies for specimens that would previously have been lumped together as *Rhinolophus clivosus* initiated a more widespread investigation of cranio-dental (using traditional morphometric analysis) and baculum morphologies in the existing collection, and for a more limited set of specimens an analysis of variation in cochlea morphology. Traditional and geometric morphometric analyses of the cochlea were based on information from micro-focus X-ray CT scans and reconstructions of the internal cochlea space. Traditional morphometric analysis of cranio-dental measurements does not distinguish different species as clearly as baculum morphology. Traditional morphometric analysis of cranio-dental measurements does, however, support the elevation of *Rhinolophus fumigatus aethiops* to full species. The investigation of baculum morphology revealed some ontogenetic changes within taxa. It also supports the recognition of another *R. clivosus* like species, although it is not clear if this should relate to any of the available synonyms. Variation in cochlea morphology between the species follows an allometric relationship, with the exception of *R. clivosus*. A thorough understanding of various morphologies not only assists in recording characteristics of each species, but can also indicate cryptic species. In future the addition of DNA sequence information to this suite of data will help identify whether the species distinctions these morphologies suggest reflect actual phylogenetic relationships, or are misleading due to congruent evolution.

Desert water and large herbivores: what drives bat community structure?

Theresa Laverty, Joel Berger

Though rarely considered biodiversity hotspots, deserts often harbor a surprising number of unique species, including bats. Desert life is concentrated around scarce areas with surface water, typically springs within ephemeral rivers. Yet the importance of surface water for drinking by bats has been debated. Vegetation and insects cluster in riparian areas, so abiotic variables like surface water area and quality may at least limit desert bat communities indirectly through influences on habitat or prey populations. One ignored, but possibly important, biotic determinant of bat abundance and diversity is the community of large herbivores with which bats are codistributed. Our research focuses on these two potential drivers of bat community structure, surface water and large herbivores, in one of the world's oldest deserts, the Namib. We target bats that use water for drinking and/or foraging opportunities by sampling with mist nets and acoustic detectors above natural springs and manmade boreholes. This year, we are addressing the effects of elephants and other large herbivores on vegetation in the northern Namib Desert, and inspecting for subsequent changes in insect biomass, water quality, and bat community structure. Preliminary analyses indicate that herbivore biomass has a weak, positive association with the abundance of at least one bat species, *Chaerephon nigeriae*. While most molossid species occur throughout the region, other families of bats associate with specific water characteristics. Higher bat species richness is captured at water bodies with lower pH. The presence of boreholes may not only change large herbivore distributions within desert river systems, but also affect Namib bat communities. For instance, *Sauromys petrophilus* capture rates are approximately twice as high at boreholes than at natural springs. In the face of even greater rainfall variation with climate change, understanding the role desert water plays in structuring bat communities is essential to bat conservation.

The South African and African take on the wind energy-bat conflict: where we are at and where we hope to be

Kate MacEwan

South Africa has completed four rounds of renewable energy bidding, up to the end of 2015, with another round underway in 2016. A total of 38 wind energy facilities are either fully operational, under construction or awaiting final planning and financial approval. In total, this will amount to approximately 3500MW of wind energy from approximately 1370 turbines. Furthermore, the goal of South Africa's updated Integrated Resource Plan for Electricity 2010–2030 is to have more than 8000MW of wind energy generation by 2030.

Pre-construction bat monitoring at the earlier round wind farms in South Africa was inconsistent – well conducted at some facilities and poorly conducted or non-existent at others. Since 2012, guidelines have been in place to try and ensure that pre-construction bat monitoring follows a more consistent methodology. These guidelines are updated approximately every two years as new information becomes available. In addition, there have been operational bat monitoring guidelines in place since 2014. To my knowledge, long-term operational bat monitoring has been commissioned at 14 of the operational facilities. Data sharing is limited, however, I have analysed data from operational monitoring projects that I have access to and present here which species are being impacted on, quantities of known fatalities and evidence of seasonality of fatalities. I provide a review of the current role of government, developers, non-government organisations and other organisations in the South African wind energy bat conflict and propose ways forward.

I also provide brief insight into bats and wind energy in other African countries north of South Africa and the challenges faced there.

Spatial and temporal dynamics of lyssaviruses in bats in South Africa, 2004-2015

Wanda Markotter, Stewart McCulloch, Celeste Schepers, Jessica Coertse, Teresa Kearney, Ernest Seamark, Louis Nel, Janusz Paweska

The genus *Lyssavirus* consist of several viral species all capable of causing the fatal encephalitic diseases rabies. The African continent plays host to the highest diversity of lyssavirus species including Rabies virus (RABV), Lagos bat virus (LBV) Mokola virus (MOKV) and Duvenhage virus (DUVV). Both LBV and DUVV have been associated with African bat species where LBV appears to primarily circulate in frugivorous bats and DUVV in insectivorous bats. Since 2004 we have embarked on passive as well as active surveillance for lyssaviruses in bat species in South Africa. We undertook longitudinal studies of bat populations in Limpopo, Gauteng and Western Cape provinces as well as opportunistic surveillance across South Africa as a whole. Brain samples were tested for the presence of lyssavirus antigen using the fluorescent antibody test and realtime RT-PCR and serum samples were tested for the presence of lyssavirus antibodies using the rapid fluorescent focus inhibition test (RFFIT). Nine new isolates of Lagos bat virus and one isolate of Duvenhage virus was made from bat species sampled. Frugivorous bats (*Epomophorus wahlbergii* and *Rousettus aegyptiacus*) maintain a high level (> 30%) of seropositivity against LBV and *Nycteris thebaica* and *Miniopterus natalensis* tested seropositive against Duvenhage virus. We tested 23 other bat species for several other lyssaviruses and 19 additional species also tested seropositive. This re-emphasizes our lack of understanding of the true prevalence of lyssaviruses throughout Africa and the species involved in the epidemiology.

Seroprevalence varied greatly within populations and between seasons. These results can be used to infer times of year with increased viral circulation and thus high risk periods for subsequent zoonotic spillover events, as well as providing a guideline for which bat species require further investigation and pose the greatest potential for harbouring these rabies-related viruses.

Exposure of *Rousettus aegyptiacus* to Lagos bat virus, a rabies-related Lyssavirus

Stewart Mcculloch, Terence Scott, Nadia Storm, Marike Geldenhuys, Marinda Mortlock, Andre Coetzer, Jessica Coertse, Joe Kgaladi, Teresa Kearney, Ernest Seamark, Alan Kemp, Petrus van Vuren, Louis Nel, Janusz Paweska, Wanda Markotter

Lagos bat virus (LBV) - a member of the rabies-related lyssaviruses has historically been associated with populations of African fruit bats including *Rousettus aegyptiacus* (the Egyptian Fruit Bat). Factors driving viral circulation in these populations are poorly understood. However the colony size, age and health along with environmental influences such as temperature and humidity could have cumulative effects on zoonotic events.

In an attempt to understand the viral-host relationship, we undertook three interlinked investigations: firstly, a longitudinal study on a *R. aegyptiacus* population present year-long in the Limpopo province of South Africa; secondly, the maintenance of a captive colony under strict biosafety quarantine; and, thirdly, sampling of a colony in the Western Cape Province, with as distinct biome and as geographically removed from Limpopo as possible. These investigations included screening for neutralising antibodies by Rapid fluorescent focus inhibition test (RFFIT) with positive results suggesting exposure, whilst detection of viral nucleic acid by quantitative RT-PCR in brain material, indicating infection. Upon sampling, each individual was issued a unique alpha-numeric tattoo to facilitate monitoring in recapture events and the correlation of samples from the same individual at different time points.

An excess of 165 brain samples from vouchered or moribund individuals have been screened for the presence of viral RNA, with no Lagos bat virus nucleic acid being detected. The longitudinal study has provided monthly ecological and serological results since February 2013, with fluctuations between 29 - 86 % of the sampled population displaying a presence of antibodies against LBV. The colony in the Western Cape Province displayed a 47 % seroprevelance, indicating that LBV is dispersed throughout the range of *R. aegyptiacus'* South African population. This may be due to individual movement between roosts and synchronised parturition events, allowing for continuous interactions across the meta-population.

Pathogen detection in bats of Swaziland

Julie Shapiro, Randi Holm Jensen, Thomas Arn Hansen, Anders Johannes Hansen, Ara Monadjem, Robert McCleery

Bats are known to host many pathogens that may affect both humans and domestic animals. Although there have been no major outbreaks of emerging diseases from bats in Swaziland, both people and domestic animals may live in close contact with bats and other wildlife and there is little knowledge of the pathogens they may carry. The northeast Lowveld is a mosaic of three major land-use types: nature reserves, sugarcane plantations, and rural settlements. Many species of bat move between these land-use types. In addition, extensive areas of the Lowveld are used for cattle and livestock grazing, including zones with natural vegetation that are also home to diverse wildlife. Using high throughput shotgun sequencing, we screened 45 bats of nine different species in four different families (Emballonuridae, Molossidae, Pteropodidae, and Vespertilionidae) for both bacterial and viral pathogens. Notably, we detected coronaviruses in 18 individual bats belonging to all nine species screened. Within each family, coronavirus prevalence ranged from 37.5% to 57.1%. Many bats appeared to host multiple coronaviruses. Sequences ranged from several hundred to several thousand base pairs. Coronaviruses were detected in bats captured from all three major land-use types; bats from nature reserves appeared to have the highest diversity of coronaviruses. Several sequences were most similar to coronaviruses that have infected humans or domestic animals. This could indicate potential risks for coronavirus spillover in the region.

Targeting *Rousettus aegyptiacus* for paramyxovirus full-genomes using next-generation sequencing

Marinda Mortlock, Marike Geldenhuys, Jacqueline Weyer, Oliver Bezuidt, Cheryl Gleasner, Tracy Erkkila, Helen Cui, Janusz Paweska, Wanda Markotter

Rousettus aegyptiacus is known to harbor several viruses many of which are associated with zoonosis. Among these is the recently detected paramyxovirus, Sosuga virus (Rubulavirus), linked to human disease in East Africa. These bats are known to roost in large colonies and have a vast geographical distribution across the African continent. As part of previous paramyxovirus surveillance studies in South African bats, we detected two rubulaviruses from *R. aegyptiacus*, one being closely related to human mumps virus. Further characterization of these two viruses required isolation in cell culture. Failed attempts at isolation in standard cell lines led to the application of next-generation sequencing directly from biological samples with the aim to obtain full-genome sequences. Several viral enrichment steps were applied to select for viral particles and eliminate host genomic material. Despite the use of multiple enrichment steps, the vast majority of sequence data was derived from the host. Although paramyxovirus sequences were detected, it was not sufficient for full-genome assembly. This approach did however detect a number of other RNA and DNA viruses from the Coronaviridae, Hepeviridae, Adenoviridae and Herpesviridae families as well as an Influenza A virus from the Orthomyxoviridae family. These detections will however require follow-up analysis with PCR or virus isolation for confirmation. Our approach of deep sequencing from biological material of paramyxovirus positive samples did not prove to be optimal thus a more targeted virus specific technique (during sample preparation) will be necessary where virus isolation attempts have failed. Regardless, this study was able to detect a number of other viruses potentially indicating co-infections of these viruses within this bat species.

Drastic changes in bat community composition and activity patterns within a conservation-agricultural matrix, Swaziland

Fezile Mtsetfwa

Monocultures such as sugarcane plantations can cause a decrease in biodiversity at a landscape scale. Some African bat species however, seem to thrive in these landscapes. Such species are typically open-air foragers (with narrow bandwidth, low frequency, and low duty cycle calls), we only have a limited understanding of how intensive agricultural practices influence bat communities. This study investigated the effects of sugarcane monocultures on species and functional composition of bat communities across a conservation-agricultural matrix. We wanted to understand how bat community composition was altered by the abrupt inference of natural savannas by agro-ecosystems (specifically sugarcane). Bats were categorized into broad foraging groups based on their echolocation call structure (Molossidae/Emballonuridae: open-air; Vespertilionidae/Miniopteridae: clutter-edge; and Hipposideridae/Rhinolophidae; clutter). To measure bat activity we established six grids (each 25 ha in extent) randomly located in savanna and sugarcane habitats. At each grid we placed nine detectors 125 m apart. We recorded bat echolocation calls using ANABAT II and ANABAT Express detectors. Detectors were placed out before dusk and collected the following morning after dawn. We made recordings six times (three in summer and three in winter) over a one-year period. Bat species richness was highest in the savanna and decreased in the sugar cane plantations. In contrast, bat activity appeared to have the opposite trend, with higher activity in sugarcane plantations dominated (>70 %) by two open-air foraging species: *Chaerephon pumilus* and *Mops condylurus* (Molossidae).

Although activity was consistently higher in the sugarcane plantations, bats that exploited this habitat spent much less time within it compared to those foraging in the savanna. This study has shown that sugarcane fields have significant impacts on the structure of savanna bat communities by decreasing species richness, and altering bat activity patterns.

