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Above: Bushveld Horseshoe Bat (*Rhinolophus simulator*) drinking from pond at the Meletse Bat Research and Conservation Training Centre, Limpopo Province, South Africa.

Inside this issue

Research and Conservation Activities

Invitation to BAT1K Genome Consortium

Emma Teeling, Sonja Vernes, David Ray, Liliana Davalos, Tom Gilbert and Gene Myers

BAT1K is an new initiative aimed to sequence the genomes of all extant species of bats to chromosome level assemblies. Our goal as a consortium is to uncover the genes and genetic mechanisms behind the unique adaptations of bats, mining their genomes to uncover their secrets. This consortium is only possible by uniting bat researchers, field biologists, conservation organisations and lay people across the world to identify all bat species, so that we can uncover their secrets. We aim to form an active community of individuals with a common goal to conserve, better understand and promote bats.

BAT1K is currently in the initial stages, actively searching for funding to sequence every genera in a 5 year time span. While this is underway, we would like to ask you to join BAT1K and help us collect the samples required to make this a reality. In order to make the highest quality genomes possible, we need ideally flash frozen tissue, high molecular weight DNA, tissue cultures or access to living individuals. If you have access to any of these resources for any bat species, you can sign up at our website (bat1k.com), committing to BAT1K and pledging these resources to the project. If you want to pledge other resources (i.e. computational time, bioinformatics expertise etc.) or simply just want to be informed about the project, sign up and we will keep up to date with the progress of BAT1K.

As we are still in the initial stages, we would like anyone who is donating tissue sources to keep them frozen at <-80 degrees until funding is acquired to initiate the first phase of BAT1K. By signing up, you will be kept up to date through a regular newsletter and will be contacted as soon as Phase 1 begins.

By showing interest in this project and signing up, you can help us convince funding agencies to provide the resources required to make this project a reality. Together we will generate an unrivaled ‘genomic ark’ of bat genomes, preserving their genomic diversity for eternity. This will enable us to develop better conservation plans and ultimately stimulate global interest and appreciation of bats.

Observations, Discussions and Updates

Recent changes in African Bat Taxonomy (2015 – 2017)

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†NECROMANTIDAE Sigé, 2011

†*Necromantis* Weithofer, 1887

†*Necromantis fragmentum* Ravel, in Ravel, Adaci, Bensalah, Charruault, Essid, AMmar, Marzougui, Mahboubi, Mebrouk, Merzeraud, Vianey-Liaud, Tabuce and Marivaux, 2016

Locality and Horizon: Chambi (CBI) loci 1, 2 and 3, late lower Eocene - middle Eocene, Djebel Chambi, situated in the Kasserine region, Tunisia.

Etymology: From the Latin ‘fragmentum’, meaning fragment or debris, referring to the fragmentary character of the material attributed to this taxon.

†AEGYPTONYCTERIDAE Simmons, Seiffert and Gunnell, 2016

The suite of traits seen in *Aegyptonycteris knightae* is unique and justifies recognition of this taxon as a distinct chiropteran family, Aegyptonycteridae (type genus and species = *Aegyptonycteris knightae*).

†*Aegyptonycteris* Simmons, Seiffert and Gunnell, 2016

†*Aegyptonycteris knightae* Simmons, Seiffert and Gunnell, 2016

Locality and Horizon: Fayum Quarry BQ-2, 23 meter level, Birket Qarun Formation, Fayum Depression, Western Desert, Egypt (Fig. 1-2). Age: Late Eocene, Priabonian, ~37 Ma.

Etymology: From Aegyptus, Latinized Greek for ‘Egypt’, and nycteris, Greek for ‘bat’.

The genus name refers to the country in which this new taxon was discovered. The specific epithet is given in honour of Mary Knight, Managing Editor of the American Museum of Natural History Scientific Publications, in recognition of the enormous contributions she has made to dissemination of the results of scientific research over the years, as well as her lifelong devotion to the people and culture of Egypt.

Eidolinae Almeida, Giannini and Simmons, 2016

This subfamily was created by ALMEIDA *et al.* (2016: 84) to distinguish monophyletic groups within the Pteropodidae.

Currently recognized genera of Eidolinae: *Eidolon* Rafinesque, 1815.

Pteropodinae Gray 1821

Subfamily arrangement based on ALMEIDA *et al.* (2016: 83).

Currently recognized genera of Pteropodinae: *Acerodon* Jourdan, 1837, *Macroglossus* F. Cuvier, 1824, *Melonycteris* Dobson, 1877, *Neopteryx* Hayman, 1946, *Notopteris* Gray, 1859, *Pteralopex* Thomas, 1888, *Pteropus* Brisson, 1762, *Styloctenium* Matschie, 1899, *Syconycteris* Matschie, 1899.

Rousettinae Andersen, 1912

Subfamily arrangement based on ALMEIDA *et al.* (2016: 83).

Currently recognized tribes and genera of Rousettinae: Rousettini (*Rousettus* Gray, 1821), Eonycterini (*Eonycteris* Dobson, 1873), Scotonycterini (*Casinycteris* Thomas, 1910, *Scotonycteris* Matschie, 1894), Epomophorini (*Epomophorus* Bennett, 1836, *Epomops* Gray, 1870, *Hypsignathus* H. Allen, 1861, *Micropteropus* Matschie, 1899, *Nanonycteris* Matschie, 1899), Stenonycterini (*Stenonycteris* Gray, 1870), Myonycterini (*Lissonycteris* K. Andersen, 1912, *Megaloglossus* Pagenstecher, 1885, *Myonycteris* Matschie, 1899), Plerotini (*Plerotes* K. Andersen, 1910).

Epomophorus dobsonii Bocage, 1889

The phylogenetic analyses by ALMEIDA *et al.* (2016: 83) suggest that *dobsonii* is closely related to *Epomophorus wahlbergi* and they transferred the species from the genus *Epomops* to *Epomophorus*.

HIPPOSIDERIDAE

†_Palaeophyllophora_ Revilliod, 1917

†_Palaeophyllophora tunisiensis_ Ravel in Ravel, Adaci, Bensalah, Charruault, Essid, AMmar, Marzougui, Mahboubi, Mebrouk, Merzeraud, Vianey-Liaud, Tabuce and Marivaux, 2016

Locality and Horizon: Chambi (CBI) loci 1 and 2, late lower Eocene - middle Eocene, Djebel Chambi, situated in the Kasserine region, Tunisia.

Etymology: The species name refers to the country of origin: Tunisia.

†_Pseudorhinolophus_ Schlosser, 1887

Described as a subgenus of *Hipposideros*.

†_Hipposideros_ (_Pseudorhinolophus_) _africanum_ Ravel in Ravel, Adaci, Bensalah, Charruault, Essid, AMmar, Marzougui, Mahboubi, Mebrouk, Merzeraud, Vianey-Liaud, Tabuce and Marivaux, 2016

Locality and Horizon: Chambi (CBI) loci 1, 2 and 3, late lower Eocene - middle Eocene, Djebel Chambi, situated in the Kasserine region, Tunisia.

Etymology: The species name refers to the continent Africa and underlines the geographic originality of the of species which belongs to a genus that is otherwise only found in Europe.

Hipposideros cryptovalorona Goodman, Schoeman, Rakotoarivelo and Willows-Munro, 2016

Madagascar cryptic leaf-nosed bat (Eng.). La Phyllorhine cryptique de Madagascar (Fr.).

Analysing the cyt *b* sequences of 148 Madagascan *H. commersoni* s.l. specimens, GOODMAN *et al.* (2016: 428) found three well-supported monophyletic clades: A, B, and C. Clades B and C form a monophyletic lineage, which they were able to refer to *H. commersoni* s.s. Clade A showed a 9 to 11 % sequence variation with *H. commersoni* s.s., enough to warrant a separate species status. This new species is known from two adult females only.

Locality: Madagascar, Province de Fianarantsoa, Parc Nation- al de l'Isalo, along Sahanafa River, near foot of Bevato, 28 km south-east of Berenty-Betsileo, 22°19.0′S, 45°17.6′E, 550 m a.s.l.

Etymology: The name *cryptovalorona* is derived from the Greek 'kryptos', meaning hidden or concealed, and from the Sakalava dialect of Malagasy 'valorona', which is the local vernacular name of *Hipposideros* and refers to its distinct nasal structure, and can be translated as 'eight nose', referring to the complicated and multiple layers of the nose structure.

EMBALLONURIDAE

†_Vespertiliavus_ Schlosser, 1887

†_Vespertiliavus kasserinensis_ Ravel in Ravel, Adaci, Bensalah, Charruault, Essid, AMmar, Marzougui, Mahboubi, Mebrouk, Merzeraud, Vianey-Liaud, Tabuce and Marivaux, 2016

Locality and Horizon: Chambi (CBI) loci 1, 2 and 3, late lower Eocene - middle Eocene, Djebel Chambi, situated in the Kasserine region, Tunisia.

Etymology: The species name refers to the city of Kasserine, which is situated at the foot of the Djebel Chambi.

†_Vespertiliavus aenigma_ Ravel in Ravel, Adaci, Bensalah, Charruault, Essid, AMmar, Marzougui, Mahboubi, Mebrouk, Merzeraud, Vianey-Liaud, Tabuce and Marivaux, 2016

Locality and Horizon: Chambi (CBI) loci 1, 2 and 3, late lower Eocene - middle Eocene, Djebel Chambi, situated in the Kasserine region, Tunisia.

