Above: Trident Leaf-nosed Bat (Cloeotis percivali) exiting Gatkop Cave, Meletse Bat Research and Conservation Training Centre, Limpopo Province, South Africa.

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Observations, Discussions and Updates

Observation # 26: *Mops midas* (Sundevall, 1843) record from Lephalale, Limpopo Province, Republic of South Africa

Submitted by: Julio Balona, Gauteng & Northern Regions Bat Interest Group (GNoR BIG)
Observation by: Julio Balona, Erna Balona and Trevor Morgan (GNoR BIG), Lofty Fourie
Date of observation: January 2010; May 2011
Locality: South Africa, Limpopo Province, Lephalale town
GPS coordinates: 23.66°S; 27.73°E (approximate)

A query was emailed to GNoR BIG in January 2010 from a developer (Lofty Fourie) located in Lephalale. He explained that he had a bat problem in a townhouse complex that he had recently built on the edge of Lephalale and had managed to catch two of the bats in his house. Attached were several photographs of one of them, of which two are shown in Figure 1 and 2.

There was no indication of size given but judging from the sparse hair across the shoulders, the light grey flecks on the dark grey dorsal fur, the shape of the ears, and the geographical location, it was unlikely to be anything but a *Mops midas*. This piqued our interest somewhat since the nearest published record of this species is from the Alldays area, about 220 kilometres away.

The houses in which they were roosting have an unusual roof design in that they have no ceilings and consist of a layer of insulation underneath metal sheeting.

In an effort to confirm the identity of the bats, the site was visited by GNoR BIG in March 2010 when mistnets were erected in the garden of Lofty’s house and in front of the suspected roof entrance. No bats were captured but conditions were not ideal: it was windy and a fair amount of stray light illuminated the garden. The net at the suspected roof entrance was also of insufficient height. There was however reasonable bat activity and molossid squeaks could be heard.

A return trip in January 2011 was also unsuccessful in capturing any *M. midas*. This time scaffolding was used to erect a mistnet in front of the suspected roof entrance, but this resulted in the capture of eight *Scotophilus dingani* (A. Smith, 1833) instead.

Finally in May 2011, a bat was once again found in Lofty’s house. This time a ruler was placed next to a forearm in one of the photographs, which allowed an estimation of its length as 62 mm (see Figure 3). In a photograph of the bats face (Figure 4), the broad leading edge of pinnae are noticeable as well as wrinkled lips. With this additional information, we could confidently identify the bats as *M. midas*.

~

Observation # 27: *Mops midas* (Sundevall, 1843) record from Bela Bela, Limpopo Province, Republic of South Africa

Submitted by: Julio Balona, Trevor Morgan and Eve Pearse - Gauteng & Northern Regions Bat Interest Group (GNoR BIG)
Date of observation: mid-September 2012, late August 2015
Locality: South Africa, Limpopo Province, Farm Leeukui, ±20 km outside town of Bela Bela
GPS coordinates: 25.008°S; 28.433°E

Through some acquaintances, GNoR BIG was notified in mid-September 2012...
of a curious bat that had been seen on a building at Leeukuil farm outside Bela Bela. A single photo was sent of the beast in question (Figure 1).

Then in late August of 2015, GNoR BIG was sent photos of another bat that had fallen out of the roof of the building (Figures 2a and 2b).

From the photos the following features are noticeable in these bats:

- A tail that is not enclosed in a membrane.
- The fur forms a collar around the neck.
- There are light grey dorsal flecks.
- The snout is pig-like and the lips appear to be wrinkled.
- The leading edge of the pinnae are broad and triangular.

The above characteristics are all consistent with Mops midas and we are therefore confident that the bats belong to this species.

This is a notable new locality as the nearest published record for M. midas is in Lephalale (BALONA 2016), about one hundred and twenty kilometres north-west. Before this, the nearest recorded location was in the Lydenburg district, about two hundred kilometres east (MONADJEM et al. 2010).

Intriguingly, the residents of the farm claim that the bats are present only for about two weeks. Also, both reported bat encounters occurred at about the same time of the year. This suggests the possibility of a seasonal movement of this species through the area.

References


Keywords: echolocation call frequency, Hipposideros beatus beatus, Hipposideros beatus maximus, Democratic Republic of the Congo (DRC; Zaire)

Echolocation sounds of rhinolophid and hipposiderid bats typically contain a long constant frequency part followed by a short frequency-modulated part (cf/fm bats). In these species, the flying animal changes the frequency of the constant-frequency part in such a way that the frequency of the returning echo remains constant (Doppler effect compensation). The echo arrives in the auditory fovea of the bat, enabling flutter detection of moving prey (SCHNITZLER and DENZINGER, 2011). The frequency of the cf component is species specific, in hipposiderids often with a larger variation than in rhinolophids. For example, SCHNITZLER and DENZINGER (2011) report 81.0 to 84.2 kHz in 24 individuals of Rhinolophus ferrumequinum from one population, and 111 to 124 kHz in 18 individuals from the hipposiderid species Asellia tridens.

Here we present data on the echolocation frequency of Hipposideros beatus Andersen, 1906, which confirm the results reported by NOVICK (1958) and thus the unusually high frequency variation in this taxon (see below). H. beatus is considered to be a member of the Hipposideros caffer/ruber complex (MONADJEM et al., 2013), for which some echolocation data are available (e.g., HELLER, 1992; GUILLEN et al., 2000; HAPPOLD, 2013a).

Material and Methods

The bats were captured (but not collected) with mist-nets in Irangi, Democratic Republic of the Congo (DRC; formerly Zaire; 1.90°S 28.45°E) on 15th of March 1990 at about the same place, where we have made some other bat observations (HELLER, 1992; HELLER et al., 1994). The echolocation sounds of hand-held animals were recorded with a custom-made condenser microphone (similar to e.g., QMC SM1) and amplifier on a videorecorder converted to monitor sound (bandwidth up to 300 kHz). For evaluation, calls were re-recorded with a RACAL store DS tape recorder and after appropriate slow down (mostly 32x) analysed with a MOSIP-FFT-processor (Fa. MEDAV, D-91080 Uttenreuth).

Results

Hipposideros beatus is a small member of the caffer/ruber complex with two lateral leaflets at the nose-leaf (Figure 1) as in most other members of the group (HAPPOLD, 2013a). In our two animals (data on sex and size not available) the frequencies of the cf-part were 109.2 and 111.6 kHz. Both specimens were captured from a group of four resting under a broken tree after disturbance during day-time.
Table 1. Echolocation frequencies of *Hipposideros beatus*

<table>
<thead>
<tr>
<th>Country</th>
<th>Locality</th>
<th>Frequency</th>
<th>Publication</th>
</tr>
</thead>
<tbody>
<tr>
<td>Côte d’Ivoire</td>
<td></td>
<td>139-147 kHz (n=?)</td>
<td>HAPPOLD, 2013b, based on FAHR and EBIGBO, pers. comm.</td>
</tr>
<tr>
<td>Liberia/Guinea</td>
<td>Mt. Nimba 7.60°N, 8.39°W</td>
<td>129 kHz (n=1) Anabat SD2 bat detector</td>
<td>MONADJEM et al., 2013</td>
</tr>
<tr>
<td>Congo</td>
<td>Lac Tumba 0.77°S, 18.01°E</td>
<td>129 kHz (n=1) pulse detector microphone 108 kHz (n=1) solid dielectric microphone</td>
<td>NOVICK, 1958</td>
</tr>
<tr>
<td>Congo</td>
<td>Irangi 1.90°S, 28.45°E</td>
<td>109.2 kHz, 111.6 kHz (n=2) custom-made condensor microphone</td>
<td>this paper</td>
</tr>
</tbody>
</table>

**Discussion**

At the time we made the recordings, the results for *H. beatus* were not very surprising, since NOVICK (1958) had already found this species calling at 108 kHz from Lac Tumba in northwestern DRC. He had also reported another individual at the same site calling much higher, at 128 kHz. This specimen was recorded with another type of microphone, so that we could not exclude recording artefacts in these early days of ultrasound recording.

In addition, this observation was not mentioned in HAPPOLD (2013b). However, recent recordings in West Africa confirm the high frequency or indicate even higher call frequencies in *H. beatus* (up to 147 kHz; see Table 1). In the light of these new findings our results become more remarkable because a range of nearly 40 kHz (see Table 1) in the echolocation frequencies in a single species, even recorded at different localities, is quite unusual. From the distribution, our animals clearly belong to the subspecies *H. beatus maximus* Verschuren, 1957 (type locality DRC, Garamba National Park, 4°N, 29.25°E).

Interestingly, Novick’s recordings are also assumed to be *H. beatus maximus* (Happold, 2013b), but they were made close to the proposed border between the presently recognized subspecies *H. b. beatus* (type locality Equatorial Guinea, Rio Muni, Benito River, *fide* HAPPOLD, 2013b; about 1.52°N, 9.92°E [wikipedia]) and *H. b. maximus*. From the call frequencies (see Table 1) one could assume that Novick had by chance recorded one specimen from each subspecies at the same spot, thus indicating the existence of two full species. In *H. ruber*, the variation in call frequency (standard deviation) within one population is at maximum around 6 kHz (GUILLEN et al., 2000), sex specific differences included, thus being much smaller than the 20 kHz difference between both of Novick’s measurements. On the other hand, a difference of 20 kHz can be observed between closely related sympatric *Hipposideros* species. At our study site in Irangi, besides *H. beatus*, two other species of the group were recorded, assumed to be *H. ruber* (Noack, 1893) and *H. caffer* (Sundevall, 1846) (HELLER, 1992). The echolocation frequencies of these three species were clearly separated by around 20 kHz each: *H. beatus* 109-112 kHz, *H. ruber* 132-138 kHz and *H. caffer* 155-158 kHz, surprisingly the largest species having the highest calls and the smallest the lowest.

At present, it may be premature to change the status of the two *beatus* subspecies, but our data draw attention to this question. *H. beatus* is a taxonomically poorly known species with fascinating social behaviour: contrasting to the other members of the *caffer/ ruber* complex, it seems to be one of the few monogamous bats (BROSSET, 1982).

**Acknowledgements**

Special thanks go to Boni Ndumbo, Irangi, for his help in the field, to Dr. Steinhauer-Burkhard, Bukavu, for his logistic help in DRC, to Mr. Bussmann, Kigali, and last, but not least, to A. and C. Liegl for their manifold help during our excursion.

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from the Kivu region Central Africa Mammalia Chiroptera/ links/57e5f1308ae61374ee8e550.pdf?origin-publication_detail


Recent literature

Books


Intensification in land-use and farming practices has had largely negative effects on bats, leading to population declines and concomitant losses of ecosystem services. Current trends in land-use change suggest that agricultural areas will further expand, while production systems may either experience further intensification (particularly in developing nations) or become more environmentally friendly (especially in Europe). In this chapter, we review the existing literature on how agricultural management affects the bat assemblages and the behavior of individual bat species, as well as the literature on provision of ecosystem services by bats (pest insect suppression and pollination) in agricultural systems. Bats show highly variable responses to habitat conversion, with no significant change in species richness or measures of activity or abundance. In contrast, intensification within agricultural systems (i.e., increased agrochemical inputs, reduction of natural structuring elements such as hedges, woods, and marshes) had more consistently negative effects on abundance and species richness. Agroforestry systems appear to mitigate negative consequences of habitat conversion and intensification, often having higher abundances and activity levels than natural areas. Across bioeomes, bats play key roles in limiting populations of arthropods by consuming various agricultural pests. In tropical areas, bats are key pollinators of several commercial fruit species. However, these substantial benefits may go unrecognized by farmers, who sometimes associate bats with ecosystem disservices such as crop raiding. Given the importance of bats for global food production, future agricultural management should focus on “wildlife-friendly” farming practices that allow more bats to exploit and persist in the anthropogenic matrix so as to enhance provision of ecosystem services. Pressing research topics include (1) a better understanding of how local-level versus landscape-level management practices interact to structure bat assemblages, (2) the effects of new pesticide classes and GM crops on bat populations, and (3) how increased documentation and valuation of the ecosystem services provided by bats could improve attitudes of producers toward their conservation.