A comparison of bats diversity in the interior of Arabuko-Sokoke Forest and surrounding farmlands in Gede, Malindi-Kenya

Simon Musila

We investigated bats diversity in the interior of Arabuko-Sokoke Forest (ASF), one of the most important coastal forests in eastern Africa and surrounding farmlands, in order to understand the role of undisturbed coastal forest and farmlands in sustaining bats biodiversity. Five mist-nets were erected at 50-100m intervals, checked every 15 minutes from 1800hrs to 0100hrs; and each station sampled for a single night both in the interior of ASF and in farmlands. 57 different sites were sampled for bats both in ASF and farmlands in between November 2014-February 2016. A total of 24 bat species were recorded in the farmlands and 19 in the interior of ASF. There was no difference in Shannon-Weiner index of diversity for both habitats. No particular bat species was found restricted to the interior of ASF; however *Cardioderma cor*, *Otomops martiensseni*, *Neoromicia tenuipinnis*, *Triaenops afer* and *Neoromicia rendalli* were only recorded in farmlands. A total of 826 bats were trapped inside ASF and 3,633 in the farmlands. These included 83% and 78% of fruit bats in the forest interior and farmlands respectively. *Rousettus aegyptiacus* (54%) was the most abundant fruit bat in the farmlands while *Epomophorus wahlbergi* (46%) was most common in forest interior. *Neoromicia nana* and *Hipposideros vittatus* were the most common insect bats in the forest interior. *Cardioderma cor* (14%), *Scotophilus viridis* (1.32%), *Nycteris thebaica* (1.04%) and *Hipposideros vittatus* (0.9%) were the most common species in the farmlands. Therefore, the farmlands were richer in bats species richness and abundance than interior of ASF. Even though limited bat research has been undertaken in the already remaining natural habitats in Africa, very little if any investigation is being done in human modified habitats, but the results of this study highlight the importance of farmlands as important but ignored ecosystems for sustaining bats biodiversity in Africa.

The relative contributions of drift and selection to phenotypic divergence in the horseshoe bats *Rhinolophus simulator* and *Rhinolophus swinnyi*

Gregory Mutumi, David Jacobs, Henning Winker

Natural selection and drift can act on populations individually, simultaneously or in tandem and our understanding of phenotypic divergence depends on our ability to recognise the individual contribution of each of these processes. According to the quantitative theory of evolution (Lande's Model), if an organism has diversified through neutral evolutionary processes (mutation and drift), variation of phenotypic characteristics between populations (B) should be directly proportional to the variation within populations (W) such that B α W. Significant deviations from this null model imply that other non-neutral forces are acting on a phenotype, possibly natural selection. We measured various morphological traits, echolocation resting frequency (RF), and 3D geometric coordinates of skulls of *Rhinolophus simulator* and *R. swinnyi* individuals across their distributional range in southern Africa. We analysed the relative contributions of drift and adaptation to the within-species diversity using the Lande's Model. Morphology and RF have predominantly diversified through natural selection (as B was not directly proportional to W). Weak signals of drift were also evident on some phenotypic traits, contributing to variation within both species. 3D geometric analysis on skulls suggests that phenotypic traits on which selection acted differed between populations, implying differential ecological selection. Additionally, phenotypic divergence was not correlated to geographic distance confirming that drift was weak or non-existent. The divergences in phenotypes were thus predominantly attributable to adaptation to different habitats and less to drift.

Phenotypic variations despite gene flow: ecological adaptation of a sensory trait maintained by cultural drift

Nicolas Nesi, Lizelle Odendaal, David Jacobs, Jaqueline Bishop

The study of intraspecific variation of signalling systems can allow understanding the microevolutionary processes driving phenotypic divergence. Echolocation calls of bats are sensitive to various evolutionary forces, but processes that shape call variation remains poorly studied. In southern Africa, *Rhinolophus capensis* has marked variation in call frequency (75.7 to 86.5 kHz) and is present in a large variety of habitats form desert to close forest, making it an excellent model to study these processes. Phylogeography, genetic structure and gene flow of *R. capensis* were investigated using mitochondrial and microsatellites markers. The resultant genetic patterns were analysed in association with geographic variation in resting frequency (RF) of echolocations calls to investigate several processes as explanations for the origin and maintenance of local acoustic variation i.e. ecological adaptation, genetic drift, and cultural drift. Patterns of genetic structure were related to different habitats indicating ecological adaptation played a role in RF divergence amongst the different populations. Analyses also revealed an asymmetric gene flow pattern with male biased dispersal and female philopatry. On the basis of these analyses we suggest that geographic variation in RF have been driven by ecological adaptation despite the homogenising effect of ongoing gene flow and has been maintained by local cultural drift from horizontal learning of colony specific frequency.

Feast now, pay later: the cost of foraging at wastewater works for an urban adapter, the Banana Bat (*Neoromicia nana*)

Samantha Naidoo, Dalene Vosloo, Corrie Schoeman

Wastewater Treatment Works (WWTWs) are a ubiquitous feature of the urban landscape. WWTWs may provide profitable foraging areas for insectivorous bats because of particularly high abundances of pollution-tolerant chironomid midges. However, bats feeding on these insects may also accumulate pollutants in their tissues. There have been no studies to investigate whether African bats utilize WWTWs as foraging grounds, and potential physiological impacts from foraging at such sites. The aim of this study was to investigate the impact of WWTWs on foraging ecology and multiple tiers of physiology (haematology and genotoxicity, detoxification organs and reproduction) in an urban adapter, the banana bat (*Neoromicia nana*) in KwaZulu-Natal, South Africa. *N. nana* at wastewater-polluted sites exhibited significantly higher abundance and feeding activity, and a predominantly Dipteran diet compared to a diverse insect diet at unpolluted sites. WWTWs thus provide an abundant short-term food resource for bats. However, we found significantly higher metal levels at wastewater-polluted sites, and in the tissues of these bats compared to unpolluted sites. Further, we found significant sub-lethal haematological and genotoxic responses (decreased antioxidant capacity, increased DNA damage and haematocrits) in WWTW bats. Thus, longer-term effects should be most evident in organs involved in detoxification. Indeed, we found disrupted essential metal/mineral nutrient balance, histopathological tissue damage and whole organ effects in the liver and kidneys. Finally, we found reproductive system alterations in male *N. nana* at WWTWs. Although we did not find significant effects on sex organs, testosterone hormone concentrations were significantly lower in males at WWTWs than at unpolluted sites. In addition, their body condition indices were significantly lower than at unpolluted sites, suggesting lower quality male bats at WWTWs. Taken together, these results suggest the potential for serious long-term health risks, negative fitness implications and ultimately, population effects for these top predators within the urban landscape.

Commercial hunting of pteropodid bats in Madagascar and Mauritius

Ryszard Oleksy

Endemic Malagasy fruit bats (*Pteropus rufus* and *Eidolon dupreanum*) and the Mauritian flying fox (*P. niger*) are hunted for bushmeat or because of their perceived impact on commercial fruit. In Madagascar a study was conducted in 2009 to assess the intensity of hunting and its potential effect on bat populations. In Mauritius in 2015/16 interviews with local people aimed to assess perceptions about bats and the intensity of hunting. In Madagascar fruit bats are hunted for consumption or sale by local villagers while in Mauritius hunting aimed to reduce the numbers of bats taking commercial fruit. On both these Indian Ocean islands culling has a significant effect on the fruit bat populations.

The impact of the Mauritian Flying Fox (*Pteropus niger*) on commercial fruit plantations studied by GPS tracking and orchard assessment

Ryszard Oleksy

The Mauritius flying fox is perceived as a major pest claimed to cause substantial losses of litchi and mango fruits. Between 2015 and 2016 a study was conducted to assess the impact bats and other frugivores have on the commercial fruit plantations. Through GPS tracking the movement of bats was monitored throughout a year to investigate their feeding habits and movement ecology. Bats were highly mobile and able to travel from one end of the island to another within a night indicating that most of Mauritius acts as the home range for the entire population. Limited forest areas and thus native food availability force bats to feed in urban areas during the austral summer and they aggregate in forested areas during the winter. Orchard assessments indicated that bats are not the major pests of commercial fruit and that netting may be the most effective method of protecting crops.

Multilayered information in everyday bat vocalizations

Yosef Prat, Mor Taub, Yossi Yovel

Since ancient times, scholars have wondered about the capabilities of animal vocal communication. Yet, while human language appears to be its most sophisticated form, the evolutionary origins of this skill are still vague. One of the obstacles in such an evolutionary quest is the lack of nonhuman parallels to language or speech. Often, we are puzzled by the diversity of animal vocalizations, but are unable to interpret their biological function. Several studies have demonstrated the abilities of certain calls to convey information about their emitter, or about their context, e.g. alarms of specific dangers. However, most studies are limited to vocalizations which are distinctly identifiable or to contexts of emotionally extreme behaviors, such as courtship or distress. Bats, which heavily rely on their environment's acoustics, being both nocturnal and echolocators, serve as a perfect model for vocal communication research. We study the extremely vocal and social Egyptian fruitbat (*Rousettus aegyptiacus*). For 75 days we continuously monitored a group of bats, and recorded tens of thousands of vocalizations from everyday interactions, which seem very similar upon first hearing. Using synchronized video recordings, we identified the emitter, the target, and the context of the vocalizations. We adopted a machine-learning approach, which has been previously used in human speech recognition, in order to comprehensively analyze the spectral properties of bat calls. We found significant differences between calls emitted by different individuals, in different contexts, and even directed to different addressees, implying that an eavesdropping bat could use these discrepancies. Importantly, our analysis encompasses everyday pairwise, mostly aggressive, vocalizations. Such vocalizations, which govern the vocal communication of many species, are often overlooked in bioacoustics studies. We conclude that fruitbat social vocalizations hold multilayered information, and we propose bats as a potentially beneficial model for vocal communication and language evolution research.

Miocene fossil bats from Nosy Makamby, northwestern Madagascar

Karen Samonds, Gregg Gunnell, Steve Goodman, Nancy Simmons

The near lack of Tertiary terrestrial vertebrate fossils from Madagascar continues to inhibit direct testing of biogeographic hypothesis regarding the origin and evolution of many of its extant taxa. Extant Malagasy bats comprise 49 species, but the published fossil record consists of only 11 taxa from the Late Pleistocene and Holocene. Bats are thought to have arrived on Madagascar through multiple dispersal events, largely during the last 15 million years. We report here a collection of bat fossils recovered from Miocene sediments on the island of Nosy Makamby, northwestern Madagascar.

Fossiliferous deposits consist of medium to coarse sandstones representing a coastal plain/near-shore marine environment. Fossils were extracted using acetic acid preparation techniques and include: jaws, partial limb bones, and isolated teeth of *Hipposideros*, one small myotine lower molar, and distal humeri of *Miniopterus*. The majority of specimens are referred to *Hipposideros* based on the dental formula, small upper premolar shifted lateral in the toothrow, and distinctive morphology of the lower P2. *Hipposideros* is widely distributed throughout the Old World tropics, including *H. commersoni* and *H. sp. nov.*, currently being described, which are the largest extant microchiropteran *H. sp. nov* bats on the island today. Subfossil *H. commersoni* have also been described from Madagascar, as well as the larger extinct *H. besaoka*. The Nosy Makamby specimens represent the earliest record of fossil bats in Madagascar and the first non-marine fossils from within the island's 80-million year fossil gap (virtually no fossil vertebrates known from the later Cretaceous to the sub-Recent). A better understanding of this assemblage has great potential to help reconstruct the biogeographic history of Malagasy bats, and demonstrates the potential for recovering small fossils from nearshore marine sediments. These types of localities may currently represent the best opportunity to elucidate how, when, and from where the ancestors of Madagascar's modern animals arrived.

African bat malaria parasites – from host specificity to broad host range

Juliane Schaer, Susan Perkins, Kai Matuschewski, DeeAnn Reeder

The diversity of bats is reflected in the high diversity of their malaria parasites. Contrary to the human infecting parasites of only one genus, *Plasmodium*, diverse parasites that belong to additional eight genera are described from chiropteran hosts. Co-evolutionary patterns are apparent for some of these host-parasite systems, whereas other malaria parasite genera, e.g. *Nycteria*, are present in distant related bat families like *Nycteridae* and *Rhinolophidae*. Here, we present data from investigations of malaria parasite infections in bats from several biodiversity surveys in different West and East African countries. Microscopy and molecular methods were used to collect data on prevalence and phylogenetic relationships of chiropteran malaria parasites. We detected parasites of the genera *Plasmodium, Hepatocystis, Polychromophilus* and *Nycteria* in six different bat families and discuss the findings in the context of co-evolution and host specificity. One example is the phylogeny of African bat *Hepatocystis*. Parasites are confined to bats of the close related families Hipposideridae and Pteropodidae, but our phylogenetic analysis of parasite sequences from seven different host genera indicate that within pteropodid bats, *Hepatocystis* parasites do not exhibit host specificity. Understanding the evolution of malaria parasites and their phylogenetic context as well as identifying host switches is essential for understanding the important human malaria disease.

Taxonomic, functional and phylogenetic diversity of bats and metacommunity structure along elevational gradients in Africa

Corrie Schoeman

Tropical mountains are hotspots of biodiversity, but the factors that generate this high diversity are poorly understood. To investigate possible mechanisms that structure bat assemblages along elevational scales, I compared taxonomic, phylogenetic and functional dimensions of bat diversity at four mountains in Africa. Phylogenetic dispersion was based on relatedness of species derived from a bat supertree, whereas functional dispersion was estimated separately for skull morphology (reflecting dietary niche) and body size. I used null models to infer possible drivers of the observed patterns.

Species richness declined with elevation, yet associations between phylogenetic and functional diversity and elevation differed between indices and among mountains. Species in highland assemblages at Cederberg and Soutpansberg were phylogenetically more similar than expected by chance, whereas phylogenetic diversity of lowland and mid-elevation assemblages at Mulanje and Nimba mountains were significantly lower than expected by chance. Differences in species composition between lowland and highland assemblages and sites imply distributional limits for selected functional groups, possibly caused by environmental factors, e.g. vegetation type or changes in human land use types, and climate and/or topography, or independent speciation events in lowlands and highlands. These barriers to distribution may hinder uphill range shifts of many bat species in response to climate change, with concomitant impacts on insect control and seed dispersal on African mountains.