Etymology: From the Latin 'aenigma' meaning riddle or puzzle and referring to the originality of the morphological characters of the specimens and the difficult systematics.

†_Pseudovespertiliavus_ Ravel in Ravel, Adaci, Bensalah, Charruault, Essid, AMmar, Marzougui, Mahboubi, Mebrouk, Merzeraud, Vianey-Liaud, Tabuce and Marivaux, 2016

Etyomology: The generic name refers to the numerous morphological similarities with the genus *Vespertiliavus*.

†_Pseudovespertiliavus parva_ Ravel in Ravel, Adaci, Bensalah, Charruault, Essid, AMmar, Marzougui, Mahboubi, Mebrouk, Merzeraud, Vianey-Liaud, Tabuce and Marivaux, 2016

Locality and Horizon: Levels HGL50 and HGL50' of the Glib Zegdou, late lower Eocene - middle Eocene, situated in the Gour Lazib region (Sahara, Hammada du Dra), Algeria.

Etymology: From the Latin 'parva' meaning small, referring to the small size of this bat species.

NYCTERIDAE

†_Khoufechia_ Ravel in Ravel, Adaci, Bensalah, Charruault, Essid, AMmar, Marzougui, Mahboubi, Mebrouk, Merzeraud, Vianey-Liaud, Tabuce and Marivaux, 2016

Etymology: The generic name refers to the arab word 'Khouféche' for bat.

†_Khoufechia gunnelli_ Ravel in Ravel, Adaci, Bensalah, Charruault, Essid, AMmar, Marzougui, Mahboubi, Mebrouk, Merzeraud, Vianey-Liaud, Tabuce and Marivaux, 2016

Locality and Horizon: Chambi (CBI) loci 1, 2 and 3, late lower Eocene - middle Eocene, Djebel Chambi, situated in the Kasserine region, Tunisia.

Etymology: In honour of Gregg Gunnell for his numerous contribution to the study of paleogenic bats.

VESPERTILIONOIDEA

Family indeterminate

†_Drakonycteris_ Ravel in Ravel, Adaci, Bensalah, Charruault, Essid, AMmar, Marzougui, Mahboubi, Mebrouk, Merzeraud, Vianey-Liaud, Tabuce and Marivaux, 2016

Etymology: The generic name is a combination of the Greek words 'drakon' (δράκων) and 'nycteris' (Νυχτερίδες), meaning dragon and bat respectively. The name of the genus is an allusion to the general context that emerges from the discovery of this fossil bat on the hillside of the Glib Zegdou. In addition, it highlights the robust but original morphology of the dental equipment attributed to it.

†_Drakonycteris glibzegdouensis_ Ravel in Ravel, Adaci, Bensalah, Charruault, Essid, AMmar, Marzougui, Mahboubi, Mebrouk, Merzeraud, Vianey-Liaud, Tabuce and Marivaux, 2016

Locality and Horizon: Level HGL50 of the Glib Zegdou, late lower Eocene - middle Eocene, situated in the Gour Lazib region (Sahara, Hammada du Dra), Algeria.

Etymology: The name of the species refers to the Glib Zegdou, located in Gour Lazib, Algeria.

†*Chambinycteris* Ravel in Ravel, Adaci, Bensalah, Charruault, Essid, AMmar, Marzougui, Mahboubi, Mebrouk, Merzeraud, Vianey-Liaud, Tabuce and Marivaux, 2016

Etymology: The generic name refers to the locality (Chambi) where the specimens were collected.

†*Chambinycteris pusilli* Ravel in Ravel, Adaci, Bensalah, Charruault, Essid, AMmar, Marzougui, Mahboubi, Mebrouk, Merzeraud, Vianey-Liaud, Tabuce and Marivaux, 2016

Locality and Horizon: Chambi (CBI) loci 2 and 3, late lower Eocene - middle Eocene, Djebel Chambi, situated in the Kasserine region, Tunisia.

Etymology: The specific name comes from the Latin 'pusilli', meaning puny, because of the small size and the fragile aspect of this species.

VESPERTILIONIDAE

Neoromicia stanleyi Goodman, Kearney, Rakotoarivelo and Hassanin, 2017

Stanley's serotine (Eng.) serotine de Stanley (Fr.)

This undescribed species has been known in the literature for the past 23 years. RAUTENBACH *et al.* (1993) while documenting the karyotypes of southern African bats, found a large *Neromicia capensis* form in the eastern parts of southern Africa – which was similar in description to *Neoromicia melkorum* Roberts 1926. KEARNEY *et al.* (2002) collected bats at the type locality of *N. melkorum* in the Northern Cape and found that these larger animals had the same karyotype as *Neoromicia capensis* (A. Smith, 1829), with this species becoming smaller in size in an eastward direction (KEARNEY 2005). Hence *Neoromicia melkorum* was synonomized with *Neoromicia capensis*. But the larger sized individuals in the eastern parts of southern Africa - with a different karyotype - were recognized as a distinct species often referred to as *Neoromicia* cf. *melkorum*. ('cf.' from the Latin 'confer', meaning 'compare') so this species was like the description given, but is clearly not the same. The name cf. *melkorum* has been used in a number of publications (see appendix 1).

GOODMAN *et al.* (2016) have now formally described and named this species in honour of William ("Bill") Stanley (ca. 1957 – 2015). Bill was the mammal collection manager at the Field Museum of Natural History from 1989 to 2015, until his sudden death in the Ethiopia Highlands where he was conducting fieldwork.

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Simmons N. B., Seiffert E. R. and Gunnell G. F. 2016. A New family of large omnivorous bats (Mammalia, Chiroptera) from the Late Eocene of the Fayum Depression, Egypt, with comments on use of the name 'Eochiroptera'. *American Museum Novitates* **3857**: 1–43. doi: 10.1206/3857.1.

Appendix 1: Publications referring to "cf. *melckorum*":

± These publications only refer to the usage of "cf. *melckorum*" in other papers.

± Bates P. J. J., Ratrimomanarivo F. H., Harrison D. L. and Goodman S. M. 2006. A description of a new species of *Pipistrellus* (Chiroptera: Vespertilionidae) from Madagascar with a review of related Vespertilioninae from the island. *Acta Chiropterologica* **8(2)**: 299 - 324. doi: 10.3161/1733-5329(2006)8[299:ADOANS]2.0.CO;2.

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Goodman S. M., Rakotondramanana C. F., Ramasindrazana B., Kearney T., Monadjem A., Schoeman M. C., Taylor P. J., Naughton, K. and Appleton, B. 2015. An integrative approach to characterize Malagasy bats of the subfamily Vespertilioninae Gray, 1821, with the description of a new species of *Hypsugo*. *Zoological Journal of the Linnean Society* **173(4)**: 988 - 1018. doi: 10.1111/zoj.12223.

± Goodman S. M., Taylor P. J., Ratrimomanarivo F. and Hoofer, S. R. 2012. The genus *Neoromicia* (Family Vespertilionidae) in Madagascar, with the description of a new species. *Zootaxa* **3250**: 1 - 25.

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Rautenbach I. L., Bronner G. N. and Schlitter D. A. 1993. Karyotypic data and attendant systematic implications for the bats of southern Africa. *Koedoe* **36(2)**: 87 - 104. doi: 10.4102/koedoe.v36i2.377.

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Scientific contributions

UPDATE ON THE DISTRIBUTION OF "CHIROPTERA SP1" IN THE SOUTHERN AND EASTERN PARTS OF LA RÉUNION ISLAND BASED ON ACOUSTIC SURVEYS

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Keywords : *Scotophilus*, range expansion, acoustic identification.

La Réunion Island (2512 km^2) is a tropical volcanic island of recent origin (2–3 million years ago) in the western Indian Ocean, located to the east of Madagascar (780 km) and close to Mauritius (210 km). Despite the fact that only two species of insectivorous bats are currently recognized to occur on the island – the endemic molossid *Mormopterus francoismoutoui* Goodman *et al*., 2008, and Afro-Malagasy Region emballonurid *Taphozous mauritianus* Geoffroy, 1818 – recent acoustic surveys revealed a distinct acoustic type, which can be related to a third species (BARATAUD and GIOSA, 2013). The third form, that we refer to herein as Chiroptera sp1, might be the Pale House Bat, *Scotophilus borbonicus* Geoffroy, 1803, previously reported on La Réunion (GEOFFROY, 1803; MAILLARD, 1862; VINSON, 1868; MAC-AULIFFE, 1902; HILL, 1980; CHEKE and DAHL, 1981) and inferred to have occurred at higher altitudes until its presumed extinction in the late 19th century (CHEKE and HUME, 2008). The species was subsequently reported from Madagascar (DORST, 1947, but see GOODMAN *et al*., 2005). On La Réunion, MAILLARD (1862) called it the "upland bat" and noted that it "lives generally in the forests and is also found in the coastal zone". Based on acoustic measurements, a recent study (PRIÉ *et al*., 2016) provided strong evidence to associate the newly found Chiroptera sp1 to the genus *Scotophilus*, by performing a comparison between *M. francoismoutoui*, Chiroptera sp1 and its presumed congener *S. robustus* from Madagascar. PRIÉ *et al.* (2016) also aimed to discuss the uncertain taxonomic status of *S. borbonicus*, as the remaining specimen allocated to this species is in poor condition (GOODMAN *et al*., 2005). According to PRIÉ *et al.* (2016), Chiroptera sp1 is presumed to inhabit the northwestern part of the island in zones associated with semi-dry forest. This conclusion was based on data primarily from this portion of the island and a few additional records from southern and eastern areas.