Chapters


Humans have inadvertently changed global ecosystems and triggered the dawn of a new geological epoch, the Anthropocene. While some organisms can tolerate human activities and even flourish in anthropogenic habitats, the vast majority are experiencing dramatic population declines, pushing our planet into a sixth mass extinction. Bats are particularly susceptible to anthropogenic changes because of their low reproductive rate, longevity, and high metabolic rates. Fifteen percent of bat species are listed as threatened by the IUCN, i.e., they are considered Critically Endangered, Endangered or Vulnerable. About 16% of species are Data Deficient, highlighting the paucity of ecological studies that can support conservation status assessments. This book summarizes major topics related to the conservation of bats organized into sections that address: the response of bats to land use changes; how the emergence of viral and fungal diseases has changed bat populations; our perception of bats; and drivers of human–bat conflicts and possible resolutions and mitigation. The book ends with approaches that might advance bat conservation through conservation networks and a better understanding of human behavior and behavioral change.


Urbanisation is viewed as the most ecologically damaging change to land use worldwide, posing significant threats to global biodiversity. However, studies from around the world suggest that the impacts of urbanisation are not always negative and can differ between geographic regions and taxa. Bats are a highly diverse group of mammals that occur worldwide, and many species persist in cities. In this chapter, we synthesise current knowledge of bats in urban environments. In addition, we use a meta-analysis approach to test if the general response of bats depends on the intensity of urbanisation. We further investigate if phylogenetic relatedness or functional ecology determines adaptability of species to urban landscapes and if determining factors for urban adaptability are consistent worldwide. Our meta-analysis revealed that, in general, habitat use of bats decreases in urban areas in comparison to natural areas. A high degree of urbanisation had a stronger negative effect on habitat use compared to an intermediate degree of urbanisation. Neither phylogenetic relatedness nor functional ecology alone explained species persistence in urban environments; however, our analysis did indicate differences in the response of bats to urban development at the family level. Bats in the families Rhinolophidae and Mormoopidae exhibited a negative association with urban development, while responses in all other families were highly heterogeneous. Furthermore, our analysis of insectivorous bats.


The effects of roads on bats have been largely neglected until recently, despite growing evidence for profound effects on other wildlife. Roads destroy fragment and degrade habitat, are sources of light, noise and chemical pollution and can kill directly through collision with traffic. The negative effects of roads on wildlife cannot be refuted but at the same time road building and upgrading are seen as important economic drivers. As a consequence, infrastructure projects and protection of bats are often in conflict with each other. There is now growing evidence that fragmentation caused by roads reduces access to important habitat, leading to
lower reproductive output in bats. This barrier effect is associated with reduced foraging activity and species diversity in proximity to motorways and other major roads. The effects of light and noise pollution may add to this effect in the immediate vicinity of roads and also make bats even more reluctant to approach and cross roads. Several studies show that vehicles kill a wide range of bat species and in some situations roadkill may be high enough to lead directly to population decline. Current mitigation efforts against these effects are often ineffective, or remain largely untested. The limited information available suggests that underpasses to take bats under roads may be the most effective means of increasing the safety and permeability of roads. However, underpass design needs further study and alternative methods need to be developed and assessed.

Meyer C. F. J., M. J. Struabig and M. R. Willig - Responses of tropical bats to habitat fragmentation, logging, and deforestation. pp. 63–103. doi: 10.1007/978-3-319-25220-9_4

Land-use change is a key driver of the global biodiversity crisis and a particularly serious threat to tropical biodiversity. Throughout the tropics, the staggering pace of deforestation, logging, and conversion of forested habitat to other land uses has created highly fragmented landscapes that are increasingly dominated by human-modified habitats and degraded forests. In this chapter, we review the responses of tropical bats to a range of land-use change scenarios, focusing on the effects of habitat fragmentation, logging, and conversion of tropical forest to various forms of agricultural production. Recent landscape-scale studies have considerably advanced our understanding of how tropical bats respond to habitat fragmentation and disturbance at the population, ensemble, and assemblage level. This research emphasizes that responses of bats are often species and ensemble specific, sensitive to spatial scale, and strongly molded by the characteristics of the prevailing landscape matrix. Nonetheless, substantial knowledge gaps exist concerning other types of response by bats. Few studies have assessed responses at the genetic, behavioral, or physiological level, with regard to disease prevalence, or the extent to which human disturbance erodes the capacity of tropical bats to provide key ecosystem services. A strong geographic bias, with Asia and, most notably, Africa, being strongly understudied, precludes a comprehensive understanding of the effects of fragmentation and disturbance on tropical bats. We strongly encourage increased research in the Paleotropics and emphasize the need for long-term studies, approaches designed to integrate multiple scales, and answering questions that are key to conserving tropical bats in an era of environmental change and dominance of modified habitats (i.e., the Anthropocene).


Frosts are one of the most important habitats for insectivorous bats as they offer the potential for both roosting and foraging. We reviewed silvicultural literature from North America, Australia, and Europe and found that diverse research approaches have revealed commonalities in bat responses to forest silviculture. Almost all silvicultural treatments evaluated were compatible with some use by forest bats, though different bat ensembles respond in different ways. Ensemble ecomorphology was a consistent predictor of how bats respond to vegetative clutter and its dynamic changes as forests regenerate and develop a dense structure following harvesting. Sustaining high levels of bat diversity in timber production forests requires a mix of silvicultural treatments and exclusion areas staggered across the landscape, regardless of forest type or geographic region. Use of edge habitats, exclusion areas/set-asides, and riparian corridors for roosting and foraging by bats were consistent themes in the literature reviewed, and these habitat elements need to be considered in forest planning. Densities of hollow or dead trees sufficient to support large populations of roosting bats are unknown and remain a major knowledge gap, but will likely be species contingent. New paradigm shifts in forest management away from the use of even-aged systems to multi-spatial scale retention of mature forest including trees with cavities should be beneficial to bats, which are influenced by landscape-scale management. Such an approach is already in use in some regions, though there is a limited guidance on what constitutes a reasonable landscape threshold for retention. The effectiveness of such an approach will require long-term monitoring and research, especially with population studies which are currently lacking.


Intensification in land-use and farming practices has had largely negative effects on bats, leading to population declines and concomitant losses of ecosystem services. Current trends in land-use change suggest that agricultural areas will further expand, while production systems may either experience further intensification (particularly in developing nations) or become more environmentally friendly (especially in Europe). In this chapter, we review the existing literature on how agricultural management affects the bat assemblages and the behavior of individual bat species, as well as the literature on provision of ecosystem services by bats (pest insect suppression and pollination) in agricultural systems. Bats show highly variable responses to habitat conversion, with no significant change in species richness or measures of activity or abundance. In contrast, intensification within agricultural systems (i.e., increased agrochemical inputs, reduction of natural structuring elements such as hedges, woods, and marshes) had more consistently negative effects on abundance and species richness. Agroforestry systems appear to mitigate negative consequences of habitat conversion and intensification, often having higher abundances and activity levels than natural areas. Across biomes, bats play key roles in limiting populations of arthropods by consuming various agricultural pests. In tropical areas, bats are key pollinators of several commercial fruit species. However, these substantial benefits may go unrecognized by farmers, who sometimes associate bats with ecosystem disservices such as crop raiding. Given the importance of bats for global food production, future agricultural management should focus on “wildlife-friendly” farming practices that allow more bats to exploit and persist in the anthropogenic matrix so as to enhance provision of ecosystem services. Pressing research topics include (1) a better understanding of how local-level versus landscape-level management practices interact to structure bat assemblages, (2) the effects of new pesticide classes and GM crops on bat populations, and (3) how increased documentation and valuation of the ecosystem services provided by bats could improve attitudes of producers toward their conservation.


While artificial lighting is a major component of global change, its biological impacts have only recently been recognised. Artificial lighting attracts and repels animals in taxon-specific ways and affects physiological processes. Being nocturnal, bats are likely to be strongly affected by artificial lighting. Moreover, many species of bats are insectivorous, and insects are also strongly influenced by...
lighting. Lighting technologies are changing rapidly, with the use of light-emitting diode (LED) lamps increasing. Impacts on bats and their prey depend on the light spectra produced by street lights; ultraviolet (UV) wavelengths attract more insects and consequently insectivorous bats. Bat responses to lighting are species-specific and reflect differences in flight morphology and performance; fast-flying aerial hawking species frequently feed around street lights, whereas relatively slow-flying bats that forage in more confined spaces are often light-averse. Both high-pressure sodium and LED lights reduce commuting activity by clutter-tolerant bats of the genera Myotis and Rhinolophus, and these bats still avoided LED lights when dimmed. Light-induced reductions in the activity of frugivorous bats may affect ecosystem services by reducing dispersal of the seeds of pioneer plants and hence reforestation. Rapid changes in street lighting offer the potential to explore mitigation methods such as part-night lighting (PNL), dimming, directed lighting, and motion-sensitive lighting that may have beneficial consequences for light-averse bat species.


Natural bodies of open water in desert landscapes, such as springs and ephemeral pools, and the plant-life they support, are important resources for the survival of animals in hyper arid, arid and semi-arid (dryland) environments. Human-made artificial water sources, i.e. waste-water treatment ponds, catchments and reservoirs, have become equally important for wildlife in those areas. Bodies of open water are used by bats either for drinking and/or as sites over which to forage for aquatic emergent insects. Due to the scarcity of available water for replenishing water losses during roosting and flight, open bodies of water of many shapes and sizes may well be a key resource influencing the survival, activity, resource use and the distribution of insectivorous bats. In this chapter, we review the current knowledge of bats living in semi- and arid regions around the world and discuss the factors that influence their richness, behaviour and activity around bodies of water. We further present how increased anthropogenic changes in hydrology and water availability may influence the distribution of species of bats in desert environments and offer directions for future research on basic and applied aspects on bats and the water they use in these environments.


White-nose syndrome (WNS) is an infectious disease of hibernating bats that has killed millions of bats since it first emerged in eastern North America in 2006. The disease is caused by a pathogenic fungus, Pseudogymnoascus (formerly Geomyces) destructans that was likely introduced to North America by human trade or travel, demonstrating the serious problem of global movement of pathogens by humans in the Anthropocene. Here, we present a synthesis of the current state of knowledge on WNS, including disease mechanisms, disease ecology, global distribution and conservation and management efforts. There has been rapid research response to WNS and much about the disease is now well understood. However, critical gaps in our knowledge remain, including ways to limit spread, or effective treatment options to reduce disease mortality. There are several hibernating bat species in North America that are threatened with extinction from WNS. Protecting those species has become a race against time to find and implement creative solutions to combat the devastating impacts of this disease.


Many of the recently emerging highly virulent zoonotic diseases have a likely bat origin, for example Hendra, Nipah, Ebola and diseases caused by coronaviruses. Presumably because of their long history of coevolution, most of these viruses remain subclinical in bats, but have the potential to cause severe illnesses in domestic and wildlife animals and also humans. Spillovers from bats to humans either happen directly (via contact with infected bats) or indirectly (via intermediate hosts such as domestic or wildlife animals, by consuming food items contaminated by saliva, faeces or urine of bats, or via other environmental sources). Increasing numbers of breakouts of zoonotic viral diseases among humans and livestock have mainly been accounted to human encroachment into natural habitat, as well as agricultural intensification, deforestation and bushmeat consumption. Persecution of bats, including the destruction of their roosts and culling of whole colonies, has led not only to declines of protected bat species, but also to an increase in virus prevalence in some of these populations. Educational efforts are needed in order to prevent future spillovers of bat-borne viruses to humans and livestock, and to further protect bats from unnecessary and counterproductive culling.