Three steps forward, two steps back: conservation not necessarily a fairy tale of they lived happily ever after or is it?

Ernest Seamark, Teresa Kearney, Mark Keith, Monique Shanahan, Wanda Markotter, Stewart Mcculloch, Muriel Dietrich, Leon Labuschagne, Victor Van Cakenberghe, Kwaku Acheampong, Brock Fenton, Steven Tucker, Andre Groves, Dzibu Mphaphuli, Peter Mills, Willeen Oliver

Biodiversity stewardship is a mechanism for using contractual agreements to include private land in the South African conservation estate. This involves using notary agreements as part of the deed to protect land worthy of a Nature Reserve status (National Environmental Management: Protected Areas Act 57 of 2003). This approach provides an additional level of security especially if the property is sold.

AfricanBats, together with government conservation agencies, have embarked on a project using the biodiversity stewardship model to secure protection of an important bat cave in the northern part of South Africa. Gatkop Cave is one of two known *Miniopterus natalensis* maternity roosts in the Savanna biome of South Africa. The Natal Long-fingered bat is an appendix II listed CMS species. The cave is also used as a maternity roost by seven other cave dwelling species representing four different families (excluding Miniopteridae). It is estimated that 100,000 female *M. natalensis* give birth annually to young between November – January in Gatkop cave. This population migrate, around March, to hibernacula caves in the Cradle of Humankind World Heritage Site 160 km south of Gatkop Cave.

AfricanBats and collaborative partners have undertaken research and monitoring at Gatkop Cave since 2011. In March 2013 facilities 600m from the cave were entrusted to AfricanBats for use as a research and training base. This allowed greater onsite presence in the area that assisted in building trust with local stakeholders (a key ingredient for a successful project). However, unstable social and economic factors affecting global markets, can drastically affect projects, necessitating adaptive management approaches to management and planning. This presentation will outline what we have learned to date; the successes, failures and possible ways forward for future conservation management of not only Gatkop Cave but also other important bat caves in South Africa.

Effect of vegetative heterogeneity on bat diversity and activity in southern African savannas

Ara Monadjem, Fezile Mtsetfwa, Julie Shapiro, Robert McCleery

The presence of megaherbivores substantially changes the structure and composition of vegetation in savannas. Changes in vegetation are predicted to lead to shifts in composition and functionality of faunal communities. However, these predictions have rarely been tested. Specifically, the effects of megaherbivores on bat communities and the scale at which such effects may occur, is largely unknown. We examined impacts on bat communities at two scales: local and landscape. We sampled the bat community (excluding non-echolocating fruitbats) by employing acoustic monitoring on ten grids, each one 550 × 550 m in extent, set up in similar savanna habitats in Swaziland and South Africa. Four grids were situated within a large protected area (Kruger National Park, South Africa) that harbours megaherbivores. The remaining six grids were situated in protected areas in north-eastern Swaziland where elephants and rhinos have been absent for at least a century. Each grid contained nine plots separated by 250 m, at which a single Anabat was erected and recordings taken from sunset to sunrise. Anabat recordings were made on two nights per plot per season (dry/wet) over a two-year period, 2014 and 2015, for a total sampling effort of 720 Anabat nights. We recorded 85,616 bat passes from nine sono-species. At the local scale, we examined the impact of vegetation structure on bat diversity and activity. The null model was the best candidate model suggesting that vegetation structure at a plot scale did not affect bat diversity or activity. At the landscape scale, we examined the impact of megaherbivores on the bat community. Both bat diversity and activity was significantly higher in the absence of megaherbivores. Kruger showed large reductions in vegetative heterogeneity on multiple scales compared with Swazi sites and this reduction in heterogeneity was correlated with substantial decreases in bat diversity and activity.

Territorial singing in the African Heart-Nosed Bat

Grace Smarsh, Michael Smotherman

The diversity of song repertoires and functions of singing in mammals have been little investigated. *Cardioderma cor*, the heart-nosed bat, was first noted as a singer due to their conspicuously loud, low frequency songs. Unlike other singing bats that sing in the roost for courtship and mate defense, this species roosts in groups in the hollows of baobab trees but disperses nightly to exclusive areas where they move about foraging and singing. We tested the overarching hypothesis that singing is used to create and defend foraging territories. By mist-netting, pit-tagging, tracking and acoustically recording 12 singing individuals for 4-6 nights each we collected movement and singing behavioral data. We recorded songs throughout the tracking period. Through acoustic playbacks we tested song function. Male

C. cor individuals are spatially arranged on separate foraging areas of over 100m across that they return to nightly. They sing back and forth with neighbors from preferred perches. Low-frequency, repetitive syllables are acoustically adapted for song transmission across the cluttered bush habitat. Songs varied within and across individuals both spectrally and temporally. Song playbacks elicited strong responses in movement and singing, confirming the territorial function of singing. Variability of song further supports the possibility of other functions of singing, including discrimination of conspecifics and signaling motivational level.

Drivers of bat fly intensity and prevalence of *Rhinolophus* bat species in southern Africa

Michael Staegemann, Corrie Schoeman

Demographic and ecological characteristics render obligate cave roosting bats highly susceptible to infestation by various ectoparasites. However, the patterns and factors of ectoparasite loads among bat host species are understudied, particularly in the Old World. We tested predictions of host sex, body size, and habitat heterogeneity hypotheses to explain parasitic bat fly (Streblidae and Nycteribiidae) diversity, intensity and prevalence on six *Rhinolophus* bat species in southern Africa. We sampled and classified 930 bat flies to seven morphospecies (4 streblids and 3 nycteribiids) on 333 individual bats at 34 sites in eight biomes. Bat fly prevalence and infestation intensity was highest in the smallest species *R. swinnyi*. By contrast, probability of bat fly presence was positively associated with host body size. In support of the habitat heterogeneity hypothesis, we found a significantly positive relationship between species diversity and habitat heterogeneity. However, we found no evidence that parasitic flies favoured male or female bats. Recursive partitioning analysis showed that the best predictor of parasitic fly diversity was surrounding land cover, and to a lesser degree, body size. Our results suggest that biotic processes at the local scale and human land use and biome characteristics at the meso-scale influence bat fly diversity on rhinolophid bats. Future studies should target other species of cave-roosting bats, as well as endo-parasites, to better understand the mechanisms responsible for parasitism in Old World bats.

Ecosystem services provided by bats and birds in coffee plantations in Malawi

Emma Stone, Matthew Town, Stephen Harris, Gareth Jones

Conversion of tropical forest and agricultural intensification are important drivers of biodiversity loss globally. Malawi has the highest rate of deforestation in southern Africa and the rapid expansion of agriculture has resulted in habitat degradation and fragmentation. Bats are 'keystone' species performing fundamental ecological roles as seed dispersers and pollinators, and are of great economic importance due to their role in insect pest control. We conducted a field experiment in the Satemwa Estate coffee plantation in Southern Malawi to quantify the ecosystem services provided by bats through insect pest control. Thirty sites were selected randomly within coffee fields in 2015. At each site (block) three exclosures (n = 90 in total) were constructed from wooden frames and covered in wire mesh large enough to exclude bats and birds but allow insects. Each exclosure in each block was assigned to one of three treatments: control - comprising the external cage but no netting; birds and bats - cage closed all day and all night; and bats - cage closed at night only to exclude bats. Experiments commenced in June 2015 and ended in August 2015. We collected data on insect pest damage (leaf and berry) and harvest data in each exclosure. Leaf damage from *Leucoplema dohertyi* (Leaf skeletoniser) was significantly higher in bat exclosures than controls, and significantly lower in bird exclosures than controls. There was no difference in *Ascotis selenaria reciprocaria* (Giant looper moth) damage between treatments. Leaf damage from *Cercospora coffeicola fungus* was significantly lower in bat and bird exclosures than controls. There was no difference in proportion of bad/damaged coffee berries harvested between bat exclosures and controls, or bird exclosures and control. Bats and birds suppress skeletonisers in coffee but increase the occurrence of *Cercospora* damage, suggesting they may be vectors of *Cercospora* fungus.

Bat coronaviruses – how do they jump the species barrier?

Tasnim Suliman, Sabella Eckerle, Benjamin Meyer, Marcel Mueller, Wolfgang Preiser

Bats are known to carry numerous viruses that can potentially infect other animals including humans and result in what may range from harmless infections to global epidemics of severe diseases. Numerous coronaviruses (CoV) have been found in bats, including the progenitors of SARS-CoV that caused an epidemic in 2002/03 with over 8000 cases and a 10% fatality rate, and of MERS-CoV which has been occurring since 2012 in the Middle East, causing 1,698 infections and 609 deaths to date. SARS-CoV was transmitted to humans from civets and MERS-CoV from dromedaries. A South African bat species, *Neoromicia capensis*, was found by our group to harbour a novel CoV, named NeoCoV, that is genetically 85% identical to MERS-CoV. However, nothing is known about the hostswitching events that could have caused an adaptation of this virus to dromedary camels and / or humans, giving rise to MERS.

For unclear reasons, propagation of bat viruses in cell cultures is notoriously challenging; only one laboratory has succeeded in isolating a CoV from a Chinese horseshoe bat, while numerous other attempts across bat and virus species have failed. The use of the correct cell line is apparently critical for virus isolation; however, few bat cell lines are available and none from *N. capensis*. We have established primary cell cultures from various *N. capensis* tissue types immortalised by transduction with the large T-antigen of Simian Virus 40. Pseudoparticle technology presents a novel yet promising method of identifying suitable cell lines for the isolation of particularly elusive viruses: We use bio-safe replication-deficient virus-like particles bearing the spike proteins of NeoCoV in order to identify viruscell line compatibility before using precious bat-derived samples. These tools in combination present a practical and biologically rational manner of investigating the factors involved in the zoonoses caused by bat-borne CoVs.

Preliminary data on the distribution of insectivorous forest bats along elevational gradients in the Nigerian/Cameroon Mountains

Iroro Tanshi, Tigga Kingston

Striking changes in environmental conditions along mountains allow investigations on species distributions patterns and their drivers. Monotonous decline in species richness has been predicted for mountains where temperature and moisture are highest at the base, but species distribution patterns along elevational gradients can be idiosyncratic. Bat distributions in Afromontane areas remain poorly known, and those of the Cameroon/Nigerian Mountain range in southeastern Nigeria, a biodiversity hotspot, hitherto unstudied. We captured forest interior insectivorous bats from each of six elevational bands from 200 m asl to 1700 m asl in the Afi and Obudu Mountains of southeastern Nigeria. Bats were caught using harp traps on two consecutive nights on four transects at each elevational band. Transects were 200 m long on existing trails, with trap points set at 50 m intervals. The study was conducted between May 2015 and March 2016.

We caught 17 bat species belonging to five families, namely the Emballonuridae (1 species), Hipposideridae (5), Nycteridae (3), Rhinolophidae (4) and Vespertilionidae (4). Bat species richness declined monotonously with increasing elevation. The species ensemble on both mountains showed a nested distribution pattern. Although both *Hipposideros ruber* and *Rhinolophus alcyone* co-occur in the lowlands, only one species was dominant on either mountains; Afi (*H. ruber*) and Obudu (*R. alcyone*) Mountain respectively. Our next step will investigate the processes driving the pattern of species distribution along elevational gradients in this important biodiversity hotspot.

The controversial cull of the Mauritius Fruit Bat *Pteropus niger*

Vikash Tatayah

The Mauritius Fruit Bat *Pteropus niger*, a Vulnerable species, has been blamed for exaggerated levels of damage to commercial fruits such as lychee *Litchi chinensis* and mango *Mangifera indica*. A real bat population increase over the past decade due to lack of strong cyclones, the natural regulatory factor, has exacerbated the human-fruit bat conflict. Due to pressure from fruit growers and the public, the Government of Mauritius passed a law, the Native Terrestrial Biodiversity and National Parks Act, in October 2015, which made provision for the culling of a native species, even if red-listed. This paved the way for a highly controversial official cull of 20 000 (of a debated total population claimed to be between 50 000 and 90 000 individuals) Mauritius Fruit Bats *Pteropus niger* conducted by the armed forces, despite the lack of scientific advice to support the reported damage to fruits, and local and international outcry. Illegal hunting and persecution increased due to the perceived reduction in legal protection and lack of enforcement or even condoning of such acts. The presentation in the context of the IBRC 2016 Bat Hunting Special Session will cover aspects related to the official cull, its aftermath and the way forward.

Ecosystem services provided by bats in macadamia orchards in South Africa

Peter Taylor, Valerie Linden, Sina Weier, Ingo Grass, Dries Alberts, Teja Tscharntke

We reviewed studies estimating the economic value of crop pest predation services of bats in different agroecosystems worldwide, and we provide new data for these services in subtropical macadamia orchards in South Africa. Approaches for estimating predation services in bats have involved either a bottom-up (modelling) or a top-down (exclusion) approach. Economic models are based on parameters such as bat consumption rates of pest insects and population size, crop yield and current prices, longevity and fecundity of insect pests, losses (injury coefficient) due to insect damage and the costs of chemical pest control. Such studies usually model a single bat species and a single pest insect species, usually the dominant pest in the system. The top-down approach involved exclusion of bats from experimental plots and comparison of pest insect numbers and crop damage and yield in experimental and control plots. Studies involving predator exclusion measure the net trophic effect of all predator and prey species. Estimated values for bat predation services in dollars per hectare varied by orders of magnitude (from zero ha^{-1} pa to $730 ha^{-1} pa) depending on the method of estimation, the agricultural system studied and technological advances such as the use of pest-resistant transgenic strains. We aim to compare for the first time, independent top-down and bottom-up estimates in the same agro-ecosystem. Using a modelling approach, the avoided cost of bats in macadamia orchards in South Africa was conservatively estimated to be $1.9 million (±$1.3 million) per annum nationally, or $102 (±$66.8) per hectare per annum. Bat and bird exclusion trials in progress in macadamia orchards will provide an independent top-down estimate of the economic value of bats; initial analyses after only eight months demonstrate that bats and birds (separately and combined) can suppress insect populations, but that very high variability exists between replicate sites.