If indeed Chiroptera sp1 represents a third insectivorous bat species for La Réunion, it is important to have a clear understanding of its distribution to ensure effective management and conservation programs. While the taxon in question has yet to be captured, echolocation calls (BARATAUD and GIOSA, 2013) provide the only current basis for its identification. The aim of the current study is to (i) update information on the distribution of Chiroptera sp1 based on new acoustic records collected in the southern and eastern parts of the island and (ii) present new inferences on its ecology in order to maximize the chance of capturing the species in the near future.

MATERIAL AND METHODS

We used Song Meters SM2BAT+ (Wildlife Acoustics) with omnidirectional microphones to record bat echolocation calls. Weatherproof microphones (SMX-II, Wildlife Acoustics) were placed at least 2 m above the ground, in open flyways, and away from clutter. We placed these devices randomly in the eastern and southern portions of the island, taking into account access and insurance of the recording equipment. Song meters in WAV mode were set to save echolocation sequences of one or more calls during 5 s. This basic sampling unit of 5 s SM2Bat recording could contain data of one or more species. Parameters necessary for species identification are provided in BARATAUD and GIOSA (2013). Chiroptera sp1 is known to have a narrow bandwidth (quasi-constant frequency, QCF) bounded between 29 and 31 kHz (BARATAUD and GIOSA, 2013; PRIÉ *et al.*, 2016). Due to some overlap between the acoustic repertories of the common *Mormopterus francoismoutoui* and Chiroptera sp1, we used a three-step process to rigorously discriminate these two taxa. First, we employed Scan'R software (Binary Acoustic Technology Inc.) to filter out most of *M. francoismoutoui*, *T. mauritianus* and parasitic signals (mostly insects and terrestrial mammals such as *Rattus* spp.). A custom-made calibration was carried out to sharpen the call selection criteria, specifically on trigger level, minimum and maximum frequency cutoff, and minimum duration. Second, all calls that passed the species filters were confirmed manually by the author and M. Barataud, who has extensive experience analyzing bat echolocation data. Acoustic measurements were conducted with BatSound 4.2.1 software (Pettersson Elektronik AB, Sweden) to confirm that the calls belonged to the Chiroptera sp1 repertory. The calls were digitized (sampling rate 96 kHz) and processed through a Fast Fourier Transformation (FFT) using a Hanning Window for spectrograms (FFT size of 512 points). As recommended in BARATAUD (2015), for individual calls, manual measurements were performed associated with the power spectrum, specifically a FFT window of 256 points for quasi-constant frequency (QCF) pulses or 512 points for frequency modulated (FM) or flat-ended FM (FM-QCF) pulses. For each measured call, four parameters were determined and compared to the dichotomous key provided in BARATAUD and GIOSA (2013) to discriminate Chiroptera sp1 from *T. mauritianus* and *M. francoismoutoui*: peak frequency (Fmax), minimum frequency (Fmin), bandwidth (BW), maximum frequency (MF), and interpulse intervals (IPI). These parameters have been shown to separate acoustic differences between bat species in La Réunion (BARATAUD and GIOSA, 2013). Elevation, time of signal, and number of total files recorded per location were also noted. Third, as recommended in BARCLAY and BRIGHAM (2004), the distribution of our selected Chiroptera sp1 echolocation calls was confirmed with a reference library kindly provided by M. Barataud and recorded from captured *M. francoismoutoui* equipped with light sticks and identified flying individuals of Chiroptera sp1 recorded in 2009 and 2012 (see BARATAUD and GIOSA, 2013; PRIÉ *et al*., 2016) on La Réunion. Calls falling inside the set of values determined from the reference library were considered as belonging to Chiroptera sp1 and those falling in the overlap between *M. francoismoutoui* and Chiroptera sp1 acoustic repertories were classified as potential but unconfirmed signals.

RESULTS AND DISCUSSION

From 49 different locations in eastern and southern La Réunion, 779 hours of recordings and 82,036 call files were collected over 66 nights from February 2015 to March 2017 (see Appendix 1, Figure 1). After the three filtering steps detailed in methods section above, 16 call files of Chiroptera sp1 were confirmed from six localities. An additional 41 call files were classified as probable Chiroptera sp1, providing another 12 probable localities.

As confirmed in previous studies (BARATAUD and GIOSA, 2013; PRIÉ *et al.,* 2016), Chiroptera sp1 emitted single harmonic pulses consisting in most cases of a narrowband quasi-constant frequency component (QCF) and occasionally FM-QCF pulses (four out the 16

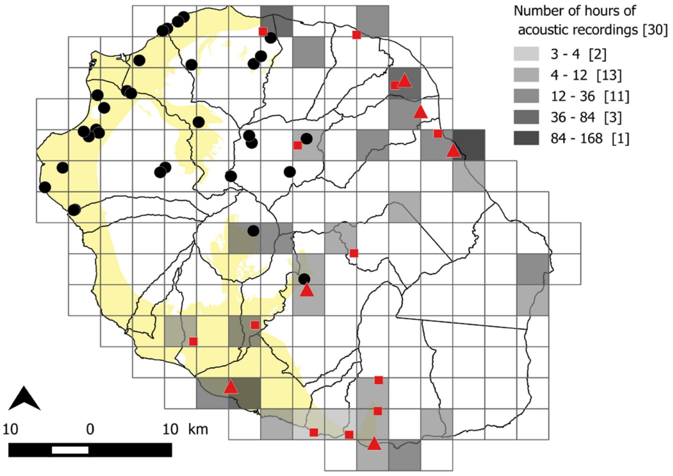

Figure 1. Distribution of Chiroptera sp1 and search effort on La Réunion. Black dots: previous data collected from PRIÉ *et al.* (2016); red triangles: new data collected specifically in the context of this study from eastern and southern areas; red squares: potential Chiroptera sp1 calls collected during the current study; yellowish areas indicates the semi-dry forest zone.

Table 1. Acoustic parameters (in kHz and msecs [IPI]) from the 16 confirmed Chiroptera sp1 call files collected in the eastern and southern parts of La Réunion.

	FM-QCF pulses		QCF pulses	
	n	*Mean (±SD)*	*n*	*Mean (±SD)*
MF	4	48.45 (±9.26)	12	31.18 (±1.69)
Fmin		32.87 (±1.89)		29.62 (±0.53)
Fmax		33.29 (±1.64)		29.82 (±0.41)
BW		15.59 (±7.67)		1.56 (±1.96)
IPI		173.25 (±78.80)		217.42 (±96.24)

confirmed Chiroptera sp1 calls). In Table 1, a summary of confirmed call acoustic measurements is presented.

All confirmed Chiroptera sp1 call sequences were recorded early in the night (from 6:30 PM to 8:43 PM) or predawn (from 5:21 AM to 5:46 AM). After adding data of calls attributed to Chiroptera sp1 from the northern part of the island (PRIÉ *et al.,* 2016), the same temporal trend is confirmed, although predawn activity is slightly extended to 6:10 AM. When considering the complete dataset, including probable Chiroptera sp1 calls, only four of the 64 call files fell outside the activity period mentioned above (11:25 PM, 2:47 AM, 3:10 AM, 4:27 AM). Chiroptera sp1 was confirmed at elevations ranging from 20 m to 1,360 m, with 70% of all probable and confirmed calls from sea-level to 90 m, although the highest volume of recordings, almost 90% (see Appendix 1), was made above 500 m. When including confirmed localities from PRIÉ *et al.* (2016), elevations ranged from sea-level to 1,900 m (Figure 2).

The acoustic data reported here extend the known limit distribution of Chiroptera sp1 on La Réunion, including eastern and southern portions of the island, as well as the eastern windward coast (Figure 1), providing evidence that this form is not restricted to dry and semi-dry environments, as previously proposed (PRIÉ *et al.*, 2016). Understanding the distribution and nightly activity of Chiroptera sp1 on La Réunion is a critical first step towards identifying its habitat requirements, its subsequent capture, and associating a species name with this taxon. The notable scarcity of signals matching the acoustic signature of Chiroptera sp1 suggests that it might fly high enough to exceed the microphone detection range or is rare compared to *M. francoismoutoui* and, to a lesser extent, *T. mauritianus*. For call files that were recorded at the edge of the microphone detection range, the signal to noise ratio was in some cases sufficiently high to obscure resolution for possible positive identification of Chiroptera sp1. Detector height may introduce biases to ground-based ultrasound survey, potentially resulting in false absences and unrepresentative activity levels (STATON and POULTON, 2012). Consequently, foraging height preferences of Chiroptera sp1 should be investigated in more detail, as this factor might explain why this species is only recorded at early and late night: as already suggested in BARATAUD and GIOSA (2013), this taxon may have a different flight behavior during the middle portion of the night as compared to early night and predawn hours. Survey protocols to specifically search for Chiroptera sp1 should include the use of detectors placed in different vertical positions, for example at ground level to up to 30 m (using different types of towers or even buildings in urban areas), as suggested by COLLINS and JONES (2009). While Chiroptera sp1 was diagnosed primarily at lower elevations (Figure 2), its presence also at higher altitudes was confirmed. Considering the larger amount of data collected in this current study was from the coastal portion of the island, it might be useful to augment surveys in the uplands, from where the species was originally considered to occur (MAILLARD, 1862; MAC AULIFFE, 1902). Finally, our results suggest the need to conduct more systematic ecological studies on this taxon, determine the best means for its capture, and if it represents *Scotophilus borbonicus*. This species is considered as critically endangered (HUTSON *et al.*, 2001) and has been tentatively confirmed from Madagascar based on older specimens (GOODMAN *et al.,* 2005).