Wind energy continues to be one of the fastest growing renewable energy sources under development, and while representing a clean energy source, it is not environmentally neutral. Large numbers of bats are being killed at utility scale wind energy facilities worldwide, raising concern about cumulative impacts of wind energy development on bat populations. We discuss our current state of knowledge on patterns of bat fatalities at wind facilities, estimates of fatalities, mitigation efforts, and policy and conservation implications. Given the magnitude and extent of fatalities of bats worldwide, the conservation implications of understanding and mitigating bat fatalities at wind energy facilities are critically important and should be proactive and based on science rather than being reactive and arbitrary.

**Mildenstein T., I. Tanshi and P. A. Racey - Exploitation of bats for bushmeat and medicine.** pp. 325–375. doi: 10.1007/978-3-319-25220-9_12.

Bat hunting for consumption as bushmeat and medicine is widespread and affects at least 167 species of bats (or c. 13 % of the world’s bat species), in Africa, Asia, across the islands of Oceania, and to a lesser extent in Central and South America. Hunting is particularly prevalent among the large-bodied fruit bats of the Old World tropics, where half (50 %, 92/183) the extant species in the family Pteropodidae are hunted. Pteropods that are hunted are six times more likely to be Red Listed as threatened: 66 % of species in IUCN threatened categories (CR, EN, VU, NT), compared to 11 % of species in the ‘Least Concern’ (LC) category. However, there still appears to be an information gap at the international level. One third of the hunted species on the Red List are not considered threatened by that hunting, and nearly a quarter of the bat species included in this review are not listed as hunted in IUCN Red List species accounts. This review has resulted in a comprehensive list of hunted bats that doubles the number of species.
known from either the IUCN Red List species accounts or a questionnaire circulated in 2004. More research is needed on the impacts of unregulated hunting, as well as on the sustainability of regulated hunting programs. In the absence of population size and growth data, legislators and managers should be precautionary in their attitude towards hunting. Roost site protection should be a priority as it is both logistically simpler than patrolling bat foraging grounds and reduces the comparatively larger scale mortality and stress that hunting at the roost can cause. Education and awareness campaigns within local communities should demonstrate how bats are a limited resource and emphasize characteristics (nocturnal, slow reproducing and colonial) that make them particularly vulnerable to hunting pressure.


Pteropodid bats damage a wide range of fruit crops, exacerbated by continuing loss of their natural forest as forests are cleared. In some countries where such damage occurs, bats are not legally protected. In others, as a result of pressure from fruit growers, legal protection is either not implemented or over-ridden by legislation specifically allowing the killing of bats. Lethal control is generally ineffective and often carried out with shotguns making it an animal welfare issue, as many more animals are injured or orphaned than are killed. Here, we review the literature and current state of the conflict between fruit growers and pteropodids and describe a wide range of potential mitigation techniques. We compile an extensive list of bats and the fruit crops on which they feed where this has resulted in conflicts, or could lead to conflict, with fruit growers. We also discuss the legal status of bats in some countries where such conflicts occur. We found the most effective means of preventing bat damage to crops is the use of fixed nets (that generally prevent entanglement) covering a whole orchard. Netting individual trees, or fruit panicles, using small net bags, is also effective. Management methods that assist netting include pruning to maintain low stature of trees. These exclusion techniques are the best management options considering both conservation and public health issues. Although lights, sonic and ultrasonic noises, noxious smells and tastes have been used to deter bats from eating fruit, there have been no large-scale systematic trials of their effectiveness. Nevertheless, broadcasting the sound of discharging shotguns followed by the sound of wounded bats has proved effective in Australia. The use of decoy fruit trees is the least investigated method of mitigation and requires detailed knowledge of the natural diet of the bat species involved. The few studies of dietary preferences undertaken to date suggest that bats prefer non-commercial fruit when it is available, and we highlight this as an area for future research.


Humans have shared buildings with bats for thousands of years, probably as early as first humans built primitive huts. Indeed, many bat species can be defined as synanthropic, i.e., they have a strong ecological association with humans. Bats have been observed using buildings as roosting and foraging sites, temporary shelters, for reproduction and hibernation. A synanthropic lifestyle may result in direct fitness benefits owing to energetic advantages in warmer roosts, which may ultimately lead to faster development of juveniles, or by being less exposed to natural predators in urban environments. All these benefits may allow bats to use buildings as stepping stones to exploit habitats otherwise devoid of roosting structures and may even lead to the expansion of geographic ranges. Yet, the coexistence with humans also comes with some risks. Bats may be exposed to chemical pollutants, particularly preservation chemicals used on lumber or during pest control measures. Bats may also be at risk of direct persecution or they may die accidentally if trapped within buildings. In general, eviction of bats from buildings should follow the general rule of avoidance–mitigation–compensation. When considering conservation measures for synanthropic bats, it is most important to assess the role of the building for different life stages of bats. Construction work at buildings should be conducted in a manner that minimizes disturbance of bats. Artificial roosts can replace lost roosts, yet bats will often not accept alternative roosts. Demographic changes in human populations may lead to the abandonment of buildings, for example, in rural areas and to increased conflicts in urban areas when old buildings are replaced by new buildings or when previously unoccupied space in buildings is renovated. We advocate maintenance and enhancement of roosts for synanthropic bats, in addition to outreach and education campaigns, to improve the tolerance of humans for synanthropic bats.


Caves and other subterranean sites such as mines are critical to the survival of hundreds of bat species worldwide, since they often provide shelter for most of a nation’s bat fauna. In the temperate zone, caves provide roosts for hibernation and for some species, breeding in summer, whereas in warmer regions, they support high species richness year round and enormous colonies that maintain substantial ecosystem services. Due to the solubility of the substrate, the highest densities of caves occur in karst landscapes. Given their importance for bats, relatively few studies have investigated factors involved in cave selection, although current evidence suggests that the density and size of caves are the best predictors of species diversity and population sizes. Thermal preferences have been established for some cave-dwelling species as well as their vulnerability to disturbance, particularly during hibernation and reproduction. Growth in limestone quarrying and cave tourism industries worldwide severely threatens cave-dwelling bats, in addition to loss of foraging habitat, hunting for bushmeat, incidental disturbance and disruptive guano harvesting. Apparent declines of cave bats in Europe and North America also pose serious concerns, as do global climate change predictions. The main conservation response to threats to cave bats in these continents has been gatering, but this remains relatively untested as a means of protecting colonies in other regions. Research on sustainable harvesting of bats as bushmeat and their responses to different types of human disturbance at caves and loss of surrounding foraging habitats is required. More caves of outstanding importance for bats at national and international levels also require protection.


Taxonomy—the description, naming, and classification of organisms—and systematics—the study of the evolutionary relationships of organisms—are both crucial components in conservation, providing a necessary framework for any conservation initiative. With more than 200 new bat species identified or raised from synonymy in the past decade and additional taxa described monthly, the Age of Discovery is ongoing for bats. New taxonomic and systematic discoveries clarify the status of populations, and the recognition of distinct species and lineages allows appropriate conservation strategies to be crafted, increasing the likelihood of success.
of recovery. In addition to identifying species and specimens, taxonomists care for vouchers, provide species lists for localities, and communicate taxonomic ideas to non-experts, especially through descriptions, keys, and field guides. Taxonomists can also provide conservation planning tools such as inventory data, estimates of extinction risk and extinction rate, and information for defining protected areas. Despite the importance of taxonomy, a lack of financial and institutional support impedes the training and employment of taxonomists and such factors need to be overcome. Taxonomic and systematic discoveries, especially those involving cryptic species and unrecognized diversity, are rapidly increasing with the advent of modern genetics. Researchers must be cautious to argue from multiple lines of evidence when naming new species and be clear about the species concept they employ, as these have wide ranging impacts beyond taxonomy. Creating new ties between taxonomists and non-experts will be crucial in conservation of a diverse range of organisms in increasingly fragile landscapes.


Conservation networks link diverse actors, either individuals or groups, across space and time. Such networks build social capital, enhance coordination, and lead to effective conservation action. Bat conservation can benefit from network approaches because the taxonomic and ecological diversity of bats, coupled with the complexity of the threats they face, necessitates a wide range of expert knowledge to effect conservation. Moreover, many species and issues transcend political boundaries, so conservation frequently requires or benefits from international cooperation. In response, several regional bat conservation networks have arisen in recent years, and we suggest, that with the globalization of threats to bats, there is now a need for a global network to strengthen bat conservation and provide a unified voice for advocacy. To retain regional autonomy and identity, we advocate a global network of the regional networks and develop a roadmap toward such a meta-network using a social network framework. We first review the structure and function of existing networks and then suggest ways in which existing networks might be strengthened. We then discuss how regional gaps in global coverage might best be filled, before suggesting ways in which regional networks might be linked for global coverage.


Bat populations around the world are declining as a consequence of human activities. Bat conservation thus hinges on changing human behavior, but to do so, we must understand the origins and drivers of the behavior. As natural scientists, most bat biologists lack the knowledge and training to implement rigorous studies of the human dimensions of bat conservation, yet such studies are needed to guide successful intervention. As we travel through the Anthropocene, it is critical that bat conservation biologists adopt an interdisciplinary approach and work with researchers from the social sciences who hold these skills and knowledge. To facilitate conversation and collaboration with conservation social scientists, I review the key theoretical and empirical perspectives on human behavior toward wildlife and report on studies of bats in these contexts wherever possible. I also recommend ways in which bat biologists can use some of this knowledge to enhance less structured or opportunistic outreach efforts encountered during our research activities.

Papers


On-going fragmentation of tropical forest ecosystems and associated depletion of seed dispersers threatens the long-term survival of animal-dispersed plants. These threats do not only affect biodiversity and species abundance, but ultimately ecosystem functions and services. Thus, seed dispersers such as the straw-coloured fruit bat, *E. helvum*, which traverse long distances across fragmented landscapes, are particularly important for maintaining genetic connectivity and colonizing new sites for plant species. Using high-resolution GPS-tracking of movements, field observations and gut retention experiments, we quantify dispersal distances for small- and large-seeded fruits foraged by *E. helvum* during periods of colony population low (wet season) and high (dry season) in an urban and a rural landscape in the forest zone of Ghana. Gut passage time averaged 116 min (range 4–1143 min), comparable to other fruit bats. Movements were generally longer in the urban than in the rural landscape and also longer in the dry than in the wet season. As the majority of seeds are dispersed only to feeding roosts, median dispersal distances were similar for both large (42–67 m) and small (42–65 m) seeds. However, small seeds were potentially dispersed up to 75.4 km, four times further than the previous maximum distance estimated for a similar-sized frugivore. Maximum seed dispersal distances for small seeds were almost twice as long in the rural (49.7 km) compared to the urban (31.2 km) landscape. Within the urban landscape, estimated maximum dispersal distances for small seeds were three times longer during the dry season (75.4 km) compared to the wet season (22.8 km); in contrast, distances in the rural landscape were three times longer in the wet season (67 km) compared to the dry season (24.4). Dispersal distances for large seeds during the dry season (551 m) in the rural landscape were almost twice that in the wet season (319 m). We found no influence of food phenology on dispersal distances. The maximum likelihood for seed dispersal beyond feeding roosts (mean distance from food tree 263 m) was 4.7%. Small seeds were dispersed over even longer distances, >500 and >1000 m, with a likelihood of 3.0 % and 2.3 % respectively. Our data show that *E. helvum* retains ingested seeds for very long periods and may traverse large distances, probably making it an important long distance seed disperser in tropical Africa. We suggest *E. helvum* is important for ecosystem functioning and urge its conservation.