Bat species diversity of Liwonde National Park, Malawi with comments on breeding, morphometrics and possible new species for Malawi

Matthew Town, Gareth Jones, Stephen Harris, Emma Stone

Malawi is important for the conservation of bats in Africa (Hudson et al. 2001). Bats represent 30% of mammalian diversity in Malawi, however, little is known about the species in the region. Malawi has the highest deforestation rates in southern Africa (2.4%/yr, UNEP2002). The lack of knowledge of bats in the region limits conservation management. Bat surveys were conducted between September 2014 and 2016, inside and outside Liwonde National park. Three habitats (open mopane, riverine and arable) were surveyed using harp traps and mist nets. Thirty-five sites were sampled over 122 nights for a total of 427 hours. Morphometric and breeding data was supplemented by data gathered from roosts and opportunistic surveys. Captured bats were identified using published papers (Cotterill 2001, Monadjem et al. 2010, Ratcliffe 2002), wing punches and faecal samples collected and morphometric measurements recorded. A total of 1148 bats of up to 38 species were captured and 32 roosts identified within the area. Three species previously not recorded in Malawi, *Scotophilus leucogaster, Mimitellus thomasi* and *Triaenops persicus* have been identified (pending genetic confirmation). The most abundant species in the park appears to be *Scotophilus leucogaster*. High numbers of *Scotophilus viridis* were caught. The reproductive condition and morphometrics of these two species is summarised. A limited amount of measurements and other information gathered regarding the poorly known *Myotis welwitschi, Scotophilus nigrita, Scotoecus hindei/albigula* and *Mimitellus thomasi* are also included for incorporation into the greater database of information on African bats. Our data makes an important contribution towards our knowledge of the bats of Africa. As a result of the country's geographical location between the eastern and southern regions of the continent, data gathered from species in the area augments current distribution maps, facilitating our understanding of patterns of speciation and recognition of environmental factors affecting species distributions.

Bats on the slopes of Mt. Kilimanjaro, Tanzania and their role as seed dispersers

Anna-Valeska Vogeler, Lisa Ehrmantraut, Marco Tschapka

Frugivorous bats fulfill crucial roles as seed dispersers in tropical ecosystems, as they may carry fruits over considerable distances away from the parent tree and occur in all kind of habitats. Therefore, they are important agents of reforestation in disturbed habitats. However, the specific role of pteropodid bats as seed dispersers in Africa is yet unclear, as well as the consequences of the degradation and fragmentation of their natural habitats for the animals. Movements of frugivorous bats along altitudinal and disturbance gradients according to food availability may constitute important processes in fragmented habitats. We examined occurrence of pteropodids in six natural and anthropogenic habitat types (savannah, maize, homegarden, coffee plantation, lower montane forest, riparian strips) at different altitudes along the slopes of Mt. Kilimanjaro, Tanzania and assessed their diet through fecal analysis. We also recorded comprehensive trait data sets of bat and food plant species to investigate changes in interaction and functional diversity along these altitudinal and land-use gradients. The objectives of this study were to identify dispersed plant species and to explore the morphological adaptions of the interacting species. Most seeds recorded in bat faeces came from figs (*Ficus* spp., Moraceae) that are frequently found in riparian strips along stream sites on the slopes of Mt. Kilimanjaro. Riparian habitats play crucial roles as hunting habitats for insectivorous bats, and our data suggest that also the frugivorous pteropodid bats may benefit from these habitats by both an increased availability of food resources and the linear nature of riparian strips that facilitates commuting flight. Riparian strips in the Mt. Kilimanjaro area therefore seem to be not only important foraging areas for all bats but the seed-dispersing fruit bats promote also genetic connectivity between forests and the surrounding habitats such as savannah and anthropogenically deforestated sites.

Bats and pollution: should we still consider in vivo responses in ecotoxicological studies?

Dalene Vosloo, Corrie Schoeman, Sarina Claassens, Samantha Naidoo

Researchers are under increasing pressure not to use mammals, or at least reduce the number of individuals used, in invasive research. Animalivorous bats are considered useful bioindicators of disturbed environments. Specifically, as apex predators, they accumulate pollutants from lower trophic levels and because they are long-lived, they represent an ideal model organism to describe potential pollutant effects in humans.

Research in our laboratories has highlighted the advantages of describing integrated physiological responses of bats to polluted environments. Using tissues sampled from *Neoromicia nana*, an insectivorous bat that often forages at wastewater treatment works (WWTW), our findings include metal accumulation in liver and kidneys, and damage to liver, kidneys and blood cells. High hematocrit, high muscle lactate levels and increased reliance on anaerobic muscle fibers are indicative of tissue hypoxia and energy restriction. This energy restriction does not necessarily result in leaner bats, as glycogen, lipid and protein stores in muscles and liver were maintained, although we found that male WWTW bats had lower body condition and sex hormones than those from reference sites. High mono- and polyunsaturated fatty acids and leptin levels in in the brown adipose tissue of WWTW bats may change the way in which they utilise daily torpor bouts to conserve energy between feedings. Collectively our results indicate that *N. nana* bats are vulnerable to pollutants in their immediate environment, with effects on general maintenance, growth and reproduction. In vivo studies such as these are particularly important in developing countries where people living in settlements downstream from WWTW-polluted environments may be vulnerable to high pollutant levels in their main source of water. We argue that in vivo studies are key in studying mechanisms of toxicity, or in developing biomarkers of pollutant effects.

Forest degradation and fragmentation effects on bats at Kakamega forest, western Kenya

Paul Webala, Jeremiah Mwaura

Habitat loss and fragmentation are serious threats to biodiversity, especially in tropical rainforests, with arguably highest biodiversity, but where deforestation rates are highest. Nonetheless, little is known about such perturbations on biotas. We investigated effects of forest degradation and fragmentation on the relative abundance of bat species and community composition at Kakamega forest, western Kenya, based on captures and bat activity (passes) at two locations (edge and interior) at 36 sites in three forest fragments of differing sizes and fragment characteristics (fragment size, tree density, basal area (DBH) and degree of degradation (indexed as density of stumps, charcoal kilns, footpaths and measure of forest cover). A total of 1296 mist-net hours and 1786 harp-trap hours resulted in the capture of 4983 bats representing 26 species and 8 families. Additionally, 74754 bat passes belonging to 14 insectivorous bat species were recorded using Pettersson bat detectors. For frugivores, habitat use was similar on forest edges of all three forest fragments. However, these fruit bats utilized the interior of the smaller and more open Malava forest fragment more significantly than the less disturbed, more dense and closed Kisere and Main Kakamega forest fragments. In contrast, both captures and bat activity indicated that highly cluttered or narrow space animalivores (presumably “forest specialists”) predominated in the forest interior of the Main Kakamega forest than in the smaller Malava forest. Principal Components analysis (PCA) showed that forest cover explained the occurrence of many forest specialists in the forest interior while frugivores were associated with disturbance indicators. The highly disturbed and open Malava forest fragment, with the least and highest tree and stump density, respectively, favoured species open-space or edge bats. Conversely, specialist species almost exclusively occurred in the less disturbed, larger and closed canopy Main Kakamega forest, and may prove especially vulnerable to forest fragmentation.

Bat species diversity and distribution in a disturbed regime at the Lake Bogoria National Reserve, Kenya

David Wechuli

Human population growth drives encroachment and progressive conversion of natural habitats for agriculture. We evaluated human impacts on bat species diversity and distribution among four vegetation formations in and around Lake Bogoria National Reserve between November, 2012 and July, 2013. Plants were surveyed using the Braun-Blanquet cover-abundance method, whereas bats were sampled using standard mist nets erected on poles at ground level. Floristic similarity analysis revealed two broad vegetation assemblages namely, *Acacia* woodland/*Acacia–Commiphora* woodland and riverine vegetation. Two hundred and thirty-three bats representing eleven genera in seven families were recorded. These were: *Epomophorus minimus, Rhinolophus landeri, Hipposideros caffer, Cardioderma cor, Lavia frons, Nycteris hispida, Chaerephon pumilus, Mops condylurus, Neoromicia capensis, Scotoecus hirundo* and *Scotophilus dinganii*. Species richness estimators indicated that sampling for bats was exhaustive at ground level. Bat species richness and diversity were highest in the more structurally complex *Acacia* woodland compared to the more homogenous farmlands where we recorded only common and generalist species that often occur in open habitats or on forest edges.

The higher bat species richness and diversity in the *Acacia* woodland as compared to farmlands underscores the importance of remnant natural savannah woodlands in the conservation of bats and other elements of biodiversity.

Poster presentations

Dietary composition and resource partitioning among insectivorous bats in central Ghana

Ebenezer Badu, Evans Nkrumah, Peter Vallo, Heather Baldwin, Priscilla Anti, Stefan Klose, Samuel Oppong, Elisabeth Kalko, Christian Drosten, Marco Tschapka

We investigated the level of dietary partitioning of cave roosting insectivorous bats from central Ghana, Africa. Data were collected using mist-nets from five bat caves from July 2011 to May 2012. A total of 1312 faecal pellets were collected from six species: *Hipposideros gigas, Hipposideros abae, Hipposideros* cf. *ruber, Hipposideros jonesi, Coleura afra* and *Nycteris* cf. *thebaica*. Data were analyzed for dietary composition, and relationship of body mass to prey hardness and dietary breadth. Our results indicate the dominance of Lepidoptera, Coleoptera and Orthoptera in the diet of these bats differing significantly in their level of consumption; Lepidoptera (ANOVA, F(5,1306) = 105.316, P < 0.001), Coleoptera (ANOVA, F(5,1306) = 75.595, P < 0.001) and Orthoptera (ANOVA, F(5,1306) = 537.540, P < 0.001. We found that *H. gigas* and *H. abae* primarily fed on Coleoptera (95% and 64.6% by volume respectively) while *H. jonesi* and *H.* cf. *ruber* fed mainly on Lepidoptera (61.7% and 98.1% by volume respectively). *Nycteris* cf. *thebaica* (Nycteridae) consumed mostly Orthoptera (76.6% by volume) whereas Lepidoptera composed 48.9% by volume of the diet of *Coleura afra*. Additionally, we found a significant and strong positive relation between the mean body mass and hardness index of *Hipposideros* bats (rs =1.000, df=2, p < 0.01), and there was no significant relation between mean body mass and dietary breadth (rs = 0.200, df=2, p = 0.80). These two Hipposiderid species *H. gigas* and *H. jonesi* may be considered coleopteran and Lepidoptera specialist respectively for the narrowest dietary breadth.

The role of volatiles in the dispersal of fig seeds (Moraceae) by frugivorous bats in southern Africa

K. Govender, A. Shuttleworth, C. Downs, S. Johnson

Olfaction is a key sense for mammals and it has been shown that fruit-eating bats use olfactory cues during foraging. However, little has been documented about the volatiles used by bats to locate fruits and determine their palatability. Ripe figs (*Ficus* sp.) are an essential source of food for frugivorous bats and they in turn disperse the fig seeds. This study aimed to determine the volatile organic compounds (VOCs) emitted by fig syconia (Moraceae) as they develop from unripe to ripe figs and to determine the responses of bats to these compounds. We found significant changes in VOCs in the scent of unripe and ripe fig fruits across day and night using the dynamic headspace sampling and gas chromatography-mass spectrometry. Spectral analysis also revealed colour changes as figs ripen and analysis using a generic animal colour vision model suggests that bats can perceive these changes. Field-based choice experiments indicated that Wahlberg's Epauletted Fruit Bat (*Epomophorus wahlbergi*) prefer ripe fruits over green ones. These bats also responded to synthetic compounds matching those identified from headspace samples of different fig developmental stages. Determining the responses of fruit-eating bats to the volatiles and colour of fig fruits is important for understanding the evolution of fruit characteristics in *Ficus* and also for understanding the foraging behaviour and seed dispersal role of bats.

Assessment of bats in the Kafa Biosphere Reserve in Ethiopia

Ingrid Kaipf

In the framework of the project 'Biodiversity under Climate Change: Community-Based Conservation, Management and Development Concepts for the Wild Coffee Forests' implemented by The Nature and Biodiversity Conservation Union (NABU) and supported by the International Climate Initiative of the German Federal Ministry for the Environment, Nature Conservation, Building and Nuclear Safety (BMUB), an International Biodiversity Assessment at the Kafa Biosphere Reserve/Ethiopia has been conducted. A team of almost 30 German and Ethiopian experts undertook intense fieldwork for 2 weeks in December 2014. The overall goal of the assessment was to specify and verify flora and fauna assessments, which formerly have been done at the Kafa region. The data and experts' recommendation on indicator species will be use for the development of a biodiversity monitoring for Kafa Biosphere Reserve. In our bat study, we registered by capture or sound recordings 29 bat and four fruit-bat species. We got new records of five bat and one fruit-bat species for Kafa Biosphere Reserve. We also recorded by echolocation calls a new species of the Horseshoe bat family for Ethiopia. Our results assume that it will be necessary to develop an old tree management and cave protecting concept for the Biosphere Reserve to conserve bat roots.