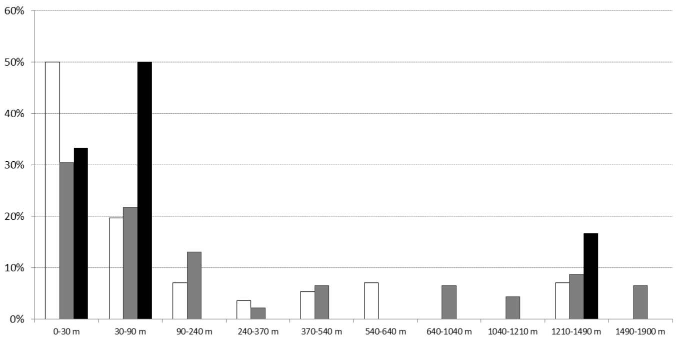

Figure 2. Elevational range of collected calls of Chiroptera sp1. White bars: relative percentage of all confirmed and probable calls obtained during the current study; gray bars: relative percentage of all confirmed calls from the current study and PRIÉ et al. (2016); black bars: relative percentage of all confirmed calls from the current study.

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Appendix 1.

Location of bat acoustic inventory stations. PC: probable calls; CC: confirmed calls; NC: unconfirmed presence of Chiroptera sp1. Number of recorded hours (NRH): *n*=779; Total number of monitoring nights (TNMN): *n*=66; Total number of files (TNF): *n*=82036). X and Y in UTM40S.

Date	Commune	Locality	Elevation (m)	NRH	X	Y	TNMN	TNF	Chiroptera sp1
26/02/2015	Petite Ile	Grande Anse Beach	0	2	349329	7636215	1	221	
26/02/2015	Petite Ile	Grande Anse Beach	0	2	349329	7636448	1	238	PC
11/05/2015	Bras-Panon	Liberia forest - Kiosque	680	12	357343	7674281	1	3770	
11/05/2015	Bras-Panon	Liberia forest - Parking	640	12	356619	7673974	1	195	
16/12/2015	Le Tampon	Bois Court	1360	12	348451	7654701	1	187	CC
16/12/2015	Saint-Pierre	Grand Bois	130	12	346509	7638535	1	3265	
16/12/2015	Saint-Louis	Plaine du Gol	150	12	334264	7647950	1	511	PC
09/01/2016	Saint-Joseph	Langevin	70	12	360900	7635104	1	49	
09/01/2016	Saint-Joseph	Manapany	20	3	353723	7635920	1	666	PC
10/01/2016	Sainte-Marie	Duparc	80	12	345550	7687570	1	3349	
05/02/2016	Saint-André	Cité Lamarck	110	36	359469	7680990	1	8538	PC
22/03/2016	Saint-Pierre	ZAC Canabady	80	12	341570	7641130	1	2243	
30/03/2016	Saint Denis	Chaudron	20	12	342731	7688867	1	1533	
30/03/2016	Saint Denis	Chaudron	20	12	342744	7688862	1	731	
30/03/2016	Saint Denis	Chaudron	20	12	342810	7688929	1	1101	
12/07/2016	Saint-Philippe	Cap Méchant	40	12	365940	7635924	1	3336	
12/07/2016	Sainte-Rose	Piton Sainte-Rose	90	24	378093	7658433	2	239	
13/07/2016	Bras-Panon	Rivière du Mât-les-Hauts	140	24	358933	7679325	2	770	
26/07/2016	Entre-Deux	Ravine Citron	490	24	341976	7650058	1	1855	PC

Date	Commune	Locality	Elevation (m)	NRH	X	Y	TNMN	TNF	Chiroptera sp1
17/08/2016	Le Tampon	Grand Bassin	690	12	347880	7656910	1	343	
23/08/2016	Saint-André	Near Jumbo Score	80	12	360654	7681696	1	1846	
23/08/2016	Saint-André	Near Jumbo Score	80	12	360969	7681731	1	1664	
27/09/2016	Saint-Pierre	Industrial area n°4 - Cliffs	60	12	338945	7642191	1	254	CC
27/09/2016	Saint-Pierre	Industrial area n°4 - Savanna	60	12	338893	7641720	1	90	
27/09/2016	Saint-Pierre	Pont Ravine des Cabris	40	12	338483	7642013	1	1278	
30/09/2016	Saint-Benoît	Patu de Rosemont High School	20	36	366762	7672672	3	1481	CC
30/09/2016	Saint-Benoît	Patu de Rosemont High School	20	36	366719	7672629	3	1247	
30/09/2016	Saint-Benoît	Patu de Rosemont High School	20	24	366765	7672687	3	5575	PC
25/11/2016	Saint-André	Near Jumbo Score	80	12	360654	7681696	1	1508	CC
25/11/2016	Saint-André	Near Jumbo Score	80	12	360891	7681754	1	338	
04/01/2017	Salazie	Mare à Citron	640	12	347300	7673240	1	1760	PC
11/01/2017	Saint-Pierre	Industrial area n°4 - Cliffs	60	12	338945	7642191	1	453	CC
11/01/2017	Saint-Pierre	Industrial area n°4 - Savanna	60	12	338893	7641720	1	197	
11/01/2017	Saint-Pierre	Pont Ravine des Cabris	40	12	338483	7642013	1	3769	
06/02/2017	Saint-Denis	Moufia	70	12	342970	7687940	1	170	PC
15/02/2017	Sainte Marie	Beaumont	300	24	347420	7684500	2	2310	
15/02/2017	Bras Panon	City center	50	24	362650	7677680	2	745	CC
20/02/2017	Saint-Benoît	Patu de Rosemont High School	20	24	366762	7672672	2	2860	CC
20/02/2017	Saint-Benoît	Patu de Rosemont High School	20	16	366765	7672687	2	7667	
20/02/2017	Saint-Benoît	Patu de Rosemont High School	20	24	366719	7672629	2	1321	
13/03/2017	Saint-Joseph	Langevin	70	12	360900	7635104	1	2024	
13/03/2017	Saint-Joseph	Piton Babet	20	12	356869	7634877	1	1670	CC
17/03/2017	Sainte-Suzanne	City center	30	24	354671	7687498	2	4641	PC
19/03/2017	Plaine des Palmistes	Col de Bellevue	1490	12	354332	7659328	1	1477	PC
19/03/2017	Plaine des Palmistes	Pyramide	890	12	359286	7664198	1	120	
20/03/2017	Saint-Benoît	Le Bourbier	50	24	364804	7674767	2	233	
23/03/2017	Sainte-Rose	Bois Blanc	130	12	377174	7655788	1	19	

Date	Commune	Locality	Elevation (m)	NRH	X	Y	TNMN	TNF	Chiroptera sp1
23/03/2017	Sainte-Anne	City center	10	12	369426	7668491	1	1234	
23/03/2017	Sainte-Rose	Enclos	80	12	375881	7652029	1	61	
23/03/2017	Saint-Joseph	Lit Rivière des Remparts	170	12	357321	7638971	1	589	PC
23/03/2017	Saint-Joseph	Lit Rivière des Remparts - Cressonière	350	12	357416	7642943	1	295	PC

Recent literature

Papers

Banyard A. C. and Fooks, A. R. 2017. The impact of novel lyssavirus discovery. *Microbiology Australia*: 17-21. doi: 10.1071/MA17006.

The global discovery of novel lyssaviruses is of continued scientific interest through its importance to both public and animal health. Lyssaviruses cause an invariably fatal encephalitis that is more commonly known as rabies. The term rabies has a long history in human society, as rabies virus (RABV) is the only pathogen that is associated with 100% fatality once the onset of clinical disease has started. Although predominantly associated across the globe with domestic and feral dog populations, the association of bats is clear. Whilst evolutionarily associated with bats, RABV is most commonly transmitted to human populations through the bite of an infected dog and dogs are considered the primary reservoir of disease. Indeed, RABV does cause more than an estimated 70 000 deaths every year globally in human populations and whilst this is largely in areas where the disease is endemic, areas that remain free of rabies must remain vigilant to the risk of re-incursion of disease. Characterisation of novel lyssaviruses is of importance on several levels. Not least to investigate the pathogenesis and potential transmission routes of different lyssavirus species but also to assess the potential effect of post-exposure treatments and vaccination should human exposure occur. Bat lyssaviruses and the problems associated with novel discoveries and the potential impact they have on both human and animal populations are discussed.