Although Togo is a relatively small country in West Africa, it is characterized by a wide variety of vegetation zones ranging from moist forests to arid savannahs, including the “Dahomey Gap”. There has been no comprehensive documentation of the native mammal fauna of Togo since 1893. Our review of the extant and extirpated mammals of Togo includes 178 species, with Chiroptera (52 species) and Rodentia (47 species) being the most speciose groups. This number does not include additional species recorded along the borders of Togo, and whose presence inside the country is not verified. Seven species of mammals are presumably linked for global coverage.

Cohabitation between humans and microchiropteran bats is becoming an upscaling issue in the French island of La Réunion, as buildings can be crucial to the life histories of endemic species like Mormopterus francoismoutoui. Managing human-bat conflicts might play a key role in the survival of this endemic species, whose populations could rely on only a few natural or artificial permanent breeding colonies. Relocation projects are currently conducted on the island, involving bat boxes as alternative routes for displaced colonies. As such, two successful colonizations of bat boxes by M. francoismoutoui were observed in the East and the North of the island, initiating the first steps for the development and management of bats colonies relocation in the area. Guidelines are preserved, based on local and international feedback, in order to provide technical and scientific tools to resolve conflicts between humans and bats in the context of Réunion Island.


Infestation of Ixodes vespertilionis Koch, 1844 on Myotis punicus Felten, 1977 from two sites (Trios Tunnel and Sidi Trad cave) in north-eastern Algeria was studied. An overall infestation of 41.4% for all stages was found among bats collected from both sites. By stage, a total of eight females, 70 nymphs, and 107 larvae were recovered from both populations. The number of females recovered per bat at Sidi Trad ranged from 0-1, for nymphs 0-2, and for larvae 0-2. While no female ticks were collected at Trios Tunnel, the number of nymphs ranged from 0-2 and for larvae 0-2. At Trios Tunnel, the number of nymphs was significantly higher during April and June but not for July and September. On the other hand, the number of larvae increased from July to November, while at Sidi Trad cave, female ticks were recovered during April and May and then disappeared until the end of the study period. Significant differences were noted during all the months when compared with all stages. Nymphs infested bats significantly during April and May, declined in June and July, and then became steady until October. Larvae peaked in July, with low frequency in April, and then fluctuated from August to November.


The isolation of populations in the Iberian, Italian and Balkan peninsulas during the ice ages define four main paradigms that explain much of the known distribution of intraspecific genetic diversity in Europe. In this study we investigated the phylogeography of a wide-spread bat species, the bent-winged bat, Miniopterus schreibersii around the Mediterranean basin and in the Caucasus. Environmental Niche Modeling (ENM) analysis was applied to predict both the current distribution of the species and its distribution during the last glacial maximum (LGM). The combination of genetics and ENM results suggest that the populations of M. schreibersii in Europe, the Caucasus and Anatolia went extinct during the LGM, and the refugium for the species was a relatively small area to the east of the Levantine Sea, corresponding to the Mediterranean coasts of present-day Syria, Lebanon, Israel, and northeastern and northwestern Egypt. Subsequently the species first repopulated Anatolia, diversified there, and afterwards expanded into the Caucasus, continental Europe and North Africa after the end of the LGM. The fossil record in Iberia and the ENM results indicate continuous presence of Miniopterus in this peninsula that most probably was related to the Maghrebian lineage during the LGM, which did not persist afterwards. Using our results combined with similar findings in previous studies, we propose a new paradigm explaining the general distribution of genetic diversity in Europe involving the recolonization of the continent, with the main contribution from refugial populations in Anatolia and the Middle East. The study shows how genetics and ENM approaches can complement each other in providing a more detailed picture of intraspecific evolution.


Re-examination, using molecular tools, of the diversity of haemosporidian parasites (among which the agents of human malaria are the best known) has generally led to rearrangements of traditional classifications. In this study, we explored the diversity of haemosporidian parasites infecting vertebrate species (particularly mammals, birds and reptiles) living in the forests of Gabon (Central Africa), by analyzing a collection of 492 bushmeat samples. We found that samples from five mammalian species (four duiker and one pangolin species), one bird and one turtle species were infected by haemosporidian parasites. In duikers (from which most of the infected specimens were obtained), we demonstrated the existence of at least two distinct parasite lineages related to Polychromophilus species (i.e., bat haemosporidian parasites) and to sauropid Plasmodium (from birds and lizards). Molecular screening of sylvatic mosquitoes captured during a longitudinal survey revealed the presence of these haemosporidian parasite lineages also in several Anopheles species, suggesting a potential role in their transmission. Our results show that, differently from
what was previously thought, several independent clades of haemosporidian parasites (family Plasmodiidae) infect mammals and are transmitted by anopheline mosquitoes.


The transformation of native habitats into forest plantations for industrial purposes frequently has negative consequences for biodiversity. We evaluated the impact of eucalypt plantations on native bats in a Mediterranean area, taking Portugal as a case study. We compared the overall bat activity, species richness and Kuhl’s bat *Pipistrellus kuhlii* (the most abundant bat species in the area) activity between eucalypt plantations and native montado habitat, and examined the influence of stand, landscape and survey variables within plantations on the response variables. A set of 11 plantation stands, three landscape and two survey variables were employed as predictor variables using a zero-inflated Poisson generalized linear mixed model. Hawking and generalist bats of the genus *Pipistrellus* were the most frequently detected species. Bat activity, species richness and *P. kuhlii* activity were higher in native montado than in any of the eucalypt stands. Mature eucalypt plantations showed the highest bat activity, while clear-cut areas showed the lowest. Generally, within eucalypt stands, complex high-level vegetation structure, from the ground level up to 3 m high, and proximity to water points were associated with higher levels of bat and *P. kuhlii* activity and species richness. The results suggest that in order to promote bat diversity and activity in exotic eucalypt plantations in the Mediterranean region, it is important to provide a high density of water points, maintain plots of mature plantations and promote understorey clutter.


Bats of the family Pteropodidae, also known as megabats or Old World fruit bats, are widely distributed in tropical areas of Africa, Asia, and Oceania. Of 45 genera in the family, 12 are endemic to the Afro-tropical region and two others have representative species on the African continent. African megabats inhabit wooded habitats and are nearly ubiquitous on the mainland and nearby islands with the exception of desert areas. Some species have been implicated as possible reservoirs of the Ebola Zaire virus. We studied the phylogenetic relationships of mainland African megabats using both mitochondrial and nuclear loci in separate and combined analyses. The phylogenetic trees obtained showed four main African clades: *Eidolon*, Scotonycterini (including two genera), African *Rousettus* (three species), and the previously identified ‘endemic African clade’ (nine genera). The latter three lineages form a clade that also includes the Asian species of *Rousettus* and the Asian genus *Eonycteris*. *Eidolon* does not show close relationships to other African genera, instead nestling elsewhere in the megabat tree. Although our results confirm many of the conclusions of previous studies, they challenge the taxonomic status and placement of *Epomops dobsonii* and *Micropteropus*, and provide evidence indicating that a new classification at subfamilial and tribal levels is highly desirable. The principal clades we detected represent four independent colonizations of Africa from most probably Asian ancestors. Estimates of divergence dates suggest that these events occurred in different periods and that although local diversification appears to have started in the late Miocene, the more extensive diversification that produced the modern fauna occurred much later, in the Pleistocene.


The past year has marked the most devastating Ebola outbreak the world has ever witnessed, with over 28,000 cases and over 11,000 deaths. Ebola virus (EBOV) has now been around for almost 50 years. In this review, we discuss past and present outbreaks of EBOV and how those variants evolved over time. We explore and discuss selective pressures that drive the evolution of different Ebola variants, and how they may modify the efficacy of therapeutic treatments and vaccines currently being developed. Finally, given the unprecedented size and speed of the outbreak, as well as the extended period of replication in human hosts, specific attention is given to the 2014-2015 West African outbreak variant (Makona).


In addition to several emerging viruses, bats have been reported to host multiple bacteria but their zoonotic threats remain poorly understood, especially in Africa where the diversity of bats is important. Here, we investigated the presence and diversity of *Bartonella* and *Rickettsia* spp. in bats and their ectoparasites (Diptera and Siphonaptera) collected across South Africa and Swaziland. We collected 384 blood samples and 14 ectoparasites across 29 different bat species and found positive samples in four insectivorous and two frugivorous bat species, as well as their Nycteribiidae flies. Phylogenetic analyses revealed diverse *Bartonella* genotypes and one main group of *Rickettsia*, distinct from those previously reported in bats and their ectoparasites, and for some closely related to human pathogens. Our results suggest a differential pattern of host specificity depending on bat species. *Bartonella* spp. identified in bat flies and blood were identical supporting that bat flies may serve as vectors. Our results represent the first report of bat-borne *Bartonella* and *Rickettsia* spp. in these countries and highlight the potential role of bats as reservoirs of human bacterial pathogens.


Despite many studies illustrating the perils of utilising mitochondrial DNA in phylogenetic studies, it remains one of the most widely used genetic markers for this purpose. Over the last decade, nuclear introns have been proposed as alternative markers for phylogenetic reconstruction. However, the resolution capabilities of mtDNA and nuclear introns have rarely been quantified and compared. In the current study we generated a novel ~5 kb dataset comprising six nuclear introns and a mtDNA fragment. We assessed the relative resolution capabilities of the six intronic fragments with respect to each other, when used in various combinations together, and when compared to the traditionally used mtDNA. We focused on a major clade in the horseshoe bat
family (Afro-Palaearctic clade; Rhinolophidae) as our case study. This old, widely distributed and speciose group contains a high level of conserved morphology. This morphological stasis renders the reconstruction of the phylogeny of this group with traditional morphological characters complex. We sampled multiple individuals per species to represent their geographic distributions as best as possible (122 individuals, 24 species, 68 localities). We reconstructed the species phylogeny using several complementary methods (partitioned Maximum Likelihood and Bayesian and Bayesian multispecies coalescent) and made inferences based on consensus across these methods. We computed pairwise comparisons based on Robinson-Foulds tree distance metric between all Bayesian topologies generated (27,000) for every gene(s) and visualised the tree space using multidimensional scaling (MDS) plots. Using our supported species phylogeny we estimated the ancestral state of key traits of interest within this group, e.g. echolocation peak frequency which has been implicated in speciation. Our results revealed many potential cryptic species within this group, even in taxa where this was not suspected a priori and also found evidence for mtDNA introgression. We demonstrated that by using just two introns one can recover a better supported species tree than when using the mtDNA alone, despite the shorter overall length of the combined introns. Additionally, when combining any single intron with mtDNA, we showed that the result is highly similar to the mtDNA gene tree and far from the true species tree and therefore this approach should be avoided. We caution against the indiscriminate use of mtDNA in phylogenetic studies and advocate for pilot studies to select nuclear introns. The selection of marker type and number is a crucial step that is best on critical examination of preliminary or previously published data. Based on our findings and previous publications, we recommend the following markers to recover phylogenetic relationships between recently diverged taxa (~<20 My) in bats and other mammals: ACOX2, COPS7A, BGN, ROGDI and STAT5A.