AfricanBats: resources and training being provided to enhance conservation of African bats

Teresa Kearney, Victor Van Cakenberghe, Mark Keith, Leon Labuschagne, Kwaku Acheampong, Ernest Seamark

AfricanBats aims to conserve Africa's bat biodiversity through education, capacity building, research and management. The organization was registered in South Africa as a Not-For-Profit company in 2012, and as a Public Benefit Organization and Non-Profit Organization in 2015. These formal registrations legitimize the aims of AfricanBats and provide the legal framework for the acquisition of funding and assets to support its work. For the past two years the Rufford Foundation has provided much of the support to AfricanBats. Both the African Bat Conservation News (ABCN) (ISSN 1812-1268), which started in 2004, and the African Chiroptera Report (ACR) (ISSN 1990-6471), which was first released in 2006, have been incorporated into AfricanBats. These freely available, online resources are accessible via the AfricanBats webpage www.africanbats.org. ABCN is a forum for observations, notes, ideas and discussions on conservation of African bats that is published quarterly. The ACR is currently updated and released annually, and collates published information on African bats in relation to updated classifications, and species distributions drawn from a database of 114,434 specimen records. Although a relatively new organization AfricanBats is making noticeable contributions to education and capacity building. Since 2012, AfricanBats has given nine introductory courses on bats to 42 participants from tertiary institutions and conservation and health related government agencies. An annual bat fieldworkers course was started in 2014, which to date has trained seven post-graduates from Kenya, Namibia, South Africa, and Swaziland, in best practice field techniques associated with bat field work. Graduates of this training are now being incorporated into a mentorship program associated with the capacity training. This not only allows for additional skills development, but also increases the reach of suitably skilled bat fieldworkers in Africa. For the second year running two more students will be base with AfricanBats as part of the DST/NRF internship programme.

How bat and bird communities affect insect damage of macadamia trees

Valerie Linden

Bats and birds provide ecosystem services that can be of major economic importance in agricultural systems. By consuming a great amount of pest insect species they potentially decrease the damage to crops and thereby increase the harvest and crop quality. To prove the potential economic value of bats and birds, I am using exclusion experiments to compare the effect of the absence of them in a paired design. The study is being conducted on Macadamia trees in northern South Africa. Four different treatments (with 6 replicates) are being applied, a full exclosure, which is closed 24h, excluding birds and bats during day and night, a night and a day exclosure, that are being opened/closed in the mornings and evenings, excluding either bats or birds respectively and a control treatment, which is an empty cage, allowing birds and bats to enter at all times. Two sets of all four exclusion treatments are placed on six different farms, one set in the direct vicinity of natural vegetation and another one inside the orchard or next to a road. A total number of 96 trees are being sampled. Insect, bird and bat abundance is being monitored over two years. The exclusion experiments are running since September 2015. The main response variable is the nut quality which will be examined per treatment at the end of each harvesting season (April/May). The nut quality is expected to be lower for those trees where bats and/or birds were excluded, compared to those trees where they had access to. The effect of treatments is expected to be higher for those trees close to natural vegetation. The data from the first couple of months already show a significantly lower arthropod abundance in the control treatments and higher variances between the treatments at the exclosure sets next to natural vegetation

Your mother is always with you. Retrieving bat pups fallen on the ground

Marco Riccucci

After birth, the falling of pups to the ground is an occasional but not uncommon event. Retrieval of the offspring by the mother is probably more usual than it appears from the evidence available so far. It seems that some species always attempt this operation while others tend to abandon the fallen pups. Knowledge on this particular behavior is still limited, therefore the data displayed here are subject to substantial additions and changes. In Vienna (Austria), where there are as many as 22 species of bats, the retrieval of pups is not a common practice, especially for *Hypsugo savii*, probably due to the height and density of buildings. Also two Lasiurini (*Lasiurus borealis* and *Lasiurus cinereus)* are not able to do this, due to an intrinsic weight problem: both species have multiple births and if pups fall to the ground recovery is therefore problematic. When pups fall from the roost it immediately starts squeaking an audible distress call to get the attention of their mothers. They are generally retrieved in a short time or the following night but there are cases when the recovery process takes place up to three nights later.

These species are used to retrieve their offsprings fallen to the ground: P: Pteropodidae; Ph: Phyllostomidae; V: Vespertilionidae; Mi: Miniopteridae; M: Molossidae *Chaerephon pumilus*, M *Corynorhinus rafinesquii,* V *Epomophorus wahlbergi,* P *Eptesicus fuscus,* V *Eptesicus serotinus,* V *Miniopterus schreibersii,* Mi *Mops condylurus,* M *Myotis myotis,* V *Myotis nattereri,*V *Myotis lucifugus,* V *Myotis sodalis,* V *Myotis thysanodes,* V *Myotis yumanensis,* V *Neoromicia capensis,*V *Nycticeius humeralis,* V *Phyllostomus hastatus,* Ph *Pipistrellus kuhlii,* V *Pipistrellus nathusii,*V *Pipistrellus pipistrellus,* V*; Pipistrellus pygmaeus,* V *Plecotus auritus,* V *Scotophilus dinganii,* V *Tadarida brasiliensis,* M.

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

Leigh Richards, Peter Taylor, Ara Monadjem

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) provide possible lineage-specific cranial characters to aid in taxonomic diagnoses of the recently described genetic lineages within the complex, and b) 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 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.

The bats of the Congo and of Rwanda and Burundi revisited

Victor Van Cakenberghe, Prescott Musaba, Guy-Crispin Gembu, Erik Verheyen, **Ernest Seamark**

In 1966, Robert William Hayman, Xavier Misonne and Walter Verheyen published their listing of the Congolese, Rwandan and Burundian bat specimens in the collections in the museums of Tervueren, Brussels, London, Geneva, and New York (Hayman et al., 1966). In the fifty years that have passed since, some major changes have been introduced in the taxonomy of the Chiroptera: new species have been discovered, (cryptic) species have been split off, species have been moved to other genera. Furthermore, additional material has been collected (or was already present in collections that were not available to the authors at the time). For the current project, we re-evaluated the data presented by Hayman et al., and supplemented this with specimen records found in the literature and in online catalogs. All references to the original publication have been tracked. When available, we also recorded additional information such as locality, sex and age, collector, collection date and preservation type of the voucher specimen. The distribution maps of the Congolese taxa are revised to represent the current taxonomy. These distribution maps are presented in perspective against the global distribution of the taxon. An updated gazetteer is also compiled where historical locality names and coordinates are checked, corrected if needed, and standardized. The assignment of the localities has been modified to link them to the current provinces. An updated key to the various taxa is presented, to aid future work on the Chiroptera of the Democratic Republic of the Congo, Rwanda and Burundi.

Humoral immune response of *Rousettus aegyptiacus* to the glycoprotein, nucleoprotein and structural proteins of Marburg virus

Nadia Storm, Petrus Jansen van Vuren, Wanda Markotter, Janusz Paweska

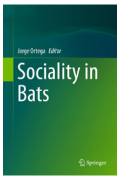
Marburg virus (MARV) is a filovirus that causes severe haemorrhagic fever in humans and non-human primates. Antibodies play a significant role in protection against lethal MARV disease. Characterising the humoral immune response of a natural reservoir host may provide insights into which antibodies may be important for protection of humans against MARV infection, as well as which proteins may be important to target for diagnosis and surveillance studies. The *Rousettus aegyptiacus* fruit bat has been identified as a reservoir host for MARV, however, little is known about the serological responses elicited by this host in response to MARV infection. The aim of this study was therefore to determine the specific serological responses of experimentally MARV infected *Rousettus aegyptiacus* to the glycoprotein, nucleoprotein and viral structural proteins using enzyme-linked immunosorbent assays based on recombinant MARV proteins. Results showed that the greatest immune response was directed against the glycoprotein and nucleoprotein. However, in the experimentally infected bats, antibodies against the glycoprotein of MARV waned after peaking at 12 days post-infection, while antibodies against the nucleoprotein was more pronounced and reached a plateau between days 12 and 42 post-infection. This implies that the nucleoprotein might be more important than the glycoprotein in conferring protection against MARV disease in *Rousettus aegyptiacus,* and that serological assays based on the nucleoprotein should be included for surveillance studies in these bats.

Changes of bat species composition over altitudinal gradients on northern and southern aspects of the Soutpansberg mountain range, South Africa

Sina Weier

In order to gain insight into the pattern of bat species composition over altitude and the environmental variables driving the observed pattern, we compared data from moist southern and drier northern aspects of the Soutpansberg range in northern South Africa. Acoustical monitoring and additional capturing of bats was used for analysis of species distribution patterns and comparisons of community composition. Bat activity generally followed a linear decline with increasing altitude, possibly related to reproductive females preferring lower altitudes. Species richness followed a hump-shaped distribution on the northern aspect and across the transect, whereas a pattern of a linear decline was observed on the southern aspect. Our study strongly supports a previously published climate model for insectivorous bats which assumes that water availability linked with temperature determines the shape of altitudinal distribution in bat species. Step-wise selection from multiple regression models retained habitat type and/or measures of habitat structure in all final models, supporting several other studies in that vegetation correlated to altitude is a primary determinant of bat species distribution over altitude. This study also supports that the Soutpansberg is a biodiversity hotspot for bats and emphasises that conservation efforts should by no means ignore the lower altitudes.

Books



Sociality in bats

Ortega, J. (Ed). 2016. *Sociality in bats*. Cham: Springer International Publishing. 301 pp.

This book provides new insights into the social behavior of bats - one of the most fascinating topics currently being pursued by researchers. After an introduction reviewing the history of research in bat behavioral ecology, it covers three major themes: bat sociality *per se* (Part I), bat communication (Part II), and ecological aspects (Part III). Part I offers a concise overview of the social organization and systems of bats, introducing readers to the complexity and dynamics of group structures. Part II is devoted to the innovative field of social communication, focusing on bat songs, dialects and calls. Part III discusses the influence of the environment on bat behavior, particularly with regard to roosting and foraging. This book addresses the needs of researchers working in behavioral sciences, evolution and ecology.

Chapters

Bradbury, J. W. 2016. Introduction. pp. 1–7. doi: 10.1007/978-3-319-38953-0_1.

Compared with other taxa such as primates or songbirds, studies of bat social behavior and communication are a relatively recent development. Despite this late start, bats now constitute some of the key tests of general theories in behavioral ecology. Here, I briefly review some of the history of research in bat behavioral ecology, and hopefully set the scene for the exciting new extensions presented in this volume.

Furmankiewicz, J. 2016. The social organization and behavior of the Brown Long-Eared Bat *Plecotus auritus*. pp. 11–46. doi: 10.1007/978-3-319-38953-0_2.

The complexity of the social behavior and social organization of bats arises from the philopatry of females, stable group composition, and hence cooperation with colony members, which in turn influences the mating system of particular species. Understanding the relationship between social organization and mating system is crucial for understanding the behavior of animals. I have studied the social organization and social and mating behavior of a temperate zone species of bat, the brown long-eared bat *Plecotus auritus*, for over 13 years in SW Poland using genetic and behavioral methods. The obtained results enable me to complete and explain the pattern of social organization and mating behavior in this species. *P. auritus* lives in small, stable, and isolated maternity colonies (usually up to 40–50 individuals, including adult resident males) and swarms in underground hibernacula during autumn and spring. Members of the colony use low frequency contact calls when they emerge and return to the roosts and during dawn swarming. The peak of this vocal activity falls between July and September and in the morning. Around 28–38 % of colony members emerge or return in pairs, or sometimes in groups of 3–4 individuals emitting social calls. Before leaving the roost, and after arrival, 10–16 % of bat activity involves tandem flights. This behavior may play a role in the maintenance of social bonds between mates in the roost. Some members of the maternity colonies and solitary males frequently travel to the underground hibernacula from day roosts as far away as 31.5 km every autumn and spring to swarm with bats from other colonies. Swarming populations are large and may gather up to several hundred individuals from several colonies. Swarming bats usually stay in swarming sites for several hours before returning to a day roost, vocalizing and intensively flying, sometimes in groups of 2 or more individuals. Colonies and groups of swarming bats show high gene diversities and low inbreeding coefficients, and they are not genetically isolated by distance, which suggests high gene flow between sites and the mating function of autumn and spring swarming. Therefore, inbreeding is avoided in these philopatric and spatially isolated colonies by swarming behavior and mating in hibernacula in the autumn and spring. This work indicates that *P. auritus* appears to be unusual among European temperate zone bat species in its maternity colony composition and stability (resident females accompanied by resident males), biphasic swarming season (in autumn and spring), and distinctive vocal activity in swarming sites and maternity colonies. The social structure and behavior of *P. auritus* is complex and suggests the existence of close and stable society-like groups in this species.

Nagy, M. and Knörnschild, M. 2016. Sex-biased dispersal and social systems of Neotropical Emballonurids. pp. 47–63. doi: 10.1007/978-3-319-38953-0_3.

The most common pattern of sex-biased dispersal in mammals including temperate bats is that females remain philopatric and males disperse from their natal groups. In contrast, sex-biased dispersal patterns in tropical bat species appear much more variable, ranging from all-offspring dispersal to female-biased dispersal and male-biased dispersal. The identity of the philopatric sex is essential for the kin structure of social groups (i.e. matrilineal relatives in species with female philopatry and patrilineal relatives in species with male philopatry) and thus for the evolution of social behavior. This book chapter contrasts sex-biased dispersal and the social systems of three well-studied Neotropical bat species of the family Emballonuridae. Two of these Neotropical Emballonurids exhibit exceptional female-biased dispersal and male philopatry in combination with resource-defense polygyny (greater sac-winged bat *Saccopteryx bilineata*) or female-defense polygyny (proboscis bat *Rhynchonycteris naso*). However, in the gray sac-winged bat (*Balantiopteryx plicata*) females are the more philopatric sex and the social system involves some sort of sexual segregation with mating probably taking place at male mating aggregations. To conclude, we discuss the evolutionary pressures driving the observed dispersal patterns and how sexual selection in Neotropical Emballonurids with male philopatry might shape bat sociality.