Benda P., Reiter A., Uhrin M. and Varadínová Z. 2016. A New Species of Pipistrelle Bat (Chiroptera: Vespertilionidae) from Southern Arabia. *Acta Chiropterologica* 18(2): 301–323. doi: 10.3161/15081109ACC2016.18.2.001.

A new species of the genus *Pipistrellus* is described from the Dhofar region, southern Arabia. The new species occurs in a very limited area lesser than 1,000 km^2, situated in the belt of relative humid savannah habitats of coastal Arabia between easternmost Yemen and south-western Oman. This bat represents the eighth pipistrelle species known from Arabia and fourth bat species endemic to southern Arabia. The new species is positioned morphologically and genetically very close to the group of the Oriental species of the genus *Pipistrellus* and represents the westernmost offshoot of the Oriental vespertilionid bat fauna, isolated for more than 1,500 km across the Indian Ocean from the area of continuous distribution of this fauna in the Indian Subcontinent.

Bendjeddou M. L., Loumassine H. E., Metallaoui W., Chiheb K., Farfar A., Bounaceur F., Boukheroufa F., Bouslama Z. and Dietz C. 2016. First record of *Nyctinomus aegyptiacus* for Tunisia. *Vespertillo* 18: 23–27.

We report on the first record of the Egyptian free-tailed bat (*Nyctinomus aegyptiacus* Geoffroy, 1818) in Tunisia. The finding refers to a voucher specimen collected at Ksar Ghilane (Jbil National Park). Morphological characters and measurements of the specimen are presented.

Bray T. C. and Benda P. 2016. Distribution of *Asellia tridens* (Chiroptera: Hipposideridae) lineages including representatives from Saudi Arabia. *Zoology in the Middle East* 62(4): 283–287. doi: 10.1080/09397140.2016.1250708.

The genus *Asellia* was recently revised, giving an insight into the genetic and morphological characteristics of a group whose distribution spans from North Africa into Asia. We studied the genus further by considering additional mitochondrial markers and sampling localities. The deepest previously identified split in *A. tridens* is supported (Middle East/North Africa), along with the association of North and West African lineages. Central Saudi Arabia is found to represent the easternmost extent of a North African haplogroup when considering concatenated fragments of Cytochrome-*b*, NADH Dehydrogenase 2, and Cytochrome Oxidase 1 genes. New distribution data further emphasises the diversity found in the Middle East and suggests some mixing of haplotypes over long distances.

Chawana R., Patzke N., Alagaili A. N., Bennett N. C., Mohammed O. B., Kaswera-Kyamakya C., Gilissen E., Ihunwo A. O., Pettigrew J. D. and Manger P. R. 2016. The distribution of Ki-67 and Doublecortin Immunopositive Cells in the brains of three Microchiropteran species, *Hipposideros fuliginosus*, *Triaenops persicus*, and *Asellia tridens*. *Anatomical Record* 299(11): 1548–1560. doi: 10.1002/ar.23460.

The current study uses Ki-67 and doublecortin (DCX) immunohistochemistry to delineate potential neurogenic zones, migratory pathways and terminal fields associated with adult neurogenesis in the brains of three microchiropterans. As with most mammals studied to date, the canonical subgranular and subventricular neurogenic zones were observed. Distinct labelling of newly born cells and immature neurons within the dentate gyrus of the hippocampus was observed in all species. A distinct rostral migratory stream, that appears to split around the medial aspect of the caudate nucleus was observed. These two rostral stream divisions appear to merge at the rostroventral corner of the caudate nucleus to turn and enter the olfactory bulb, where a large terminal field of immature neurons was observed. DCX immunolabelled neurons were observed mostly in the rostral neocortex, but a potential migratory stream to the neocortex was not identified. A broad swathe of newly born cells and immature neurons was found between the caudoventral division of the rostral migratory stream and the piriform cortex. In addition occasional immature neurons were observed in the amygdala and DCX immunopositive axons were observed in the anterior commissure. While the majority of these features have been found in several mammal species, the large number of DCX immunolabelled cells found between the rostral migratory stream and the piriform cortex and the presence of DCX immunostained axons in the anterior commissure are features only observed in microchiropterans and insectivores to date. In the diphyletic scenario of chiropteran evolution, these observations align the microchiropterans with the insectivores.

Coimbra J. P., Pettigrew J. D., Kaswera-Kyamakya C., Gilissen E., Collin S. P. and Manger P. R. 2017. Retinal ganglion cell topography and spatial resolving power in African megachiropterans: Influence of roosting microhabitat and foraging. *Journal of Comparative Neurology* 525(1): 186–203. doi: 10.1002/cne.24055.

Megachiropteran bats (megabats) show remarkable diversity in microhabitat occupation and trophic specializations, but information on how vision relates to their behavioral ecology is scarce. Using stereology and retinal whole mounts, we measured the topographic distribution of retinal ganglion cells and determined the spatial resolution of eight African megachiropterans with distinct roosting and feeding ecologies. We found that species roosting in open microhabitats have a pronounced streak of high retinal ganglion cell density, whereas those favoring more enclosed microhabitats have a less pronounced streak (or its absence in *Hypsignathus monstrosus*). An exception is the cave-dwelling *Rousettus aegyptiacus,* which has a pronounced horizontal streak that potentially correlates with its occurrence in more open environments during foraging. In all species, we found a temporal area with maximum retinal ganglion cell density (~5,000–7,000 cells/mm$_2$) that affords enhanced resolution in the frontal visual field. Our estimates of spatial resolution based on peak retinal ganglion cell density and eye size (~6–12 mm in axial length) range between ~2 and 4 cycles/degree. Species that occur in more enclosed microhabitats and feed on plant material have lower spatial resolution (~2 cycles/degree) compared with those that roost in open and semiopen areas (~3–3.8 cycles/degree). We suggest that the larger eye and concomitant higher spatial resolution (~4 cycles/degree) in *H. monstrosus* may have facilitated the carnivorous aspect of its diet. In conclusion, variations in the topographic organization and magnitude of retinal ganglion density reflect the specific ecological needs to detect food/predators and the structural complexity of the environments.

Curtis A. A. and Simmons N. B. 2017. Unique turbinal morphology in horseshoe bats (Chiroptera: Rhinolophidae). *The Anatomical Record* 300: 309–325. doi: 10.1002/ar.23516.

The mammalian nasal fossa contains a set of delicate and often structurally complex bones called turbinals. Turbinals and associated mucosae function in regulating respiratory heat and water loss, increasing surface area for olfactory tissue, and directing airflow within the nasal fossa. We used high-resolution micro-CT scanning to investigate a unique maxilloturbinal morphology in 37 species from the bat family Rhinolophidae, which we compared with those of families Hippoideridae, Megadermatidae, and Pteropodidae. Rhinolophids exhibit numerous structural modifications along the nasopharyngeal tract associated with emission of high duty cycle echolocation calls via the nostrils. In rhinolophids, we found that the maxilloturbinals and a portion of ethmoturbinal I form a pair of strand-like bony structures on each side of the nasal chamber. These structures project anteriorly from the transverse lamina and complete a hairpin turn to project posteriorly down the nasopharyngeal duct, and vary in length among species. The strand-like maxilloturbinals in Rhinolophidae were not observed in our outgroups and represent a synapomorphy for this family, and are unique in form among mammals. Within Rhinolophidae, maxilloturbinal size and cross-sectional shape were correlated with phylogeny. We hypothesize that strand-shaped maxilloturbinals may function to reduce respiratory heat and water loss without greatly impacting echolocation call transmission since they provide increased mucosal surface area for heat and moisture exchange but occupy minimal space. Alternatively, they may play a role in transmission of echolocation calls since they are located directly along the path sound travels between the larynx and nostrils during call emission.

Dickson K. V. R., Davies C. W. T., Routh A., Killick R. and Barbon A. R. 2016. Radiographic cardiac silhouette measurement in captive Livingstone's Fruit Bats (*Pteropus livingstonii*). *Journal of Zoo and Wildlife Medicine* 47(4): 963–969. doi: 10.1638/2015-0126.1.

Cardiomyopathies have been increasingly noted in the captive population of Livingstone's fruit bat (*Pteropus livingstonii*). The aim of this study was to produce a set of repeatable quantitative reference measurements that could be used to assess the cardiac size during radiographic examination of this species. Ventro-dorsal and lateral radiographs (n = 129) from a total of 42 individual Livingstone's fruit bats were examined. The control group radiographs (n = 102) consisted of 34 healthy individuals. Radiographic measurements were taken of structures within the thorax and then converted into ratios. These ratios from radiographs (n = 27) were also calculated for eight individuals with diagnosed cardiomyopathy. Vertebral Heart Scores (VHS) were calculated from right lateral radiographs and compared between the two groups. From all the data, only the width of the cardiac silhouette to the width of the thorax (the W: T ratio) in the ventro-dorsal view and the VHS were found to be significantly different between both groups (P <, 0.05). The group with cardiomyopathies had a mean W: T ratio of 0.59 (±60.005) and a VHS of 9.77 (±60.89), while a mean W: T ratio of 0.54 (±60.004) and a VHS of 8.71 (±60.93) was established for healthy specimens.

Dietrich M., Kearney T., Seamark E. C. J. and Markotter W. 2017. The excreted microbiota of bats: evidence of niche specialisation based on multiple body habitats. *FEMS Microbiology Letters* 364(1): fnw284. doi: 10.1093/femsle/fnw284.