Bats are the only mammals capable of powered flight, but little is known about the genetic determinants that shape their wings. Here we generated a genome for Miniopterus natalensis and performed RNA-seq and ChIP-seq (H3K27ac and H3K27me3) analyses on its developing forelimb and hindlimb autopods at sequential embryonic stages to decipher the molecular events that underlie bat wing development. Over 7,000 genes and several long noncoding RNAs, including Tbx5-as1 and Hottip, were differentially expressed between forelimb and hindlimb, and across different stages. ChIP-seq analysis identified thousands of regions that are differentially modified in forelimb and hindlimb. Comparative genomics found 2,796 bat-accelerated regions within H3K27ac peaks, several of which cluster near limb-associated genes. Pathway analyses highlighted multiple ribosomal proteins and known limb patterning signaling pathways as differentially regulated and implicated increased forelimb mesenchymal condensation in differential growth. In combination, our work outlines multiple genetic components that likely contribute to bat wing formation, providing insights into this morphological innovation.


In recent decades, the extent of primary forest in tropical regions has decreased drastically, with concurrent increases in the extent of tropical secondary forest. This has important implications for conservation management. We present novel data on species diversity and composition for three taxa (bats, geometrid moths and plants) in forests at two stages of secondary growth located in the Aberdare Mountains in Central Kenya. We found no significant differences in alpha diversity for any of the sampled groups between forest types. However, we found disturbance-driven differences of tree and herb community compositions and correlations between tree and moth – and tree and shrub community compositions. Changes in community compositions were more pronounced using an abundance-based indicator (Bray–Curtis) in comparison with an incidence based (Sørensen). Our results demonstrate that solely working with alpha diversity values can be misleading in conservation planning as they might not reflect compositional changes between habitats. Furthermore, abundance-based compositional measures appear to be superior to incidence-based measures for detecting subtle effects of disturbance on biodiversity.


The origins of interactions between angiosperms and fruit-eating seed dispersers have attracted much attention following a seminal paper on this topic by Tiffney (1984). This review synthesizes evidence pertaining to key events during the evolution of angiosperm-frugivore interactions and suggests implications of this evidence for interpretations of angiosperm-frugivore coevolution. The most important conclusions are: (i) the diversification of angiosperm seed size and fleshy fruits commenced around 80 million years ago (Mya). The diversity of seed sizes, fruit sizes and fruit types peaked in the Eocene around 55 to 50 Mya. During this first phase of the interaction, angiosperms and animals evolving frugivory expanded into niche space not previously utilized by these groups, as frugivores and previously not existing fruit traits appeared. From the Eocene until the present, angiosperm-frugivore interactions have occurred within a broad frame of existing niche space, as defined by fruit traits and frugivory, motivating a separation of the angiosperm-frugivore interactions into two phases, before and after the peak in the early Eocene. (ii) The extinct multituberculates were probably the most important frugivores during the early radiation phase of angiosperm seeds and fleshy fruits. Primates and rodents are likely to have been important in the latter part of this first phase. (iii) Flying frugivores, birds and bats, evolved during the second phase, mainly during the Oligocene and Miocene, thus exploiting an existing diversity of fleshy fruits. (iv) A drastic climate shift around the Eocene-Oligocene boundary (around 34 Mya) resulted in more semi-open woodland vegetation, creating patchily occurring food resources for frugivores. This promoted evolution of a ‘flying frugivore niche’ exploited by birds and bats. In particular, passerines became a dominant frugivore group worldwide. (v) Fleshy fruits evolved at numerous occasions in many angiosperm families, and many of the originations of fleshy fruits occurred well after the peak in the early Eocene. (vi) During periods associated with environmental change altering coevolutionary networks and opening of niche space, reciprocal coevolution may result in strong directional selection formative for both fruit and frugivore evolution. Further evidence is needed to test this hypothesis. Based on the abundance of plant lineages with various forms of fleshy fruits, and the diversity of frugivores, it is suggested that periods of rapid coevolution in angiosperms and frugivores occurred numerous times during the 80 million years of angiosperm-frugivore evolution.
Most molecular phylogenetic studies place all placental mammals into four superordinal groups, Laurasiatheria (e.g. dogs, bats, whales), Euarchontoglires (e.g. humans, rodents, colugos), Xenarthra (e.g. armadillos, anteaters) and Afrotheria (e.g. elephants, sea cows, tenrecs), and estimate that these clades last shared a common ancestor 90–110 million years ago. This phylogeny has provided a framework for numerous functional and comparative studies. Despite the high level of congruence among most molecular studies, questions still remain regarding the position and divergence time of the root of placental mammals, and certain ‘hard nodes’ such as the Laurasiatheria polytomy and Paenungulata that seem impossible to resolve. Here, we explore recent consensus and conflict among mammalian phylogenetic studies and explore the reasons for the remaining conflicts. The question of whether the mammal tree of life is or can be ever resolved is also addressed. This article is part of the themed issue ‘Dating species divergences using rocks and clocks’.

Pathogenic \textit{Leptospira} are the causative agents of leptospirosis, a disease of global concern with major impact in tropical regions. Despite the importance of this zoonosis for human health, the evolutionary and ecological drivers shaping bacterial communities in host reservoirs remain poorly investigated. Here, we describe \textit{Leptospira} communities hosted by Malagasy bats, composed of mostly endemic species, in order to characterize host–pathogen associations and investigate their evolutionary histories. We screened 947 individual bats (representing 31 species, 18 genera and seven families) for \textit{Leptospira} infection and subsequently genotyped positive samples using three different bacterial loci. Molecular identification showed that these \textit{Leptospira} are notably diverse and include several distinct lineages mostly belonging to \textit{Leptospira borgpetersenii} and \textit{L. kirschneri}. The exploration of the most probable host-pathogen evolutionary scenarios suggests that bacterial genetic diversity results from a combination of events related to the ecology and the evolutionary history of their hosts. Importantly, based on the data set presented herein, the notable host-specificity we have uncovered, together with a lack of geographical structuration of bacterial genetic diversity, indicates that the \textit{Leptospira} community at a given site depends on the co-occurring bat species assemblage. The implications of such tight host-specificity on the epidemiology of leptospirosis are discussed.

We present information on the prey taken by the Bat Hawk \textit{Macheiramphus alcinus} in two different areas of lowland western central Madagascar. These are the first dietary data from Madagascar for this widespread Old World species. The recovered remains were almost exclusively of bats and birds, with a few examples of reptiles and insects. In total, 178 pellets were analysed. On the basis of minimum number of individuals and biomass, bats accounted for 58.3% and 30.3%, respectively, and birds 36.1% and 69.7%, respectively. Amongst the nine species of bats recovered from the pellets, four were represented by multiple individuals, particularly taxa belonging to the families Molossidae and Vespertilionidae that fly in open areas, and for the 11 species of identified birds, all were represented by a single individual. These patterns are interpreted as a specialisation of feeding on bats during a narrow window of time at dusk, as they leave day roost sites, and then using birds in a more general manner to fill in nutritional needs.

Populations of the Malagasy \textit{Hipposideros commersoni} (family Hipposideridae) are threatened by deforestation and hunting. Maximum likelihood and Bayesian analysis of 149 cytochrome b sequences found this species to be paraphyletic and composed of three well-supported monophyletic clades. Clades B and C form a monophyletic lineage that can be referred to \textit{H. commersoni}; these two clades are separated by 6% sequence variation. Clade A represents a distinct evolutionary lineage separate (9–11% average sequence divergence) from \textit{H. commersoni} (clades B and C) and is named herein as a new species, \textit{Hipposideros cryptovalorona} sp. nov. In the phylogeny presented herein, this species is strongly associated with the outgroup taxa \textit{Hipposideros gigas} and \textit{Hipposideros vittatus}, both restricted to Africa. External, cranial and dental measurements taken from the same individuals used in the molecular study indicate no clear distinction in morphology amongst these three clades; this includes noseleaf structure and craniodental characteristics. Principal component analyses showed limited separation of the three clades. Comparison to a Quaternary fossil species from north-west Madagascar, \textit{Hipposideros besaoka}, found little morphological overlap between any of the three clades and this extinct species. Hence, at least three species of \textit{Hipposideros} have occurred on Madagascar since the Late Pleistocene, two extant (\textit{H. commersoni} s.s. and \textit{H. cryptovalorona} sp. nov.) and one extinct (\textit{H. besaoka}).

\textit{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 (\textit{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 host-specificity patterns. 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 Epaulletted Fruit Bat (\textit{Epomophorus wahlbergi} Sundevall) prefer ripe fruits over green ones. These bats also responded to synthetic compounds matching those identified from headspace samples of ripe figs.
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.


Phylogenomics has largely succeeded in its aim of accurately inferring species trees, even when there are high levels of discordance among individual gene trees. These resolved species trees can be used to ask many questions about trait evolution, including the direction of change and number of times traits have evolved. However, the mapping of traits onto trees generally uses only a single representation of the species tree, ignoring variation in the gene trees used to construct it. Recognizing that genes underlie traits, these results imply that many traits follow topologies that are discordant with the species topology. As a consequence, standard methods for character mapping will incorrectly infer the number of times a trait has evolved. This phenomenon, dubbed “hemiplasy,” poses many problems in analyses of character evolution. Here we outline these problems, explaining where and when they are likely to occur. We offer several ways in which the possible presence of hemiplasy can be diagnosed, and discuss multiple approaches to dealing with the problems presented by underlying gene tree discordance when carrying out character mapping. Finally, we discuss the implications of hemiplasy for general phylogenetic inference, including the possible drawbacks of the widespread push for “resolved” species trees.


The flea genus Araeopsylla Jordan and Rothschild, 1921 contains nine species distributed throughout the Palearctic, Ethiopian and Oriental Regions primarily on mollosid bats. A new species of bat flea, Araeopsylla goodmani, is described. This new species is represented by three females collected from one male specimen of the mollosid bat Chaerophon jobimena Goodman & Cardiff, 2004 from Fianarantsoa Province, Madagascar. A second new species, Araeopsylla smiti, is described from one male from the Rift Valley, Kenya. It was collected from the molosid bat Chaerophon bivittatus (Heuglin, 1861). This represents the first record of Araeopsylla in Kenya. Previous records of Araeopsylla in the Malagasy region included Araeopsylla martialis (Rothschild, 1903) from Reunion Island and Madagascar. One hundred fifty-eight specimens (64♂, 83♀) on 28 specimens of Araeopsylla smiti, which is the first record from this host species and the first time the genus Araeopsylla has been documented in Madagascar. Although Lagaropsylla consularis Smit, 1957 and Lagaropsylla idae Smit, 1957 have been reported in Madagascar previously, Mops leucostigma Allen, 1918 is a new host record for L. idae. The flea intensity of L. idae (64♂, 83♀) on 28 specimens of M. leucostigma was extremely high at 5.3 fleas per host. A key to the genus Araeopsylla is provided.


In this study we tested the hypothesis that the decrease in habitat quality at wastewater treatment works (WWTW), such as limited prey diversity and exposure to the toxic cocktail of pollutants, affect fatty acid profiles of interscapular brown adipose tissue (iBAT) in bats. Further, the antioxidant capacity of oxidative tissues such as pectoral and cardiac muscle may not be adequate to protect those tissues against reactive molecules resulting from polyunsaturated fatty acid auto-oxidation in the WWTW bats. Bats were sampled at two urban WWTW, and two unpolluted reference sites in KwaZulu-Natal, South Africa. Brown adipose tissue (BrAT) mass was lower in WWTW bats than in reference site bats. We found lower levels of saturated phospholipid fatty acids and higher levels of mono- and polyunsaturated fatty acids in WWTW bats than in reference site bats, while C18 desaturation and n-6 to n-3 ratios were higher in the WWTW bats. This was not associated with high lipid peroxidation levels in pectoral and cardiac muscle. Combined, these results indicate that WWTW bats rely on iBAT as an energy source, and opportunistic foraging on abundant, pollutant-tolerant prey may change fatty acid profiles in their tissue, with possible effects on mitochondrial functioning, torpor and energy usage.