Patriquin, K. J. and Ratcliffe, J. M. 2016. Should I stay or should I go? Fission–Fusion dynamics in bats. pp. 65–103. doi: 10.1007/978-3-319-38953-0_4.

Animal species with fission–fusion dynamics are characterized by variable group size and composition, as individuals move freely among a social network. Patterns consistent with fission–fusion dynamics appear to be widespread in bats and interest in these patterns has advanced our general understanding of proximate and ultimate explanations for fission–fusion dynamics. Here, we explore the following questions: (1) Why do bats switch roosts? (2) Why do not group members move together? (3) Do bats form social bonds despite frequent roost switching? (4) If group members do form social relationships, what shapes these relationships? (5) How are social relationships maintained in these dynamic systems? (6) What does our understanding about fission–fusion in bats tell us about the evolution of fission–fusion dynamics in general? In our review, we show that bats switch roosts for a combination of reasons, including to reduce predation, parasites, and disease, and to minimize commutes. The strongest evidence, however, suggests bats switch roosts to seek more suitable roosts when roost quality changes. However, the degree to which each of these factors influences roost switching varies between individuals, across species, and depends on preferred roost type and roost availability. Group members may not move together because they experience different perceived costs and benefits of remaining in a group. Bats apparently use a combination of spatial and sensory information to relocate group members and maintain social bonds. Bat populations with fission–fusion dynamics likely benefit from social thermoregulation, and share information about roosts and foraging sites. Although our understanding of these dynamics has improved in recent years, many questions remain. For instance, a better understanding of the proximate factors driving fission–fusion dynamics is required. Establishing the levels at which bats sharing the same roost interact, together with network analyses, would also advance our understanding of relationships within these dynamic groups. Together, answers to these and other questions will help us to better manage bat populations and their habitat.

Webber, Q. M. R. and Willis, C. K. R. 2016. Sociality, parasites, and pathogens in bats. pp. 105–139. doi: 10.1007/978-3-319-38953-0_5.

Little is known about the ecology of many of the parasites and pathogens affecting bats, but host social behavior almost certainly plays an important role in bat-parasite dynamics. Understanding parasite dynamics for bats is important from a human public health perspective because of their role as natural reservoirs for recent high-profile emerging zoonotic pathogens (e.g. Ebola, Hendra) and from a bat conservation perspective because of the recent emergence of white-nose syndrome (WNS) in North America highlighting the potential population impacts of parasites and pathogens. Although some bat species are among the most gregarious of mammals, species vary widely in terms of their social behavior and this variation could influence pathogen transmission and impacts. Here, we review the literature on links between bat social behavior and parasite dynamics. Using standardized search terms in Web of Science, we identified articles that explicitly tested or discussed links between some aspect of bat sociality and parasite transmission or host population impacts. We identified social network analysis, epidemiological modeling, and interspecific comparative analyses as the most commonly used methods to quantify relationships between social behavior and parasite-risk in bats while WNS, Hendra virus, and arthropod ectoparasites were the most commonly studied host-parasite systems. We summarize known host-parasite relationships in these three systems and propose testable hypotheses that could improve our understanding of links between host sociality and parasite-dynamics in bats.

Bohn, K., Montiel-Reyes, F. and Salazar, I. 2016. The complex songs of two molossid species. pp. 143–160. doi: 10.1007/978-3-319-38953-0_6.

Birds are well known for songs while bats are well known for their developed sonar system. The chiropteran echolocation system has a long and extensive history of research because of the highly specialized neurocircuitry required for vocal production, perception, and vocal-motor integration. However, recent research has revealed that in addition to echolocation, bats produce highly sophisticated social vocalizations whose complexity is only rivaled by birds, humans, and cetaceans. In this chapter we discuss and define the terms “song” and “courtship call”, outline how acoustic signals are analyzed, and review what families of bats produce songs and calls. We then compare behavior, song structure, individual variation, and regional dialects in two species of Molossids, *Tadarida brasiliensis* and *Nyctinomops laticaudatus*. *T. brasiliensis* is a bat that sings like a bird—they produce songs with three key songbird features: hierarchical structure, syntactical organization, and syntactical flexibility. *T. brasiliensis* songs are composed of four main syllable types: chirp A (“A”), chirp B (“B”), trill and buzz. Syllables are combined to form three phrases, chirp, trill, and buzz and phrases are then combined to form songs (hierarchical structure). Specific syntactical rules are followed for combining phrases (syntactical organization). However, the number of syllables within a phrase and the number and order of phrases vary from one rendition to the next (syntactical flexibility). *N. laticaudatus* produce the same types of syllables and phrases as *T. brasiliensis*. However, the spectro-temporal structure of A and B syllables of *N. laticaudatus* are quite different, and they show much lower syntactical flexibility in combining phrases. Finally, while *T. brasiliensis* males produce highly stereotyped chirp syllables that do not vary between regions, *N. laticaudatus* chirp syllables are not stereotyped within males but do vary across regions. These findings are the first to show that complex songs are not only produced by a single bat species and that many aspects of songs are highly conserved across species.

Chaverri, G. and Gillam, E. H. 2016. Acoustic communication and group cohesion in Spix’s Disc-winged bats. pp. 161–178. doi: 10.1007/978-3-319-38953-0_7.

Acoustic communication is an especially important means by which social and highly mobile organisms, such as bats, locate group members. Contact calls are known to be used by many species of bats, including those that use permanent roosting structures; these roosts may facilitate group cohesion because individuals can rely on spatial memory and fidelity to a roosting location to relocate group members. However, the Neotropical insectivorous bat *Thyroptera tricolor* is known to form extremely cohesive social aggregations despite moving daily between roost-sites. This species uses developing tubular leaves of plants such as *Heliconia* species that unfurl in a few hours, rendering them unsuitable in less than 24 h. Our research shows that *T. tricolor* uses a combination of two social signals, “inquiry” and “response” calls, to locate each other during flight and while roosting. Individuals may recognize, and be able to preferentially associate with, group members due to strong individual signatures in these two types of calls; group cohesion may be further facilitated by recognition based on spatial location, as this species uses small roosting home ranges and exhibits extreme philopatry to the natal territory. Coupling spatial memory with acoustic communication may be an especially effective mechanism of recognition in this system, as tubular roosts cause significant distortion of acoustic signals used during contact calling. The tubular leaves, however, also provide a significant increase in signal amplitude that may allow bats to locate each other over longer distances. Our work with *T. tricolor* not only highlights the important role that social calls play in maintaining cohesive groups in highly mobile species, but the role that roosting structures may play in facilitating sociality in bats.

Knörnschild, M., Eckenweber M., Fernandez, A. A. and Nagy, M. 2016. Sexually selected vocalizations of neotropical bats. pp. 179–195. doi: 10.1007/978-3-319-38953-0_8.

Acoustic signals are by far the best studied component of bats’ social communication. Various different vocalization types cover diverse social interactions, which are either under natural selection pressures, such as mother–pup recognition and group cohesion, or under sexual selection pressures, such as male–male aggression, territoriality, and courtship. Here, we summarize the current knowledge about sexually selected vocalizations in Neotropical bats. Specifically, we highlight research findings on sexually selected vocalizations in two species whose social organization and natural history are well understood, namely Seba’s Short-tailed Bat *Carollia perspicillata* (Phyllostomidae) and the Greater Sac-winged Bat *Saccopteryx bilineata* (Emballonuridae). Males of both species exhibit resource-defense polygyny and use distinct vocalizations during aggressive male–male interactions and to announce territory ownership. While territorial vocalizations are structurally more complex in *S. bilineata* than in *C. perspicillata*, the latter species uses a more sophisticated, ritualized suite of behavioral displays to mediate male–male aggression than *S. bilineata*. Moreover, males of both species exhibit acoustic courtship which displays with differing degrees of complexity. In *S. bilineata*, courtship vocalizations are long and elaborate, while courtship vocalizations of *C. perspicillata* are comparatively simpler, with one variable syllable repeated in succession. As a synopsis, we discuss whether differences in social organization and behavioral interactions may have implications for the structural complexity and information content of sexually selected vocalizations.

Smotherman, M., Bohn, K., Davis, K., Rogers, K. and Schwartz, C. P. 2016. Daily and seasonal patterns of singing by the Mexican Free-Tailed Bat, *Tadarida brasiliensis*. pp. 197–209. doi: 10.1007/978-3-319-38953-0_9.

Singing is a specialized vocal behavior that supports courtship and territoriality but costs energy and time. Singing behaviors are well documented in the Mexican free-tailed bat, *Tadarida brasiliensis*, but many important questions about the functional significance of singing in this species remain unanswered. To better understand how singing benefits this species we analyzed daily and seasonal temporal patterns of singing in both a natural and a captive colony for extended periods of time and measured the average call and song rates over the course of seven days and over one entire year. Analyses revealed that under natural conditions singing was most prevalent at onset of the spring and fall migration periods but also continued at a less frequent rate throughout the summer months. Singing rates were highest during the spring mating season, but singing also continued through the summer months in exclusively male colonies. In a natural roost, males sang the most just before sunrise, but also sang prolifically just after sunset and sporadically throughout the night. This pattern suggested that singing patterns were driven by the activity of conspecifics leaving and returning to the roost, and also indicated that singers may spend less time foraging than their roost-mates. We tested this by measuring movements and singing patterns in a captive colony, where roost-mates were confined to flying around the vivarium at night. Under these conditions captive bats sang continuously at high rates throughout the night. We propose that singing by *T. brasiliensis* evolved initially to facilitate migration by facilitating more rapid localization of roosts by bats passing through novel territories, particularly just before sunrise. Singers sacrifice foraging time but may gain a reproductive advantage by attracting more bats to their roost during the spring mating season, which may explain why males but not females of this species sing.

Wright, G. S. 2016. Social learning and information transfer in bats: Conspecific influence regarding roosts, calls, and food. pp. 211–230. doi: 10.1007/978-3-319-38953-0_10.

Using social information can be an efficient way to respond to changing situations or learn skills. Most bat species (Order Chiroptera) are gregarious and could theoretically benefit from socially obtained information about food or roosts. Many bats experience opportunities for social learning, and recent years have seen a variety of studies addressing this phenomenon in the Chiroptera. Because bats are aerial, small, nocturnal, and emit calls outside the range of human hearing, they are notoriously difficult to study, and distinguishing between individuals when multiple bats are present can be especially challenging. Recent advances in technology, including high-quality synchronized video and audio recordings, and the use of passive integrated transponder (PIT) tags and radio-tracking, have allowed for detailed information to be obtained about individuals in multi-bat settings. Recent studies have shown that bats can learn from one another about food type, food location, and other food-related cues. In addition, social information can play a role in roost site selection and the acquisition and modification of vocalizations. Here, I review recent research documenting vocal learning in bats, as well as interactions between individuals in foraging and roosting contexts and the impact of these interactions on bats’ behavior and success. I also report on novel findings wherein individuals of a frugivorous bat species display decreased foraging success in the presence of other naïve individuals and discuss possible reasons for this result. Finally, future directions for research on social learning in bats, which could employ such technologies as thermal imaging cameras, GPS tracking, and on-board microphones, are discussed.

Fishman, M. S. 2016. Indiana Bat (*Myotis sodalis*) day roost selection in the southeastern Ontario Lake Plain of New York State. pp. 233–245. doi: 10.1007/978-3-319-38953-0_11.

Available habitat for the endangered Indiana bat (*Myotis sodalis*) varies widely across the species’ broad range and the species’ degree of habitat use specificity is not known; therefore, it is necessary to characterize the species’ habitat use patterns regionally to provide suitable guidelines for wildlife managers to conserve the species throughout its range. Understanding day roost characteristics is particularly important because habitat suitability for Indiana bats is thought to be based on the availability of suitable day roost structures. Despite having been extensively studied at the core of their range, few studies of Indiana bat day roost characteristics have been published from the northeast periphery of the species’ range, and no studies have been published from central New York State, where populations have been in steep decline due to White-Nose Syndrome since 2006. I studied day roosts of 20 female and 7 male Indiana bats in the Ontario Lake Plain northwest of Syracuse, New York, USA during the spring of 2006 and summers of 2007 and 2008 and identified 96 individual Indiana bat roost trees. Indiana bats roosted in 10 species of trees, of which *Carya ovata*, *Acer* spp., and *Ulmus americana* were most frequent. The mean diameter of roost trees was 41.55 ± 7.53 cm, which was similar to roost trees in other regions, but larger than the mean diameter of available trees in the same stands used by roosting Indiana bats. Male and female bats used similarly sized trees. I conclude that size of roost trees in central New York are similar to those throughout the Indiana bat's range, that the most frequently selected tree species differ regionally, and that patterns of male versus female roost selection varies regionally. This study provides regionally specific quantitative and qualitative metrics by which managers can identify potential Indiana bat habitat for land use planning and conservation.

Sagot, M. 2016. Effects of range, habitat and roosting ecology in patterns of group association in bats. pp. 247–259. doi: 10.1007/978-3-319-38953-0_12.