Animal-associated microbiotas form complex communities, which play crucial functions for their host, including susceptibility to infections. Despite increasing attention to bats as reservoirs of zoonotic pathogens, their microbiota is poorly documented, especially for samples potentially implicated in pathogen transmission such as urine and saliva. Here, using low-biomass individual samples, we examined the composition and structure of bacterial communities excreted by insectivorous bats, focusing on three body habitats (saliva, urine and faeces). We show that niche specialization occurs as bacterial community composition was distinct across body habitats with the majority of phylotypes being body habitat-specific. Our results suggest that urine harbors more diverse bacterial communities than saliva and faeces and reveal potentially zoonotic bacteria such as *Leptospira*, *Rickettsia*, *Bartonella* and *Coxiella* in all body habitats. Our study emphasized that, in addition to the traditional use of gut-associated samples such as faeces, both urine and saliva are also of interest because of their diverse microbiota and the potential transmission of pathogenic bacteria. Our results represent a critical baseline for future studies investigating the interactions between microbiota and infection dynamics in bats.

El Sayed S. M., Abdelrahman A. A., Ozbak H. A., Hemeg H. A., Kheyami A. M., Rezk N., El-Ghoul M. B., Nabo M. M. H. and Fathy Y. M. 2016. Updates in diagnosis and management of Ebola hemorrhagic fever. *Journal of Research in Medical Sciences* 21: 84. doi: 10.4103/1735-1995.192500.

Ebola hemorrhagic fever is a lethal viral disease transmitted by contact with infected people and animals. Ebola infection represents a worldwide health threat causing enormous mortality rates and fatal epidemics. Major concern is pilgrimage seasons with possible transmission to Middle East populations. In this review, we aim to shed light on Ebola hemorrhagic fever as regard: virology, transmission, biology, pathogenesis, clinical picture, and complications to get the best results for prevention and management. We also aim to guide future research to new therapeutic perspectives to precise targets. Our methodology was to review the literature extensively to make an overall view of the biology of Ebola virus infection, its serious health effects and possible therapeutic benefits using currently available remedies and future perspectives. Key findings in Ebola patients are fever, hepatic impairment, hepatocellular necrosis, lymphopenia (for T-lymphocyte and natural killer cells) with lymphocyte apoptosis, hemorrhagic manifestations, and complications. Pathogenesis in Ebola infection includes oxidative stress, immune suppression of both cell-mediated and humoral immunities, hepatic and adrenal impairment and failure, hemorrhagic fever, activation of deleterious inflammatory pathways, for example, tumor necrosis factor-related apoptosis-inducing ligand, and factor of apoptotic signal death receptor pathways causing lymphocyte depletion. Several inflammatory mediators and cytokines are involved in pathogenesis, for example, interleukin-2, 6, 8, and 10 and others. In conclusion, Ebola hemorrhagic fever is a serious fatal viral infection that can be prevented using strict health measures and can be treated to some extent using some currently available remedies. Newer treatment lines, for example, prophetic medicine remedies as nigella sativa may be promising.

Farkašová H., Hron T., Pačes J., Hulva P., Benda P., Gifford R.J. and Elleder D. 2017. Discovery of an endogenous Deltaretrovirus in the genome of long-fingered bats (Chiroptera: Miniopteridae). *Proceedings of the National Academy of Sciences* 114(12): 3145–3150. doi: 10.1073/pnas.1621224114.

Retroviruses can create endogenous forms on infiltration into the germline cells of their hosts. These forms are then vertically transmitted and can be considered as genetic fossils of ancient viruses. All retrovirus genera, with the exception of deltaretroviruses, have had their representation identified in the host genome as a virus fossil record. Here we describe an endogenous Deltaretrovirus, identified in the germline of long-fingered bats (Miniopteridae). A single, heavily deleted copy of this retrovirus has been found in the genome of miniopterid species, but not in the genomes of the phylogenetically closest bat families, Vespertilionidae and Cistugonidae. Therefore, the endogenization occurred in a time interval between 20 and 45 million years ago. This discovery closes the last major gap in the retroviral fossil record and provides important insights into the history of deltaretroviruses in mammals.

Formella M. and Gatherer D. 2016. The serology of Ebolavirus-a wider geographical range, a wider genus of viruses, or a wider range of virulence? *Journal of General Virology* 97(12): 3120–3130. doi: 10.1099/jgv.0.000638.

Viruses of the genus *Ebolavirus* are the causative agents of Ebola virus disease (EVD), of which there have been only 25 recorded outbreaks since the discovery of Zaire and Sudan ebolaviruses in the late 1970s. Until the west African outbreak commencing in late 2013, EVD was confined to an area of central Africa stretching from the coast of Gabon through the Congo river basin and eastward to the Great Lakes. Nevertheless, population serological studies since 1976, most of which were carried out in the first two decades after that date, have suggested a wider distribution and more frequent occurrence across tropical Africa. We review this body of work, discussing the various methods employed over the years and the degree to which they can currently be regarded as reliable. We conclude that there is adequate evidence for a wider geographical range of exposure to *Ebolavirus* or related filoviruses and discuss three possibilities that could account for this: (a) EVD outbreaks have been misidentified as other diseases in the past; (b) unidentified, and clinically milder, species of the genus *Ebolavirus* circulate over a wider range than the most pathogenic species; and (c) EVD may be subclinical with a frequency high enough that smaller outbreaks may be unidentified. We conclude that the second option is the most likely and therefore predict the future discovery of other, less virulent, members of the genus *Ebolavirus*.

Fountain K. I., Stevens, K. B., Lloyd, D. H. and Loeffler A. 2017. Skin disease in captive bats: results of an online survey of zoos and rehabilitators in Europe, North America and Australasia. Veterinary Dermatology 28: 219-e52. doi: 0.1111/vde.12410.

Background – Bats may be held captive in zoos and breeding programmes, and for rehabilitation due to illness, abandonment or injury.

Objectives – To describe the frequency and characteristics of skin disease in captive bats.

Methods – Zoos (n = 164) in Europe, North America, Australia and New Zealand, Wildlife Disease Association members and rehabilitators were invited to complete online questionnaires on skin lesions and housing. Associations between lesion type and site, frequency, species, age, suspected cause and season, and their association with housing in zoos were tested using chi-squared and two-sample z-tests.

Results – Skin lesions were seen by 38.5% (15 of 39) of responding zoos and more frequently by rehabilitators (66.7%, 18 of 27; P = 0.024). Of the total of 153 lesions of any type reported by zoos and rehabilitators, almost two thirds occurred on the pinnae (49 of 153, 32%) or wing membranes (45 of 153, 29%). Amongst pinnal lesions, crusting (27%), swelling and redness (25%) and necrosis (20%) were most frequent. In zoos, pinnal (P = 0.001) and wing lesions (P = 0.045) were associated with “season”, being more common in winter. Pruritus was rare but more often reported from rehabilitation centres (12 of 77 observed lesions) than from zoos (1 of 76) (P = 0.0015). Lesions most often affected adult and geriatric bats in zoos, and juveniles and adults in rehabilitation. Eight respondents reported that skin disease necessitated euthanasia in individual bats. There was no significant association between type of housing and lesions.

Conclusion – Pinnal and wing lesions were common in captive bats, often with necrosis. Further research into the causes is needed to improve health and welfare of captive bats.

Goodman S. M., Kearney T., Ratsimbazafy M. M. and Hassanin A. 2017. Description of a new species of *Neoromicia* (Chiroptera: Vespertilionidae) from southern Africa: A name for “*N.* cf. *melckorum*”. *Zootaxa* 4236(2): 351–374. doi: 10.11646/zootaxa.4236.2.10.

The taxonomy of sub-Saharan small insectivore bats of the family Vespertilionidae is unresolved and currently five named species of the genus *Neoromicia* are recognized from southern Africa, with *N. melckorum* considered a synonym of *N. capensis*. Since several years, the name “*N.* cf. *melckorum*” has been used in the literature to designate an apparently un- described and moderately large bodied vespertilionid bat known from different localities in southern and southeastern Africa. Using new data from molecular genetics, bacular morphology, and cranio-dental characters, we conclude that *N. melckorum* sensu stricto is indeed nested within *N. capensis* and obtain the needed evidence to formally describe "*N.* cf. *melckorum*", named herein as *N. stanleyi* sp. nov. On the basis of molecular and bacular evidence, *N. stanleyi* is found in Botswana, Zimbabwe, and Zambia, and using a combination of other characters is presumed to occur in northern South Africa and Malawi. Bayesian and maximum likelihood analyses based on 12S rRNA sequences indicate that it belongs to a clade containing four species of *Neoromicia* (*N. capensis, N. malagasyensis, N. matroka*, and *N. robertsi*) and *Laephotis*. *Neoromicia stanleyi* shows at least 3.2% nucleotide divergence from its closest relatives. It is larger in cranial characters than other members of the *capensis* group occurring in the southern portion of Africa, and a number of bacular characters distinguish *N. stanleyi* from *N. capensis*.

Greiman S. E., Vaughan J. A., Elmahy R., Adisakwattana P., Van Ha N., Fayton T. J., Khalil A. I. and Tkach V. V. 2017. Real-time PCR detection and phylogenetic relationships of *Neorickettsia* spp. in digeneans from Egypt, Philippines, Thailand, Vietnam and the United States. *Parasitology International* 66(1): 1003–1007. doi: 10.1016/j.parint.2016.08.002.