A survey was conducted to establish bat roosts in public primary and secondary schools and the nature of nuisances they constitute to effective teaching and learning process in Zaria. The entire public pre-tertiary school structures within Zaria metropolis were examined for bat roost by internal and external inspections. Concerns on the presence of roosting bats were sought through questionnaire given to 384 school children and heads of schools occupied by bats were interviewed. The survey revealed that, of the total 75 schools located within the metropolis, 21 (28%) had roosting bats. All the schools with colony of roosting bats were plagued with bat nuisances such as distracting noise, stains, damaged ceilings, droppings and odour that threaten the health, safety and learning conditions of school children. Although most of the school children (70.7%) feel tense on seeing bat, 52.7% were however uncertain as to whether presence of bats could affect their academic performance or not. Heads of schools (43%) reported great concern on health and safety issues. Collaboration between school managements and local wildlife ecologists is recommended to address these nuisances.


As part of the project ‘Biodiversity under Climate Change: Community-Based Conservation, Management and Development Concepts for the Wild Coffee Forests’ funded by the German Federal Ministry for the Environment, Nature Conservation, Building
and Nuclear Safety (BMUB) within the framework of the International Climate Initiative, NABU has conducted an International Biodiversity Assessment at the Kafa Biosphere Reserve. A team of 16 German, 1 Dutch and 12 Ethiopian experts supported by 22 field local guides conducted intense field work from the 3rd to the 13th of December 2014 (European calendar). The overall goal of the assessment was to specify and verify flora and fauna assessments conducted in the Kafa Zone before 2014, record and list species, identify indicator and flagship species and determine their status (threat/least concern, underlying causes for threat, decline etc.). This report presents the findings and analysed data of the assessment by each field group. Following this report, all data will be analysed and incorporated into a biodiversity monitoring scheme and recommendations for conservation and management will be developed. This will help to preserve the area’s unique diversity and secure a regular monitoring.


Based on a fine review of bat literature in Burkina Faso, we identified the south-western and south-eastern parts of the country as gap regions where a study that aims to fill gap in bat diversity estimation could be conducted. In total, 72 sampling sites distributed in 32 localities were surveyed between April 2008 and September 2009. 407 mist-nets-nights of 12 and 6 m were used for a total effort of 2937.3 net-hours. 1639 specimens were captured in total distributed in 45 species, 22 genera and 9 families. 15 species including 2 frugivorous and 13 insectivorous were recorded for the first time in Burkina Faso. These new species recorded increased the bats diversity of Burkina Faso from 36 to 51.


Knowledge and protection of biodiversity are important issues the environment. To this end, we have studied the diversity of bats in Burkina Faso using new field data, complemented by all available data. In total 3 483 specimens have been used to estimate species richness of bats in Burkina Faso. 51 species belonging to 24 genera and 9 families were used for the analysis of the structure. Insectivorus have greater species diversity compared to that of frugivorous. According to our estimates, from 87,93 to 92,73 % of bats present in Burkina Faso have been identified. *Epomophorus gambianus, Micropteropus pusillus* and *Nanonycteris veldkampii* are the three most commonly encountered frugivores bats. As for insectivores, most common species are *Scotophilus leucogaster, Hipposideros ruber* and *Neoromicia guineensis*. Bats species richness is greater in Sudanian area than in Sahelian area while protected areas contribute to the tranquility of the species.


Recently, a new paramyxovirus closely related to human mumps virus (MuV) was detected in bats. We generated recombinant MuVs carrying either or both of the fusion and hemagglutinin-neuraminidase bat virus glycoproteins. These viruses showed replication kinetics similar to human MuV in cultured cells and were neutralized efficiently by serum from healthy humans.


Chronic stress may negatively impact fitness and survival in wildlife. Stress hormone analysis from feces is a non-invasive tool for identifying stressors and deducing about individual and population level fitness. Although many bat populations are endangered, fecal stress hormone analysis has not been established in bats as a method for focusing conservation efforts. The isabelline serotine bat, *Eptesicus isabellinus*, is exposed to human disturbance as its roosts are mostly found in anthropogenic structures. Moreover, this bat is host to various diseases and survival rates between colonies may vary significantly. To validate the analysis of fecal glucocorticoid metabolites, we applied an adrenocorticotropic hormone (ACTH) challenge and tested four different enzyme immunoassays (EIA) for measuring glucocorticoid concentrations. Cortisol and its metabolites showed the highest increase in blood and feces after the ACTH challenge, but corticosterone and its metabolites also increased significantly. Baseline fecal cortisol metabolite (FCM) concentrations did not increase until 1.5 h after the animals were captured, which is a convenient time lag for sample collection from captured animals. We furthermore compared baseline FCM concentrations between five colonies of *E. isabellinus* in Andalusia, Spain, and tested for their correlation with survival rates. FCM concentrations did not vary between colonies, but FCM levels increased with the animals’ age. FCM analysis may prove a useful tool for identifying bat colonies that carry either or both of the fusion and hemagglutinin-neuraminidase bat virus glycoproteins. These viruses showed replication kinetics similar to human MuV in cultured cells and were neutralized efficiently by serum from healthy humans.


Despite a relatively long search for the origin of ebolaviruses, their reservoirs remain elusive. Researchers might have to consider testing alternative hypotheses about how these viruses persist and emerge to advance ebolavirus research. This article aims to encourage researchers to bring forward such hypotheses, to discuss them scientifically and to open alternative research avenues regarding the origin and ecology of ebolaviruses.


Egyptian fruit bats (*Rousettus aegyptiacus*) are one of many species within zoologic collections that frequently develop iron storage disease. The goals of this retrospective multi-institutional study were to determine the tissue distribution of iron storage in captive
The incidence of intercurrent neoplasia and infection, which may be directly or indirectly related to iron overload. Tissue sections from 83 adult Egyptian fruit bats were histologically evaluated by using tissue sections stained with hematoxylin and eosin, trichrome, and Prussian blue techniques. The liver and spleen consistently had the largest amount of iron, but significant amounts of iron were also detected in the pancreas, kidney, skeletal muscle, and lung. Hepatocellular carcinoma (HCC; 11) was the most common neoplasm, followed by cholangiocarcinoma (4). Extrabiliary neoplasms included bronchioloalveolar adenoma (3), pulmonary carcinomas and (1), oral sarcoma (1), renal adenocarcinoma (1), transitional cell carcinoma of the urinary bladder (1), mammary gland adenoma (1), and parathyroid adenoma (1). There were also metastatic neoplasms of undetermined primary origin that included three poorly differentiated carcinomas, a poorly differentiated sarcoma, and a neuroendocrine tumor. Bats with hemochromatosis were significantly more likely to have HCC than bats with hemosiderosis ($P = 0.032$). Cardiomyopathy was identified in 35/77 bats with evaluable heart tissue, but no direct association was found between cardiac damage and the amount of iron observed within the liver or heart. Hepatic abscesses occurred in multiple bats, although a significant association was not observed between hemochromatosis and bacterial infection. To the authors’ knowledge, this is the first publication providing evidence of a positive correlation between hemochromatosis and HCC in any species other than humans.


**BACKGROUND:** In recent years, the scope and importance of emergent vector-borne diseases has increased dramatically. In Algeria, only limited information is currently available concerning the presence and prevalence of these zoonotic diseases. For this reason, we conducted a survey of hematophagous ectoparasites of domestic mammals and/or spleens of wild animals in El Tarf and Souk Ahras, Algeria. METHODS: Using real-time PCR, standard PCR and sequencing, the presence of Bartonella spp., Rickettsia spp., Borrelia spp. and Coxieilla burnetii was evaluated in 268/1626 ticks, 136 fleas, 11 Nycetieribididae flies and 16 spleens of domestic and/or wild animals from the El Tarf and Souk Ahras areas. RESULTS: For the first time in Algeria, Bartonella tamiiae was detected in 12/19 (63.2%)Ixodes师范tillions ticks, 8/11 (72.7%) Nycetieribididae spp. flies and in 6/10 (60%) bat spleens (Chiropieria spp.). DNA from Coxieilla burnetii, the agent of tick-borne lymphadenopathy, was detected in 1/1 (100%) Haemaphysalis punctata and 2/3 (66.7%) Dermacentor marginatus ticks collected from two boars (Sus scrofa algeria) respectively. R. massiliae, an agent of spotted fever, was detected in 38/94 (40.4%) Rhipicephalus sanguineus sensu latu collected from cattle, sheep, dogs, boars and jackals. DNA of R. aeschlimannii was detected in 6/20 (30%) Hyalomma anatolicum excavatum and in 6/20 (30%) H. scupense from cattle. Finally, R. felis, an emerging rickettsial pathogen, was detected in 80/110 (72.7%) Archaeoprylla Erinacei and 2/1 (100%) Ctenocephalides felis of hedgehogs (Attelatrix algerus). CONCLUSION: In this study, we expanded knowledge about the repertoire of ticks and flea-borne bacteria present in ectoparasites and tissues of domestic and wild animals in Algeria.


Phylogenies of parasites provide hypotheses on the history of their movements between hosts, leading to important insights regarding the processes of host switching that underlie modern-day epidemics. Haemosporidian (malaria) parasites lack a well resolved phylogeny, which has impeded the study of evolutionary processes associated with host-switching in this group. Here we present a novel phylogenetic hypothesis that suggests bats served as the ancestral hosts of malaria parasites in primates and rodents. Expanding upon current taxon sampling of Afrotropical bat and bird parasites, we find strong support for all major nodes and show little host specificity. These results highlight the importance of broad taxonomic sampling when analyzing phylogenetic relationships, and have important implications for our understanding of key host switching events in the history of malaria parasite evolution.


An eco-epidemiological investigation was carried out on Madagascar bat communities to better understand the evolutionary mechanisms and environmental factors that affect virus transmission among bat species in closely related members of the genus Morbillivirus, currently referred to as Unclassified Morbilli-related paramyxoviruses (UMRVs). A total of 947 bats were investigated originating from 52 capture sites (22 caves, 18 buildings, and 12 outdoor sites) distributed over different bioclimatic zones of the island. Using RT-PCR targeting the L-polymerase gene of the Paramyxoviridae family, we found that 10.5% of sampled bats were infected, representing six out of seven families and 15 out of 31 species analyzed. Univariate analysis indicates that both abiotic and biotic factors may promote viral infection. Using generalized linear modeling of UMRV infection overlaid on biotic and abiotic variables, we demonstrate that sympatric occurrence of bats is a major factor for virus transmission. Phylogenetic analyses revealed that all paramyxoviruses infecting Malagasy bats are UMRVs and showed little host specificity. Analyses using the maximum
parsimony reconciliation tool CoRe-PA, indicate that host-switching, rather than co-speciation, is the dominant macro-evolutionary mechanism of UMRVs among Malagasy bats.


Crimean Congo hemorrhagic fever virus (CCHFV) is a highly virulent tick-borne pathogen that causes hemorrhagic fever in humans. The geographic range of human CCHF cases largely reflects the presence of ticks. However, highly similar CCHFV lineages occur in geographically distant regions. Tick-infested migratory birds have been suggested, but not confirmed, to contribute to the dispersal. Bats have recently been shown to carry nonviruses distinct from CCHFV. In order to assess the presence of CCHFV in a wide range of bat species over a wide geographic range, we analyzed 1,153 sera from 16 different bat species collected in Congo, Gabon, Ghana, Germany, and Panama. Using a CCHFV glycoprotein-based indirect immunofluorescence test (IIFT), we identified reactive antibodies in 10.0% (114/1,153) of tested bats, pertaining to 12/16 tested species. Depending on the species, 3.6%–42.9% of cave-dwelling bats and 0.6%–7.1% of foliage-living bats were seropositive (two-tailed t-test, p = 0.0447 cave versus foliage). 11/30 IIFT-reactive sera from 10 different African bat species had neutralizing activity in a virus-like particle assay. Neutralization of full CCHFV was confirmed in 5 of 7 sera. Widespread infection of cave-dwelling bats may indicate a role for bats in the life cycle and geographic dispersal of CCHFV.