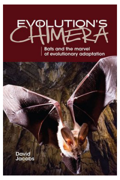
There is a wide variety of ecological factors that can potentially act as selective pressures driving the evolution of social behavior in bats. For instance, many behavioral ecologists recognize a relationship between social behavior, geographic distribution, and variation in resource abundance and distribution. Moreover, some bat species can use preexisting roosts such as tree cavities and caves, while others are able to modify nests, burrows, or foliage to create their own shelters. Thus, it is not surprising that the diverse social interactions found in bats have also been attributed to lifespan, availability, and distribution of roost sites. Here, I aim to determine if roost lifespan, number of roosts used and/or range size are important determinants of group stability. I conducted a literature review to collect information on group stability, roost lifespan, number or roosts used and range size, and I tested for correlated evolution between these variables. I found that roost lifespan, number of roosts and range size did not predict group stability. However, there was an association between range size and number of roosts used. Species with wider ranges encounter diverse habitats, environmental conditions, and roost types with different lifespans. Thus, it is not surprising that bats modify their social structure to adapt to these specific local conditions. Studying how different ecological characteristics interact to produce differences in group stability, provide the basis for understanding the complex route to sociality.

Silvis, A., Abaid, N., Ford, W. M. and Britzke, E. R. 2016. Responses of bat social groups to roost loss: More questions than answers. pp. 261–280. doi: 10.1007/978-3-319-38953-0_13.

Though characterization of, and understanding determinants of, social structure in bats is increasing, little is known about how bat social groups respond to disturbance resulting in roost loss. Given that many species of bats roost in ephemeral or transitory resources such as plants, it is clear that bat social groups can tolerate some level of roost loss. Understanding responses of bat social groups to roost loss can provide insight into social structure that have applied conservation use. Herein, we review the existing literature on the effects of disturbance on bat social groups, and present a parameterizable agent-based model that can be used to explore the relationships among roost dynamics, population dynamics, and social behavior.

Villalobos-Chaves, D., Bonaccorso, F. J., Rodríguez-Herrera, B., Cordero-Schmidt, E., Arias-Aguilar, A. and Todd, C. M. 2016. The influence of sex and reproductive status on foraging behavior and seed dispersal by *Uroderma convexum* (Chiroptera: Phyllostomidae). pp. 281–301. doi: 10.1007/978-3-319-38953-0_14.

Uroderma convexum construct and occupy tents. Tents serve as day shelters and reproductive sites, but also frequently are used as night feeding roosts. We observed and radio-tagged *U. convexum* occupying tents at Sarapiquí, Costa Rica. Social groups of *U. convexum* were composed of one adult male, reproductive females, and immature bats apparently forming a polygynous harem organization. We report spatial information (core-use, foraging range, habitat coverage use) and seed dispersal behavior for seven radio-tagged bats. Bats spend much of their foraging time in the riparian habitats; however, they also forage in mature and secondary forest and several anthropogenic habitats, dispersing at least eleven species of plants of different life forms. Bats establish night feeding roosts up to 1800 m from their day roost. Feeding roosts are in foliage close to plants producing ripe fruits and both feeding roosts and resource plants vary in space over time. Most of the time, adult males restrict movements to fruiting plants within 100 m of their tents and frequently return within the foraging period of the night, thus males disperse a large proportion of the seeds they handle exclusively within perturbed areas associated with the tents. In contrast to males, adult females usually do not return to a tent until near dawn and move over greater distances, frequently dispersing seeds into multiple habitats. Social organization, sex, and reproductive status appear to influence the outcomes of foraging behavior and seed dispersal of the bats.



Evolution's Chimera: Bats and the marvel of evolutionary adaptation

Jacobs, D. 2016. *Evolution's Chimera: Bats and the marvel of evolutionary adaptation*. University of Cape Town Press. 154 pp. Available at - https://juta.co.za/products/evolutions-chimera.

In Greek mythology, the chimera was a hybrid monster. Similarly, bats look like they have the body of a mouse, the face of a gargoyle or fox, and the wings of a pterosaur, giving rise to this book's title. *Evolution's Chimera* describes the amazing physical and behavioural adaptations of bats, using them to illustrate the processes of natural evolution.

Bats comprise a quarter of all mammals in the world and are the only mammals that can fly. They occupy every landmass and almost every habitat on Earth. They make up the second-most diverse group of mammals on the planet, numbering more than 1 270 species. And they are among the oldest mammals. They are therefore ideal for the study of how evolution generates biological diversity.

Papers

Cooper-Bohannon, R., Rebelo, H., Jones, G., Cotterill, F. (W.), Monadjem, A., Schoeman, M. C., Taylor, P. and Park, K. 2016. Predicting bat distributions and diversity hotspots in southern Africa. *Hystrix, Italian Journal of Mammalogy, 27 (1)*: 1–11. doi: 10.4404/hystrix-27.1-11722.

Species distribution models were used to predict bat species richness across southern Africa and to identify potential drivers of these spatial patterns. We also identified species richness within each biotic zone and the distributions of species considered of high conservation priority. We used this information to highlight conservation priorities for bats in southern Africa (defined here as between the latitudes of 8° S, slightly north of Zambia, to the southern tip of Africa 34° S, an area of approximately 9781840 km^2). We used maximum entropy modelling (Maxent) to model habitat suitability for 58 bat species in order to determine the key eco-geographical variables influencing their distributions. The potential distribution of each bat species was affected by different ecogeographic variables but in general, water availability (both temporary and permanent), seasonal precipitation, vegetation, and karst (caves/limestone) areas were the most important factors. The highest levels of species richness were found mainly in the eastern dry savanna area and some areas of wet savanna. Of the species considered to be of high priority due to a combination of restricted distributions or niches and/or endemism (7 fruit bats, 23 cave-dwellers, 18 endemic and near-endemic, 14 niche-restricted and 15 range-restricted), nine species were considered to be at most risk. We found that range-restricted species were commonly found in areas with low species richness; therefore, conservation decisions need to take into account not only species richness but also species considered to be particularly vulnerable across the biogeographical area of interest.

Dalhoumi, R., Aissa, P. and Aulagnier, S. 2016. Bat species richness and activity in the Bou Hedma National Park (central Tunisia). *Turkish Journal of Zoology* 40: 1–13. doi: 10.3906/zoo-1505-46.

In order to investigate the likely contact of the Mediterranean and Saharan faunas, we surveyed bats in six different habitats of Bou Hedma National Park for 1 year. We sampled bats monthly by mist-netting and echolocation call detection at two basins, Bordj and Nouh, the Bou Hedma wadi, and open and dense acacia forest and steppe. We identified 13 species, among which *Pipistrellus kuhlii*, *Eptesicus isabellinus*, and *Miniopterus schreibersi* were the most abundant and frequent, followed by *Tadarida teniotis*, *Plecotus gaisleri*, and two Saharan species, *Rhinopoma cystops* and *Otonycteris hemprichii*. We also rarely recorded four rhinolophids: *Rhinolophus euryale*, *R. ferrumequinum*, *R. hipposideros*, and *R. mehelyi*. Bat activity was recorded throughout the year in the six habitats, water bodies being more attractive than dry habitats for both Mediterranean and Saharan taxa. The wadi was the preferred habitat of *R. cystops*, *T. teniotis*, and *O. hemprichii*. The open acacia forest was attractive only during the flowering season. Species richness and bat activity peaked in late spring and reached the lowest values, but was still present, during winter.

Dalhoumi, R., Aissa, P. and Aulagnier, S. 2016. Seasonal variations of sexual size dimorphism in two Mediterranean bat species from Tunisia: the Kuhl's pipistrelle (*Pipistrellus kuhlii*) and the Isabelline serotine (*Eptesicus isabellinus*). *Folia Zoologica* 65(2): 157–163.

Body mass variations of *Pipistrellus kuhlii* and *Eptesicus isabellinus* were studied in the Bou Hedma National Park (central Tunisia) from June 2010 to June 2011. In both species, adult females were significantly heavier than males throughout the year. Seasonal variations were larger in adult females, body mass peaking during late pregnancy. After a secondary peak in September-October observed in both sexes in *E. isabellinus*, in males only in *P. kuhlii*, body mass reached a minimum value in winter when activity is low. Significant differences were also noticed between years in June for both species. Such pattern of seasonal variations of sexual size dimorphism is typical of hibernating vespertilionids.

Djilali, K., Sekour, M., Souttou, K., Ababsa, L., Guezoul, O., Denys, C. and Doumandji, S. 2016. Diet of Short-eared Owl *Asio flammeus* (Pontoppidan, 1763) in desert area at Hassi El Gara (El Golea, Algeria). *Zoology and Ecology* 26(3): 159–165. doi: 10.1080/21658005.2016.1184907.

The diet of the Short-eared Owl *Asio flammeus* was analysed in an arid environment in Hassi El Gara located in the southeast of El Golea (Ghardaia, Algeria). The diet was determined by analysing 138 pellets. Our data showed that the diet was dominated by mammals (Chiroptera and Rodentia). Based on relative biomass, birds were the main prey species. Mammals were the second most important prey. Mammals were the major food item throughout the seasons and their contribution to the diet ranged from 50.7 % in spring to 73.6 % in summer. Birds were the second numerous prey with 8.1 % in summer and 29.6 % in spring. The dominant prey species was *Myotis* sp., making up 37.8 %. It was followed by *Gerbillus nanus* (5.4 %), *Columba livia* (4.3 %) and *Bufo mauritanicus* (4.1 %).

Guernier, V., Lagadec, E., Cordonin, C., Le Minter, G., Gomard, Y., Pagès, F., Jaffar-Bandjee, M-C., Michault, A., Tortosa, P. and Dellagi, K. 2016. Human Leptospirosis on Reunion Island, Indian Ocean: Are Rodents the (Only) Ones to Blame? *PLOS Neglected Tropical Diseases* 10(6): e0004733. doi: 10.1371/journal.pntd.0004733.

Background Although leptospirosis is a zoonosis of major concern on tropical islands, the molecular epidemiology of the disease aiming at linking human cases to specific animal reservoirs has been rarely explored within these peculiar ecosystems. **Methodology/Principal Findings** Five species of wild small mammals (n = 995) as well as domestic animals (n = 101) were screened for *Leptospira* infection on Reunion Island; positive samples were subsequently genotyped and compared to *Leptospira* from clinical cases diagnosed in 2012 - 2013 (n = 66), using MLST analysis. We identified two pathogenic species in human cases, namely *Leptospira interrogans* and *Leptospira borgpetersenii*. *Leptospira interrogans* was by far dominant both in clinical samples (96.6 %) and in infected animal samples (95.8 %), with *Rattus* spp and dogs being its exclusive carriers. The genetic diversity within *L. interrogans* was apparently limited to two sequence types (STs): ST02, identified among most clinical samples and in all rats with complete MLST, and ST34, identified in six humans, but not in rats. Noteworthy, *L. interrogans* detected in two stray dogs partially matched with ST02 and ST34. *Leptospira borgpetersenii* was identified in two clinical samples only (3.4 %), as well as in cows and mice; four haplotypes were identified, of which two seemingly identical in clinical and animal samples. *Leptospira borgpetersenii* haplotypes detected in human cases were clearly distinct from the lineage detected so far in the endemic bat species *Mormopterus francoismoutoui*, thus excluding a role for this volant mammal in the local human epidemiology of the disease. **Conclusions/Significance** Our data confirm rats as a major reservoir of *Leptospira* on Reunion Island, but also pinpoint a possible role of dogs, cows and mice in the local epidemiology of human leptospirosis. This study shows that a comprehensive molecular characterization of pathogenic *Leptospira* in both clinical and animal samples helps to gaining insight into leptospirosis epidemiology within a specific environmental setting. **Author Summary** Leptospirosis is a zoonosis caused by infection with pathogenic *Leptospira* species. A broad range of animals, including rodents, pets and livestock, are maintenance hosts for leptospires. However, assessing the relative importance of each host in the contamination of the environment and, in fine, in the infection of humans, has rarely been performed. In this study, we surveyed various wild and domestic animal species and their *Leptospira* carriage in Reunion Island, where human leptospirosis is endemic. We determined and compared the *Leptospira* genetic diversity at the species and infra-species levels in laboratory confirmed human cases and in infected animals. The two *Leptospira* species infecting humans, *Leptospira interrogans* and *Leptospira borgpetersenii*, could be traced back to different animal species: rats and dogs for the former species, cows and mice for the latter. The *Leptospira* infecting the single bat species endemic to the island was not found to be involved in human leptospirosis. Aside from rats, which were expected to play a role in the local epidemiology of the disease, the putative role of dogs, cattle and mice in human epidemiology on Reunion Island, pinpointed by our data, deserves a specific investigation. These results have strong implications in terms of local control actions aimed at reducing the burden of human leptospirosis.

Han, B. A., Schmidt, J. P., Alexander, L. W., Bowden, S. E., Hayman, D. T. S. and Drake, J. M. 2016. Undiscovered bat hosts of filoviruses. *PLoS Neglected Tropical Diseases* 10(7): e0004815. doi:. 10.1371/journal.pntd.0004815

Ebola and other filoviruses pose significant public health and conservation threats by causing high mortality in primates, including humans. Preventing future outbreaks of ebolavirus depends on identifying wildlife reservoirs, but extraordinarily high biodiversity of potential hosts in temporally dynamic environments of equatorial Africa contributes to sporadic, unpredictable outbreaks that have hampered efforts to identify wild reservoirs for nearly 40 years. Using a machine learning algorithm, generalized boosted regression, we characterize potential filovirus-positive bat species with estimated 87 % accuracy. Our model produces two specific outputs with immediate utility for guiding filovirus surveillance in the wild. First, we report a profile of intrinsic traits that discriminates hosts from non-hosts, providing a biological caricature of a filovirus-positive bat species. This profile emphasizes traits describing adult and neonate body sizes and rates of reproductive fitness, as well as species' geographic range overlap with regions of high mammalian diversity. Second, we identify several bat species ranked most likely to be filovirus-positive on the basis of intrinsic trait similarity with known filovirus-positive bats. New bat species predicted to be positive for filoviruses are widely distributed outside of equatorial Africa, with a majority of species overlapping in Southeast Asia. Taken together, these results spotlight several potential host species and geographical regions as high-probability targets for future filovirus surveillance. **Author Summary** Preventing future outbreaks of ebolaviruses in humans and other vulnerable animal populations will require identifying the natural reservoirs of filoviruses. Accumulating indirect evidence points to certain bat species as prime suspects. To guide the search for natural filovirus reservoirs, we mined intrinsic biological data on the world's bat species to determine what features best predict filovirus hosts compared to bats at large. We report a suite of traits that distinguishes seropositive bat species from all others with an estimated 87 % accuracy. We also identify several bat species not currently known to be filovirus hosts whose trait profiles indicate should be surveillance targets. Geographic regions where numerous potential filovirus hosts co-occur (potential filovirus hotspots) suggest that filovirus distribution and diversity may be greater than previously thought.