Neorickettsia (Rickettsiales, Anaplasmataceae) is a genus of obligate intracellular bacterial endosymbionts of digeneans (Platyhelminthes, Digenea). Some *Neorickettsia* are able to invade cells of the digenean's vertebrate host and are known to cause diseases of domestic animals, wildlife, and humans. In this study we report the results of screening digenean samples for *Neorickettsia* collected from bats in Egypt and Mindoro Island, Philippines, snails and fishes from Thailand, and fishes from Vietnam and the USA. *Neorickettsia* were detected using a real-time PCR protocol targeting a 152 bp fragment of the heat shock protein coding gene, GroEL, and verified with nested PCR and sequencing of a 1853 bp long region of the GroESL operon and a 1371 bp long region of 16S rRNA. Eight unique genotypes of *Neorickettsia* were obtained from digenean samples. *Neorickettsia* sp. 8 obtained from *Lecithodendrium* sp. from Egypt; *Neorickettsia* sp. 9 and 10 obtained from two species of *Paralecithodendrium* from Mindoro, Philippines; *Neorickettsia* sp. 11 from *Lecithodendrium* sp. and *Neorickettsia* sp. 4 (previously identified from *Saccocoelioides lizae*, from China) from Thailand; *Neorickettsia* sp. 12 from *Dicrogaster* sp. Florida, USA; *Neorickettsia* sp. 13 and SF agent from Vietnam. Sequence comparison and phylogenetic analysis demonstrated that the forms, provisionally named *Neorickettsia* sp. 8-13, represent new genotypes. We have for the first time detected *Neorickettsia* in a digenean from Egypt (and the African continent as a whole), the Philippines, Thailand and Vietnam based on PCR and sequencing evidence. Our findings suggest that further surveys from the African continent, SE Asia, and island countries are likely to reveal new *Neorickettsia* lineages as well as new digenean host associations.

Hassanin A., Nesi N., Marin J., Kadjo B., Pourrut X., Leroy E., Gembu G-C.,Musaba-Akawa P. M., Ngoagouni C., Nakouné E., Ruedi M., Tshikung D., Pongembo Shongo C. and Bonillo C. 2016. Comparative phylogeography of African fruit bats (Chiroptera, Pteropodidae) provide new insights into the outbreak of Ebola virus disease in West Africa, 2014-2016. *Comptes Rendus Biologies* 339(11-12): 517–528. doi: 10.1016/j.crvi.2016.09.005.

Both *Ebolavirus* and *Marburgvirus* were detected in several fruit bat species of the family Pteropodidae, suggesting that this taxon plays a key role in the life cycle of filoviruses. After four decades of Zaire Ebolavirus (ZEBOV) outbreaks in Central Africa, the virus was detected for the first time in West Africa in 2014. To better understand the role of fruit bats as potential reservoirs and circulating hosts between Central and West Africa, we examine here the phylogeny and comparative phylogeography of Pteropodidae. Our phylogenetic results confirm the existence of four independent lineages of African fruit bats: the genera *Eidolon* and *Rousettus*, and the tribes Epomophorini and Scotonycterini, and indicate that the three species suspected to represent ZEBOV reservoir hosts (*Epomops franqueti*, *Hypsignathus monstrosus*, and *Myonycteris torquata*) belong to an African clade that diversified rapidly around 8–7 Mya. To test for phylogeographic structure and for recent gene flow from Central to West Africa, we analysed the nucleotide variation of 675 cytochrome *b* gene (Cyt*b*) sequences, representing eight fruit bat species collected in 48 geographic localities. Within Epomophorina, our mitochondrial data do not support the monophyly of two genera (*Epomops* and *Epomophorus*) and four species (*Epomophorus gambianus*, *Epomops franqueti*, *Epomops buettikoferi*, and *Micropteropus pusillus*). In *Epomops*, however, we found two geographic haplogroups corresponding to the Congo Basin and Upper Guinea forests, respectively. By contrast, we found no genetic differentiation between Central and West African populations for all species known to make seasonal movements, *Eidolon helvum*, *E. gambianus*, *H. monstrosus*, *M. pusillus*, *Nanonycteris veldkampii*, and *Rousettus aegyptiacus*. Our results suggest that only three fruit bat species were able to disperse directly ZEBOV from the Congo Basin to Upper Guinea: *E. helvum*, *H. monstrosus*, and *R. aegyptiacus*.

Hayman D. T. S., Fooks A. R., Marston D. A. and Garcia-R J. C. 2016. The global phylogeography of *Lyssaviruses* - Challenging the 'Out of Africa' hypothesis. *PLOS Neglected Tropical Diseases* 10(12): e0005266. doi: 10.1371/JOURNAL.PNTD.0005266.

Rabies virus kills tens of thousands of people globally each year, especially in resource-limited countries. Yet, there are genetically- and antigenically-related lyssaviruses, all capable of causing the disease rabies, circulating globally among bats without causing conspicuous disease outbreaks. The species richness and greater genetic diversity of African lyssaviruses, along with the lack of antibody cross-reactivity among them, has led to the hypothesis that Africa is the origin of lyssaviruses. This hypothesis was tested using a probabilistic phylogeographical approach. The nucleoprotein gene sequences from 153 representatives of 16 lyssavirus species, collected between 1956 and 2015, were used to develop a phylogenetic tree which incorporated relevant geographic and temporal data relating to the viruses. In addition, complete genome sequences from all 16 (putative) species were analysed. The most probable ancestral distribution for the internal nodes was inferred using three different approaches and was confirmed by analysis of complete genomes. These results support a Palearctic origin for lyssaviruses (posterior probability = 0.85), challenging the 'out of Africa' hypothesis, and suggest three independent transmission events to the Afrotropical region, representing the three phylogroups that form the three major lyssavirus clades.

Hayman D. T. S and Peel A. J. 2016. Can survival analyses detect hunting pressure in a highly connected species? Lessons from straw-coloured fruit bats. *Biological Conservation* 200: 131–139. doi: 10.1016/j.biocon.2016.06.003.

Animal behaviour, social structure and population dynamics affect community structure, interspecific interactions, and a species' resilience to harvesting. Building on new life history information for the straw-coloured fruit bat *(Eidolon helvum)* from multiple localities across Africa, we used survival analyses based on tooth-cementum annuli data to test alternative hypotheses relating to hunting pressure, demography and population connectivity. The estimated annual survival probability across Africa was high (≥0.64), but was greatest in colonies with the highest proportion of males. This difference in sex survival, along with age and sex capture biases and out-of-phase breeding across the species' distribution, leads us to hypothesize that *E. helvum* has a complex social structure. We found no evidence for additive mortality in heavily hunted populations, with most colonies having high survival with constant risk of mortality despite different hunting pressure.

Given *E. helvum*'s slow life history strategy, similar survival patterns and rate among colonies suggest that local movement and regional migration may compensate for local excess hunting, but these were also not detected. Our study suggests that spatio-temporal data are necessary to appropriately assess the population dynamics and conservation status of this and other species with similar traits.

Held J., Gmeiner M., Mordmüller B., Matsiégui P-B., Schaer J., Eckerle I., Weber N., Matuschewski K., Bletz S. and Schaumburg F. 2017. Bats are rare reservoirs of *Staphylococcus aureus* complex in Gabon. *Infection, Genetics and Evolution* 47: 118–120. doi: 10.1016/j.meegid.2016.11.022.

The colonization of afro-tropical wildlife with *Staphylococcus aureus* and the derived clade *Staphylococcus schweitzeri* remains largely unknown. A reservoir in bats could be of importance since bats and humans share overlapping habitats. In addition, bats are food sources in some African regions and can be the cause of zoonotic diseases. Here, we present a cross-sectional survey employing pharyngeal swabs of captured and released bats (n=133) in a forest area of Gabon. We detected low colonization rates of S. aureus (4–6%) and *S. schweitzeri* (4%) in two out of four species of fruit bats, namely *Rousettus aegyptiacus* and *Micropteropus pusillus*, but not in insectivorous bats. Multilocus sequence typing showed that *S. aureus* from Gabonese bats (ST2984, ST3259, ST3301, ST3302) were distinct from major African human associated clones (ST15, ST121, ST152). *S. schweitzeri* from bats (ST1697, ST1700) clustered with *S. schweitzeri* from other species (bats, monkeys) from Nigeria and Côte d'Ivoire. In conclusion, colonization rates of bats with *S. aureus* and *S. schweitzeri* were low in our study. Phylogenetic analysis supports an intense geographical dispersal of *S. schweitzeri* among different mammalian wildlife hosts.

Holmes E. C., Dudas G., Rambaut A. and Andersen K. G. 2016. The evolution of Ebola virus: Insights from the 2013–2016 epidemic. *Nature* 538(7624): 193–200. doi: 10.1038/nature19790.

The 2013-2016 epidemic of Ebola virus disease in West Africa was of unprecedented magnitude and changed our perspective on this lethal but sporadically emerging virus. This outbreak also marked the beginning of large-scale real-time molecular epidemiology. Here, we show how evolutionary analyses of Ebola virus genome sequences provided key insights into virus origins, evolution and spread during the epidemic. We provide basic scientists, epidemiologists, medical practitioners and other outbreak responders with an enhanced understanding of the utility and limitations of pathogen genomic sequencing. This will be crucially important in our attempts to track and control future infectious disease outbreaks.