The Banana Bat, Neoromicia nana, exploits pollution-tolerant chironomids at wastewater treatment works (WWTWs). We investigated how pollutant exposure impacts the detoxification organs, namely the liver and kidney of N. nana. (i) We performed SEM-EDS to quantify metal content and mineral nutrients, and found significant differences in essential metal (Fe and Zn) content in the liver, and significant differences in Cu and one mineral nutrient (K) in the kidneys. (ii) We performed histological analysis and found more histopathological lesions in detoxification organs of WWTW bats. (iii) We calculated hepatosomatic/renalsomatic indices (HSI/RSI) to investigate whole organ effects, and found significant increases in organ size at WWTWs. (iv) We quantified metalloenzyme 1E (MT1E), using Western Blot immunodetection. Contrary to predictions, we found no significant upregulation of MT1E in bats at WWTWs. Ultimately, N. nana exploiting WWTWs may suffer chronic health problems from sub-lethal damage to organs responsible for detoxifying pollutants.


The aim of this study was to investigate the evolutionary determinants of genetic structure in a molossid bat, Chaerephon pumilus, from South Africa based on 306 nucleotides of the mitochondrial control region and six microsatellite markers. We recovered strong mitochondrial genetic structure, with 90% of the molecular variance occurring among four phylogenetically-defined groups. Mismatch distributions and Bayesian skyline analyses of mitochondrial data indicated that the sample comprised subgroups, which were at demographic equilibrium over the Late Pleistocene era. Analyses based on microsatellite data contrasted strongly with the mitochondrial data. Three admixed populations were recovered; only 3% of the nuclear variance occurred among populations, which was low and not significant. This is indicative of little nuclear genetic structure among the groups of C. pumilus, which appear to comprise a single interbreeding population. Consistent with this, global Fis was not significant. Such high levels of mitochondrial genetic structure in the absence of significant nuclear structure are consistent with female philopatry, secondary contact between diverged genetic lineages and introgression.


The Albert Rift is an ecoregion which extends from the North of Albert Lake in Blue Mountains to the South extreme of Tanganyika Lake. This area attracts the attention of scientists. In fact it is characterized by an endemic, specific wealth and very and very high vulnerable. We would like to contribute to the knowledge of taxa of the earth’s biodiversity and aquatic one according to the logic: “World Conservation Monitoring Center”, as regards to conservation. We have also listed from bats twenty three species and two vulnerable. We would like to contribute to the knowledge of taxa of the earth’s biodiversity and aquatic one according to the logic:


Thirteen individuals of Noack's round-leaf bat, Hipposideros aff. ruber, were radio-tracked for 38 nights in an agricultural landscape in Kwamang, Ashanti Region, Ghana. Local convex hulls were used to estimate home range sizes of the bats. Based on 1,192 fixes,
the mean (± SD) home range size was 36 ha ± 35 ha. Individual home range size ranged from six to 95 ha and frequently overlapped among individuals. The foraging area covered 50% of the home range while the core area formed 2%. The mean maximum foraging distance was 1.1 km, with individual distances up to 2.6 km, suggesting *Hipposideros aff. ruber* is capable of covering relatively long distances. Male bats returned to the cave more often than females during the night. Although the cave was the main roost, each bat also had individual night roosts on trees.


Background: Evidence of haemosporidian infections in bats and bat flies has motivated a growing interest in characterizing their transmission cycles. In Gabon (Central Africa), many caves house massive colonies of bats that are known hosts of *Polychromophilus Dionisi* parasites, presumably transmitted by blood-sucking bat flies. However, the role of bat flies in bat malaria transmission remains under-documented. Methods: An entomological survey was carried out in four caves in Gabon to investigate bat fly diversity, infestation rates and host preferences and to determine their role in *Polychromophilus* parasite transmission. Bat flies were sampled for 2–4 consecutive nights each month from February to April 2011 (Faucon and Zadie caves) and from May 2012 to April 2013 (Kessipoughou and Djilibong caves). Bat flies isolated from the fur of each captured bat were morphologically identified and screened for infection by haemosporidian parasites using primers targeting the mitochondrial cytochrome b gene. Results: Among the 1,154 bats captured and identified as *Miniopterus inflatus* Thomas (n = 354), *Hipposideros caffer* Sundevall complex (n = 285), *Hipposideros gigas* Wagner (n = 317), *Rousettus aegyptiacus* Geoffroy (n = 157), and *Coleura afra* Peters (n = 41), 439 (38.0 %) were infested by bat flies. The 1,063 bat flies recovered from bats belonged to five taxa: *Nycteribia schmidti scotti* Falcoz, *Eucampsipoda africana* Theodor, *Penicillidia fulvida* Bigot, *Brachytarsina allaudi* Falcoz and *Raymondia huberi* Frauenfeld group. The mean infestation rate varied significantly according to the bat species (ANOVA, F 6,1481 = 13.15, P < 0.001) and a strong association effect between bat fly species and host bat species was observed. *Polychromophilus melanipherus* Dionisi was mainly detected in *N. s. scotti* and *P. fulvida* and less frequently in *E. africana*, *R. huberi* group and *B. allaudi* bat flies. These results suggest that *N. s. scotti* and *P. fulvida* could potentially be involved in *P. melanipherus* transmission among cave-dwelling bats. Sequence analysis revealed eight haplotypes of *P. melanipherus*. Conclusions: This work represents the first documented record of the cave-dwelling bat fly fauna in Gabon and significantly contributes to our understanding of bat fly host-feeding behavior and their respective roles in *Polychromophilus* transmission.


Whether it is justified or effective to cull populations of bats, as a means for mitigating human–animal conflict or controlling disease, is an issue that has recently resurfaced with moves by the Mauritian government to cull a population of endangered Mauritian flying foxes (*Pteropus niger*) (IUCN 2015). Similar calls for fruit bat culls by the Australian government in response to crop damage and out-breaks of Hendra virus (Walker and Nadin 2011) underscore the urgent need for a more robust, science-based approach to guide wildlife management. Here, I review the evidence and argue that culling of bat populations is not an effective means to mitigate conflict with fruit growers, nor to reduce the likelihood of zoonotic disease risk.


Ebola virus, discovered in 1976, caused the largest epidemic among humans in 2014. In this paper, we have discussed the systematic position of *Ebolaovirus*, the ecology of these viruses, the essential elements of pathogenesis of these infections as well as comparative characteristics of *Filoviruses* infectious biology. According to the paleovirological data, these features were developed during millions of years of the co-evolution process and co-existence of pathogens and hosts. It is likely that changes of Ebola virus biology are not the reason for such substantial changes in the epidemiology of Ebola virus infections. Analysis of factors associated with the characteristics of the present epidemic (size, region) indicate that the main reason for such big epidemic may be the changes related to both humans activity, mainly transformation of the environment, and the ability of bats (natural hosts of *Filoviruses*) to adapt to the new ecological conditions. These processes may cause more outbreaks in the future, also on a large scale, and require taking appropriate actions to reduce the risks.


Biodiversity is declining, with direct and indirect effects on ecosystem functions and services that are poorly quantified. Here, we develop the first global assessment of trends in pollinators, focusing on pollinating birds and mammals. A Red List Index for these species shows that, overall, pollinating bird and mammal species are deteriorating in status, with more species moving toward extinction than away from it. On average, 2.5 species per year have moved one Red List category toward extinction in recent decades, representing a substantial increase in the extinction risk across this set of species. This may be impacting the delivery of benefits that these species provide to people. We recommend that the index be expanded to include taxonomic groups that contribute more significantly to pollination, such as bees, wasps, and butterflies, thereby giving a more complete picture of the state of pollinating species worldwide.
Documenting and monitoring biodiversity are essential for the study and understanding of processes of species diversification, the assessment of conservation priorities, and conservation management decisions. This paper updates previous reports on the biodiversity of mammals in and around the Bezà Mahafaly Special Reserve in southwest Madagascar, which protects 4,200 ha of forest contiguous with broad stretches of surrounding forest. Findings come from the Bezà Mahafaly Monitoring Team and many students and researchers who have worked at the reserve. Methods used to inventory mammals include direct field observation, recording scat and tracks, camera- and live-trapping, mist-netting, and searching in dead wood. The diversity of mammals recorded has not decreased since the last published inventory in 2001, despite long-term reduction of forest cover in the area and pressures resulting from human activity. Four species are reported for the first time (Macrotarsomys bastardii, Triaenops menamana, Myotis goudoti, and Suncus murinus). One species has been eliminated as a likely case of mistaken identification (Hemicycletes semispinosus), and S. madagascariensis has been synonymized with S. etruscus. The balance of evidence indicates that Microcebus murinus is not present and that a murinus-like form occurs as a pelage color variant of M. griseorufus. Further research is needed to explain the phenotypic diversity of this population. Questions also remain about the species status of Lepilemur and Propithecus. Resolving these points, pursuing a range of key questions in ecological and evolutionary biology, and continued monitoring of the status of the mammal populations of the Bezà Mahafaly landscape are all important and urgent issues to be addressed.


Recent Literature
changing the availability of light and darkness as resources of food, information and refuge. I tested the hypothesis that urban exploiters should be more likely to utilize bright, unpredictable light pollution sources such as sport stadiums and building sites than urban avoiders. I quantified insectivorous bat activity and feeding attempts at seven sport stadiums under light and dark treatments using acoustic monitoring of echolocation calls. Species richness estimators indicated that stadium inventories were complete. Activity and feeding attempts were significantly higher at lit stadiums than dark stadiums, irrespective of season or surrounding human land use. Bats exhibited species-specific differences in utilization of stadiums. As predicted, four urban exploiters – Chaerophon pumilus, Tadarida aegytiaca, Otomops martiensseni and Scotophilus dinganii – dominated activity and feeding attempts at lit stadiums, yet one urban exploiter – Mops condylurus – was associated with dark stadiums. Activity levels at both dark and light stadiums were negatively correlated with peak echolocation frequency. Landscape-scale and finer scale abiotic variables were poor predictors of bat activity and feeding attempts. My results suggest that in addition to abiotic processes associated with urbanization, light pollution at sport stadiums may homogenize urban bat diversity by favoring selected urban exploiters.


Background: The cave-dwelling Egyptian rousette bat (ERB; Rousettus aegyptiacus) was recently identified as a natural reservoir host of marburgvirus. However, the mechanisms of transmission for the enzootic maintenance of marburgviruses within ERBs are unclear. Previous ecological investigations of large ERB colonies inhabiting Python Cave and Kitaka Mine, Uganda revealed that argasid ticks (Ornithodoros faini) are hematophagous ectoparasites of ERBs. Yet, their potential role as transmission vectors for marburgvirus has not been sufficiently assessed. Findings: In the present study, 3,125 O. faini were collected during April 2013 from the rock crevices of Python Cave, Uganda. None of the ticks tested positive for marburgvirus-specific RNA by Q-RT-PCR. The probability of failure to detect marburgvirus at a conservative prevalence of 0.1% was 0.05. Conclusions: The absence of marburgvirus RNA in O. faini suggests they do not play a significant role in the transmission and enzootic maintenance of marburgvirus within their natural reservoir host.