Lučan, R. K., Bartonička, T., Jedlička, P., Řeřucha, Š., Šálek, M., Čížek, M., Nicolaou, H. and Horáček, I. 2016. Spatial activity and feeding ecology of the endangered northern population of the Egyptian fruit bat (*Rousettus aegyptiacus*). *Journal of Mammalogy* 97(3): 815–822. doi: 10.1093/jmammal/gyw014.

We studied ranging and feeding behavior of Cypriot fruit bats during the summer and winter, which are critical periods with limited food supply and adverse conditions. Seasonal changes in ranging behavior were characterized by a steep increase in the size of core feeding areas and home ranges from summer to winter. Males and females did not differ in the size of summer and winter core areas and home ranges, but they differed in the distance they traveled to summer feeding sites. Summer food consisted of fruits of *Ficus carica* and flowers of *Agave americana*. Winter food consisted of dates, fruits of *Melia azedarach*, *Citrus reticulata*, *C. limon*, *Myrtus communis*, and the flowers of *Eucalyptus* spp. Males and females differed as to the proportion of time they spent feeding on different food types, which may be explained by sexual differences related to food quality requirements. Summer foraging activity tended to be in areas with water bodies and larger fruit orchards. Winter foraging activity occurred more in areas with larger fruit orchards, a higher number of citrus plantations and date palms, typically located in built-up areas. The body condition of the bats was worse during the summer, which we assume was the result of their more limited diet during this period, making summer a more stressful period for them than winter. Active conservation management of Cypriot fruit bats should include the construction of artificial water sources in the vicinity of fruit orchards, but also controversial practices such as supporting the occurrence of particular nonnative plant species, thereby enhancing food availability in critical times of the year.

Mélade, J., McCulloch, S., Ramasindrazana, B., Lagadec, E., Turpin, M., Pascalis, H., Goodman, S. M., Markotter, W. and Dellagi, K. 2016. Serological Evidence of Lyssaviruses among Bats on Southwestern Indian Ocean Islands. *Plos One* 11(8): e0160553. doi: 10.1371/journal.pone.0160553.

We provide serological evidence of lyssavirus circulation among bats on southwestern Indian Ocean (SWIO) islands. A total of 572 bats belonging to 22 species were collected on Anjouan, Mayotte, La Réunion, Mauritius, Mahé and Madagascar and screened by the Rapid Fluorescent Focus Inhibition Test for the presence of neutralising antibodies against the two main rabies related lyssaviruses circulating on the African continent: *Duvenhage lyssavirus* (DUVV) and *Lagos bat lyssavirus* (LBV), representing phylogroups I and II, respectively. A total of 97 and 42 sera were able to neutralise DUVV and LBV, respectively. No serum neutralised both DUVV and LBV but most DUVV-seropositive bats (n = 32/220) also neutralised *European bat lyssavirus 1* (EBLV-1) but not *Rabies lyssavirus* (RABV), the prototypic lyssavirus of phylogroup I. These results highlight that lyssaviruses belonging to phylogroups I and II circulate in regional bat populations and that the putative phylogroup I lyssavirus is antigenically closer to DUVV and EBLV-1 than to RABV. Variation between bat species, roost sites and bioclimatic regions were observed. All brain samples tested by RTPCR specific for lyssavirus RNA were negative.

Meng, F., Zhu, L., Huang, W., Irwin, D. M. and Zhang, S. 2016. Bats: Body mass index, forearm mass index, blood glucose levels and SLC2A2 genes for diabetes. *Scientific Reports* 6: 29960. doi: 10.1038/srep29960.

Bats have an unusually large volume of endocrine tissue, with a large population of beta cells, and an elevated sensitivity to glucose and insulin. This makes them excellent animal models for studying diabetes mellitus. We evaluated bats as models for diabetes in terms of lifestyle and genetic factors. For lifestyle factors, we generated data sets of 149 body mass index (BMI) and 860 forearm mass index (FMI) measurements for different species of bats. Both showed negative inter-species correlations with blood glucose levels in sixteen bats examined. The negative inter-species correlations may reflect adaptation of a small insectivorous ancestor to a larger frugivore. We identified an 11 bp deletion in the proximal promoter of SLC2A2 that we predicted would disrupt binding sites for the transcription repressor ZNF354C. In frugivorous bats this could explain the relatively high expression of this gene, resulting in a better capacity to absorb glucose and decrease blood glucose levels.

Peel, A. J., Baker, K. S., Hayman, D. T. S., Suu-Ire, R., Breed, A. C., Gembu, G-C., Lembo, T., Fernández-Loras, A., Sargan, D. R., Fooks, A. R., Cunningham, A. A. and Wood, J. L. N. 2016. Bat trait, genetic and pathogen data from large-scale investigations of African fruit bats, *Eidolon helvum*. *Scientific Data* 3: 160049. doi: 10.1038/sdata.2016.49.

Bats, including African straw-coloured fruit bats (*Eidolon helvum*), have been highlighted as reservoirs of many recently emerged zoonotic viruses. This common, widespread and ecologically important species was the focus of longitudinal and continent-wide studies of the epidemiological and ecology of Lagos bat virus, henipaviruses and Achimota viruses. Here we present a spatial, morphological, demographic, genetic and serological dataset encompassing 2827 bats from nine countries over an 8-year period. Genetic data comprises cytochrome *b* mitochondrial sequences (n= 608) and microsatellite genotypes from 18 loci (n= 544). Tooth-cementum analyses (n= 316) allowed derivation of rare age-specific serologic data for a lyssavirus, a henipavirus and two rubulaviruses. This dataset contributes a substantial volume of data on the ecology of *E. helvum* and its viruses and will be valuable for a wide range of studies, including viral transmission dynamic modelling in age-structured populations, investigation of seasonal reproductive asynchrony in wide-ranging species, ecological niche modelling, inference of island colonisation history, exploration of relationships between island and body size, and various spatial analyses of demographic, morphometric or serological data.

Pigott, D. M., Millear, A. I., Earl, L., Morozoff, C., Han, B. A., Shearer, F. M., Weiss, D. J., Brady, O. J., Kraemer, M. U. G., Moyes, C. L., Bhatt, S., Gething, P. W., Golding, N. and Hay, S. I. 2016. Updates to the zoonotic niche map of Ebola virus disease in Africa. *eLife* 5: e16412. doi: 10.7554/eLife.16412.

As the outbreak of Ebola virus disease (EVD) in West Africa is now contained, attention is turning from control to future outbreak prediction and prevention. Building on a previously published zoonotic niche map (Pigott *et al*., 2014), this study incorporates new human and animal occurrence data and expands upon the way in which potential bat EVD reservoir species are incorporated. This update demonstrates the potential for incorporating and updating data used to generate the predicted suitability map. A new data portal for sharing such maps is discussed. This output represents the most up-to-date estimate of the extent of EVD zoonotic risk in Africa. These maps can assist in strengthening surveillance and response capacity to contain viral haemorrhagic fevers.

Platt, R. N. II, Mangum, S. F. and Ray, D. A. 2016. Pinpointing the vesper bat transposon revolution using the *Miniopterus natalensis* genome. *Mobile DNA* 7(1): 12. doi: 10.1186/s13100-016-0071-y.

Background: Around 40 million years ago DNA transposons began accumulating in an ancestor of bats in the family Vespertilionidae. Since that time, Class II transposons have been continuously reinvading and accumulating in vespertilionid genomes at a rate that is unprecedented in mammals. *Miniopterus* (Miniopteridae), a genus of long-fingered bats that was recently elevated from Vespertilionidae, is the sister taxon to the vespertilionids and is often used as an outgroup when studying transposable elements in vesper bats. Previous wet-lab techniques failed to identify *Helitrons*, TcMariners, or hAT transposons in *Miniopterus*. Limitations of those methods and ambiguous results regarding the distribution of piggyBac transposons left some questions as to the distribution of Class II elements in this group. The recent release of the *Miniopterus natalensis* genome allows for transposable element discovery with a higher degree of precision. **Results**: Here we analyze the transposable element content of *M. natalensis* to pinpoint with greater accuracy the taxonomic distribution of Class II transposable elements in bats. These efforts demonstrate that, compared to the vespertilionids, Class II TEs are highly mutated and comprise only a small portion of the *M. natalensis* genome. Despite the limited Class II content, *M. natalensis* possesses a limited number of lineage-specific, low copy number piggyBacs and shares several TcMariner families with vespertilionid bats. Multiple efforts to identify *Helitrons*, one of the major TE components of vesper bat genomes, using de novo repeat identification and structural based searches failed. **Conclusions**: These observations combined with previous results inform our understanding of the events leading to the unique Class II element acquisition that characterizes vespertilionids. While it appears that a small number of TcMariner and piggyBac elements were deposited in the ancestral *Miniopterus* + vespertilionid genome, these elements are not present in *M. natalensis* genome at high copy number. Instead, this work indicates that the vesper bats alone experienced the expansion of TEs ranging from *Helitrons* to piggyBacs to hATs.

Plowright, R. K., Peel, A. J., Streicker, D. G., Gilbert, A. T., McCallum, H., Wood, J., Baker, M. L. and Restif, O. 2016. Transmission or within-host dynamics driving pulses of zoonotic viruses in reservoir-host populations. *PLoS Neglected Tropical Diseases* 10(8): e0004796. doi: 10.1371/journal.pntd.0004796.

Progress in combatting zoonoses that emerge from wildlife is often constrained by limited knowledge of the biology of pathogens within reservoir hosts. We focus on the host-pathogen dynamics of four emerging viruses associated with bats: Hendra, Nipah, Ebola, and Marburg viruses. Spillover of bat infections to humans and domestic animals often coincides with pulses of viral excretion within bat populations, but the mechanisms driving such pulses are unclear. Three hypotheses dominate current research on these emerging bat infections. First, pulses of viral excretion could reflect seasonal epidemic cycles driven by natural variations in population densities and contact rates among hosts. If lifelong immunity follows recovery, viruses may disappear locally but persist globally through migration; in either case, new outbreaks occur once births replenish the susceptible pool. Second, epidemic cycles could be the result of waning immunity within bats, allowing local circulation of viruses through oscillating herd immunity. Third, pulses could be generated by episodic shedding from persistently infected bats through a combination of physiological and ecological factors. The three scenarios can yield similar patterns in epidemiological surveys, but strategies to predict or manage spillover risk resulting from each scenario will be different. We outline an agenda for research on viruses emerging from bats that would allow for differentiation among the scenarios and inform development of evidence-based interventions to limit threats to human and animal health. These concepts and methods are applicable to a wide range of pathogens that affect humans, domestic animals, and wildlife.

Prié V., Augros S, Amirault G, Bas Y, Desmet J-F, Favre P, Giosa S, Hoarau C, Souquet M, Vinet O, Barataud M. 2016. Actualisation des critères acoustiques et synthèse des données concernant le présumé *Scotophilus* sp. à La Réunion (Mascareignes, France). *Le Vespére* 6: 385–396.

Although considerable advances have been made in documenting the bats of Madagascar and the Mascarenes (Mauritius and La Réunion), *Scotophilus borbonicus* remains enigmatic. In this paper, we present our results from over 3000 hours of acoustic sampling collected on La Réunion. The acoustic type referred to as Chiroptera sp. 1 is redescribed in the light of the newly collected data. Multivariate analyses performed on bioacoustic measurements of *Mormopterus francoismoutoui*, *Scotophilus robustus* and Chiroptera sp. 1 registered calls allows us to distinguish the acoustic types between *M. francoismoutoui* and *S. robustus* and suggests that Chiroptera sp. 1 is indeed a distinct taxon that may belong to the genus *Scotophilus*. We discuss the reasons why the name *Scotophilus borbonicus* should not be employed to denominate Chiroptera sp. 1. Based on the distribution of the bioacoustic data we collected, it is suggested that this species inhabits the north-western part of La Réunion, where semi-dry forests were historically present. The drastic forest loss in this highly urbanized area could explain why Chiroptera sp. 1, is seemingly so rare.

Schmidt, K. M. and Mühlberger, E. 2016. Marburg virus reverse genetics systems. *Viruses* 8(6): 178. doi: 10.3390/v8060178.

The highly pathogenic Marburg virus (MARV) is a member of the Filoviridae family and belongs to the group of nonsegmented negative-strand RNA viruses. Reverse genetics systems established for MARV have been used to study various aspects of the viral replication cycle, analyze host responses, image viral infection, and screen for antivirals. This article provides an overview of the currently established MARV reverse genetic systems based on minigenomes, infectious virus-like particles and full-length clones, and the research that has been conducted using these systems.

Notice Board

Conferences

European Conference of Tropical Ecology

To be held in: Brussels, Belgium, 2017.
Further information: **http://www.soctropecol-2017.eu.**

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**.
Download notes to authors from **www.africanbats.org**.

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