Species of the genus Raymondia (Diptera: Streblidae) are obligate ectoparasites of bats. They have a wide distribution across Africa and are associated with many different bat species. Here we present the first record of this family in Swaziland. The ectoparasites were of the species Raymondia alulata and were found parasitizing individuals of the species Nycteris thebaica. We review the status of Raymondia species known in Africa, including species records, hosts, and host distributions and provide an updated identification key for species in this genus.


A new fossil from the Late Eocene BQ-2 locality in the Birket Qarun Formation in the Fayum Depression of northern Egypt (dated to ~37 mybp) does not fit within the diagnosis of any previously described family of bats from Africa or any other continent. Known from a partial maxilla, this taxon has dilambdodont trisphoric molars with a well-developed, symmetrical, W-shaped ectoloph lacking a distinct mesostyle but with a strong parastyle and shallow U-shaped ectoflexus—all traits that are found in most archaic bat families and that are probably plesiomorphic for bats. However, this taxon also has an M2 with a large metaconule cusp and a large, bulbous hypcone set low on the posterolinguinal corner of the tooth, neither of which occur in any known bat family, living or extinct. Also notable is the size of the new BQ-2 bat, which appears to have been approximately the same size as the largest extant bats with dilambdodont dentitions, falling well within the size range of plant-eating megabats and carnivorous bats from several extant lineages. The combination of traits in the new BQ-2 bat suggests that it was omnivorous, probably including insects, small vertebrates, and plant material its diet. In this regard it represents an ecological niche previously unknown among archaic Eocene bats, which are otherwise thought to have been strictly animalivorous. Because extinct Eocene bat families exhibit considerable mosaic evolution in morphological traits, do not seem to have inhabited a uniform ecological niche, and do not form a monophyletic group, we argue against use of the name “Eochiroptera” to collectively refer to these taxa.


Bats are considered important bioindicators and deliver key ecosystem services to humans. However, it is not clear how the individual and combined effects of climate change and land-use change will affect their conservation in the future. We used a spatial conservation prioritization framework to determine future shifts in the priority areas for the conservation of 169 bat species under projected climate and land-use change scenarios across Africa. Specifically, we modelled species distribution models under four different climate change scenarios at the 2050 horizon. We used land-use change scenarios within the spatial conservation prioritization framework to assess habitat quality in areas where bats may shift their distributions. Overall, bats’ representation within already existing protected areas in Africa was low (~5% of their suitable habitat in protected areas which cover ~7% of Africa). Accounting for future land-use change resulted in the largest shift in spatial priority areas for conservation actions, and species representation within priority areas for conservation actions decreased by ~9%. A large proportion of spatial conservation priorities will shift from forested areas with little disturbance under present conditions to agricultural areas in the future. Planning land use to reduce impacts on bats in priority areas outside protected areas where bats will be shifting their ranges in the future is crucial to enhance their conservation and maintain the important ecosystem services they provide to humans.

Singing plays an important role in the social lives of several disparate bat species, but just how significant the behavior may be among bats generally is unknown. Recent discoveries suggest singing by bats might be surprisingly more diverse and widespread than anticipated, but if true then two questions must be addressed: firstly why has singing been so rarely documented among bats, and secondly do bats sing for the same reasons as songbirds? We address the first question by reviewing how sampling bias and technical constraints may have produced a myopic view of bat social communication. To address the second question, we review evidence from 50 years of batsong literature supporting the supposition that bat singing is linked to the same constellation of ecological variables that favored birdsong, including territoriality, polygyny, metabolic constraints, migratory behaviors and especially powered flight. We propose that bats sing like birds because they fly like birds; flight is energetically expensive and singing reduces time spent flying. Factoring in the singular importance of acoustic communication for echolocating bats, it seems likely that singing may prove to be relatively common among certain groups of bats once it becomes clear when and where to look for it.


The variety of factors that contributed to the initial undetected spread of Ebola virus disease in West Africa during 2013–2016 and the difficulty controlling the outbreak once the etiology was identified highlight priorities for disease prevention, detection, and response. These factors include occurrence in a region recovering from civil instability and lacking experience with Ebola response; inadequate surveillance, recognition of suspected cases, and Ebola diagnosis; mobile populations and extensive urban transmission; and the community’s insufficient general understanding about the disease. The magnitude of the outbreak was not attributable to a substantial change of the virus. Continued efforts during the outbreak and in preparation for future outbreak response should involve upgrading of reservoirs, improving in-country detection and response capacity, conducting survivor studies and supporting survivors, engaging in culturally appropriate public education and risk communication, building productive interagency relationships, and continuing support for basic research.


Ebola virus and Marburgvirus belong to the Filovirus family and are responsible for hemorrhagic fevers in Africa. The first documented Filovirus outbreak in Africa occurred in Central Africa and was attributed to Ebola virus species. In the last four decades, Filoviral hemorrhagic fevers (FHF) outbreaks caused by Ebola and Marburg viruses have been on the increase in Africa. The 2013-2015 outbreak has been the largest outbreak in human and has had the most devastating human and economic impact. Epidemics usually originate from a primary single introduction of the virus into simian or human population followed by an interspecies spillover. Multiple, short and isolated transmissions to humans have been also observed. Since the 1976 Yambuku (Democratic Republic of Congo) and Nzara (Sudan) epidemics, several investigations of different animal species have been undertaken but failed to identify the natural reservoirs of Ebola virus. Further studies identified bats as probable reservoirs of Ebola virus in Gabon, and major natural reservoirs of Marburg virus in Uganda, supposed central forested areas of Africa as the epicenter where these viruses originated from, before dissemination. Chimpanzees, gorillas and duikers have been identified as highly sensitive hosts of Ebola virus within wildlife. However, the relative importance of potential vertebrate hosts in the FHF's emergence into human population remains unclear. Different transmission routes involving bats have been proposed. Filoviruses have a zoootic origin; amplified and maintained in nature between potential reservoirs in a jungle cycle. Ebola virus mostly escapes these natural foci, when other sensitive secondary simian are infected and transmit the virus to human population via hunting, bat’s saliva infected wild fruit collection or land monitoring, while Marburg virus emergence was linked to monkey’s tissues handling or human entry into bat sheltering habitats. This review discusses the dissemination of filoviruses circulating within their possible chiropteran reservoir species. Vertebrate hosts suspected in the maintenance/transmission cycles are reviewed and their biocological features discussed. Despite the importance of the findings about reservoirs’ discovery, several other questions such as plurispecies associations, migration routes, breeding cycles need to be addressed and are pointed out in this review, in order to generate risk maps for filoviruses’ (re)emergence in West Africa.


We report on the isolation of a novel fusogenic orthoreovirus from bat flies (Eucampsipoda africana) associated with Egyptian fruit bats (Rousettus aegyptiacus) collected in South Africa. Complete sequences of the ten dsRNA genome segments of the virus, tentatively named Mahlapitsi virus (MAHLV), were determined. Phylogenetic analysis places this virus into a distinct clade with Baboon orthoreovirus, Bush viper reovirus and the bat-associated Broome virus. All genome segments of MAHLV contain a 5’ terminal sequence (5’-GGUCA) that is unique to all currently described viruses of the genus. The smallest genome segment is bicistronic encoding for a 14 kDa protein similar to p14 membrane fusion protein of Bush viper reovirus and an 18 kDa protein similar to p16 non-structural protein of Baboon orthoreovirus. This is the first report on isolation of an orthoreovirus from an anthropod host associated with bats, and phylogenetic and sequence data suggests that MAHLV constitutes a new species within the Orthoreovirus genus.


A recent study introduced a vaccine that controls Ebola Makona, the Zaire ebolavirus variant that has infected 28,000 people in West Africa. We propose that even such successful advances are insufficient for many emergent diseases. We review work hypothesizing that Makona, phenotypically similar to much smaller outbreaks, emerged out of shifts in land use brought about by neoliberal economics. The epidemiological consequences demand a new science that explicitly addresses the foundational
processes underlying multispecies health, including the deep-time histories, cultural infrastructure, and global economic geographies driving disease emergence. The approach, for instance, reverses the standard public health practice of segregating emergency responses and the structural context from which outbreaks originate. In Ebola's case, regional neoliberalism may affix the stochastic "friction" of ecological relationships imposed by the forest across populations, which, when above a threshold, keeps the virus from lining up transmission above replacement. Export-led logging, mining, and intensive agriculture may depress such functional noise, permitting novel spillovers larger forces of infection. Mature outbreaks, meanwhile, can continue to circulate even in the face of efficient vaccines. More research on these integral explanations is required, but the narrow albeit welcome success of the vaccine may be used to limit support of such a program.


Until recently, hantaviruses (family Bunyaviridae) were believed to originate from rodent reservoirs. However, genetically distinct hantaviruses were lately found in shrews and moles, as well as in bats from Africa and Asia. Bats (order Chiroptera) are considered important reservoir hosts for emerging human pathogens. Here, we report on the identification of a novel hantavirus, provisionally named Makokou virus (MAKV), in Noack's Roundleaf Bat (Hipposideros ruber) in Gabon, Central Africa. Phylogenetic analysis of the genomic l-segment showed that MAVK was the most closely related to other bat-borne hantaviruses and shared a most recent common ancestor with the Asian hantaviruses Xuan Son and Laibin. Breakdown of the virus load in a bat animal showed that MAVK resembles rodent-borne hantaviruses in its organ distribution in that it predominantly occurred in the spleen and kidney; this provides a first insight into the infection pattern of bat-borne hantaviruses. Ancestral state reconstruction based on a tree of l gene sequences of all relevant hantavirus lineages was combined with phylogenetic fossil host hypothesis testing, leading to a statistically significant rejection of the mammalian superorder Euarchontoglires (including rodents) but not the superorder Laurasiatheria (including shrews, moles, and bats) as potential hosts of ancestral hantaviruses at most basal tree nodes. Our data supports the emerging concept of bats as previously overlooked hantavirus reservoir hosts.


At the time of writing, West Africa is still dealing with the worst known Ebola epidemic. Quite rightly, the international focus has been on reducing the transmission rate of this disease until it is eradicated from the human population. Once the epidemic curve has declined to this point, scientific attention should be re-directed to the prevention of future zoonotic outbreaks. There already has been much written on how the West African epidemic might have been sparked, but speculation often has been presented as fact and in some cases has been contrary to available evidence. Such inaccurate reporting on the drivers of the emergence of this epidemic is unfortunate, as this can influence policy decisions while failing to identify how Ebola and other serious zoonoses should be controlled.


Viral discovery studies in bats have increased dramatically over the past decade, yet a rigorous synthesis of the published data is lacking. We extract and analyze data from 93 studies published between 2007-2013 to examine factors that increase success of viral discovery in bats, and specific trends and patterns of infection across host taxa and viral families. Over the study period, 248 novel viruses from 24 viral families have been described. Using generalized linear models, at a study level we show the number of host species and viral families tested best explained number of viruses detected. We demonstrate that prevalence varies significantly across viral family, specimen type, and host taxonomy, and calculate mean PCR prevalence by viral family and specimen type across all studies. Using a logistic model, we additionally identify factors most likely to increase viral detection at an individual level for the entire dataset and by viral families with sufficient sample sizes. Our analysis highlights major taxonomic gaps in recent bat viral discovery efforts and identifies ways to improve future viral pathogen detection through the design of more efficient and targeted sample collection and screening approaches.

Notice Board

Conferences

17th International Bat Research Conference
To be held in: Durban, South Africa, 31 July - 5 August 2016.
Further information: http://ibrc2016.co.za.

12th Conference of the European Wildlife Disease Association
To be held in: Berlin, Germany, 27 - 31 August 2016.
To be held in: Kunigami, Japan, 15 - 19 November 2016. Further information: http://www.zoology.or.jp/2016-jointmeeting/

European Conference of Tropical Ecology


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 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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