Hugueney M., Maridet O., Mein P., Mourer-Chauviré C. and Priéto J. 2015. *Lartetium africanum* (Lavocat, 1961) (Eulipotyphla · Soricidae) from Beni-Mellal (Morocco), the oldest African shrew: new descriptions, palaeoenvironment and comments on biochronological context. *Palaeobiodiversity and Palaeoenvironments* 95(3): 465–476. doi: 10.1007/s12549-015-0197-9.

Additional specimens of the poorly known African shrew *Lartetium africanum* (Lavocat, 1961) are described and complete our knowledge of this tiny animal. The results of this study justify the elevation of material originally described as a subspecies to the species rank. Soricids are hitherto unknown in older African localities. Like many other soricids, *L. africanum* lived in a rather humid habitat, close to a body of freshwater, as testified by the intercalations of travertines with reeds in the lacustrine lenses that yielded the fauna. However, the presence of associated vertebrate taxa also attest to more open environments in the surroundings and a tropical climate. Various hypotheses on the date of arrival of this taxon in Africa have been proposed since migration routes between Eurasia and Afro-Arabia were not always open during the Middle Miocene and also because magnetostratigraphic data are now known and can be compared. These hypotheses are discussed here. Recent advances in our knowledge of the palaeogeography and the comparison of *L. africanum* with western European *Lartetium* taxa suggest that Beni-Mellal could be older than previously proposed, possibly early Middle Miocene.

Ing R. K., Colombo R., Gembu G-C., Bas Y., Julien J-F., Gager Y. and Hassanin A. 2016. Echolocation calls and flight behaviour of the elusive Pied Butterfly Bat (*Glauconycteris superba*), and new data on its morphology and ecology. *Acta Chiropterologica* 18(2): 477–488. doi: 10.3161/15081109ACC2016.18.2.014.

The pied butterfly bat, *Glauconycteris superba*, is endemic to the tropical forest zone of Africa, where it was previously known from only five specimens. Here we report the capture of 10 individuals in two localities of the Democratic Republic of the Congo (Mbiye Island and Yoko forest reserve), and we present the first acoustic data of the species recorded using a conventional microphone and a home-made acoustic system for real time 3D localization. Our morphological comparisons show that females are larger and heavier than males, and that the two sexes exhibit the same fur coloration pattern. We found some individual variations concerning the width of the two lateral white stripes on the belly, and the number and extension of white shoulder-spots. The echolocation recordings show evidence for alternation between two call types (A and B), differing in frequency, bandwidth, and duration. The acoustic signals obtained before captures and after releases revealed important variations depending on the trajectories and environmental conditions. Acoustic characteristics, wing measurements, and the unique black and white fur pattern of *G. superba* suggest that it is a canopy species able to fly at high speeds. Our findings will be useful for future ecological studies to provide new data on the range, population size, trend and threats of *G. superba* in order to better assess its conservation status.

Kearney T. C., Keith M. and Seamark E. C. J. 2017. New records of bat species using Gatkop Cave in the maternal season. *Mammalia* 81(1): 41-48. doi: 10.1515/mammalia-2015-0043.

Eight bat species were recorded at Gatkop Cave, in the northern part of South Africa in December 2011 (*Cloeotis percivali*, *Hipposideros caffer*, *Myotis tricolor*, *Miniopterus natalensis*, *Nycteris thebaica*, *Rhinolophus blasii*, *Rhinolophus smithersi*, and *Rhinolophus simulator*). With the exception of *M. natalensis*, *R. simulator* and *Myo. tricolor*, the other five species were recorded for the first time at Gatkop Cave during this time of the year, when thousands of *M. natalensis* use the cave as a maternity and nursery roost. Previously it was suggested the large numbers of *M. natalensis* using Gatkop Cave during the maternal period excluded other bat species. The reason for this recorded change in species roost composition at Gatkop Cave during the maternal period in relation to previous records made from the late 1960s and the mid 1980s is not clear, two possible reasons are the loss of other roosts, or these species were previously present but were not captured as a result of the particular methods used.

Leopardi S., Oluwayelu D., Meseko C., Marciano S., Tassoni L., Bakarey S., Monne I., Cattoli G. and De Benedictis P. 2016. The close genetic relationship of lineage D *Betacoronavirus* from Nigerian and Kenyan straw-colored fruit bats (*Eidolon helvum*) is consistent with the existence of a single epidemiological unit across sub-Saharan Africa. *Virus Genes* 52(4): 573–577. doi: 10.1007/s11262-016-1331-0.

Straw-colored fruit bats (*Eidolon helvum*), which have been identified as natural hosts for several zoonotic pathogens, such as lyssaviruses, henipaviruses, and ebolavirus, are associated with human settlements in Nigeria where they are commonly consumed as a delicacy. However, information on the viruses harbored by these bats is scarce. In this study, coronavirus sequences were detected using a nested RT-PCR targeting 440 bp of the RNA-dependent RNA polymerase (RdRp) in six of 79 fecal samples collected from an urban colony of *E. helvum* in Ibadan, Nigeria. Phylogenetic analysis revealed that all six sequences were monophyletic and clustered in lineage D of *Betacoronavirus*. The extension of two fragments allowed us to classify our sequences within the RdRp Group Unit defined for Kenyan *Betacoronavirus* from the same host species. These findings are consistent with the previous suggestion on the existence of a single epidemiological unit of *E. helvum* across sub-Saharan Africa. This theory, which is supported by the genetic structure of continental *E. helvum*, could facilitate viral mixing between different colonies across the continent.

Li Q., Lu F., Dai C., Fan M., Wang W. and Wang K. 2017. Simulating the potential role of media coverage and infected bats in the 2014 Ebola outbreak. *Journal of Theoretical Biology* 412(10): 123–129. doi: 10.1016/j.jtbi.2016.10.009.

Multiple epidemiological models have been developed to model the transmission dynamics of Ebola virus (EBOV) disease in West Africa in 2014 because the severity of the epidemic is commonly overestimated. A compartmental model that incorporates the media impact and the effect of infected bats was constructed and calibrated using data reported until the end of 2014. The final cumulative number of deaths and confirmed cases were estimated to be 1.0921×10^4 (95% CI 9.7706×10^3–1.2072×10^4) and 1.5193×10^4 (95% CI 1.3593×10^4–1.6795×10^4), respectively. The epidemic was estimated to end on June 2015, which was similar to the data reported by the World Health Organization. A sensitivity analysis indicated that an increase of either the media impact or the number of infectious bats that are captured daily can increase the cumulative number of confirmed cases/deaths. Of the considered epidemiological parameters, only the media coverage can significantly reduce both the peak time and the value of the cumulative confirmed cases/deaths. Thus, we propose ‘the cumulative confirmed cases and deaths’ as another media mechanism. In conclusion, the media impact contributed to the control of the 2014 Ebola outbreak, and infectious bats may be a potential source of the epidemic.

McKee C. D., Hayman D. T. S., Kosoy M.Y. and Webb C.T. 2016. Phylogenetic and geographic patterns of bartonella host shifts among bat species. *Infection, Genetics and Evolution* 44: 382–394. doi: 10.1016/j.meegid.2016.07.033.

The influence of factors contributing to parasite diversity in individual hosts and communities are increasingly studied, but there has been less focus on the dominant processes leading to parasite diversification. Using bartonella infections in bats as a model system, we explored the influence of three processes that can contribute to bartonella diversification and lineage formation: (1) spatial correlation in the invasion and transmission of bartonella among bats (phylogeography); (2) divergent adaptation of bartonellae to bat hosts and arthropod vectors; and (3) evolutionary codivergence between bats and bartonellae. Using a combination of global fit techniques and ancestral state reconstruction, we found that codivergence appears to be the dominant process leading to diversification of bartonella in bats, with lineages of bartonellae corresponding to separate bat suborders, superfamilies, and families. Furthermore, we estimated the rates at which bartonellae shift bat hosts across taxonomic scales (suborders, superfamilies, and families) and found that transition rates decrease with increasing taxonomic distance, providing support for a mechanism that can contribute to the observed evolutionary congruence between bats and their associated bartonellae. While bartonella diversification is associated with host sympatry, the influence of this factor is minor compared to the influence of codivergence and there is a clear indication that some bartonella lineages span multiple regions, particularly between Africa and Southeast Asia. Divergent adaptation of bartonellae to bat hosts and arthropod vectors is apparent and can dilute the overall pattern of codivergence, however its importance in the formation of *Bartonella* lineages in bats is small relative to codivergence. We argue that exploring all three of these processes yields a more complete understanding of bat-bartonella relationships and the evolution of the genus *Bartonella*, generally. Application of these methods to other infectious bacteria and viruses could uncover common processes that lead to parasite diversification and the formation of host-parasite relationships.

Monadjem A., Richards L. and Denys C. 2016. An African bat hotspot: The exceptional importance of Mount Nimba for bat diversity. *Acta Chiropterologica* 18(2): 359–375. doi: 10.3161/15081109ACC2016.18.2.005.

Mount Nimba, covering 674 km^2, straddles Liberia, Guinea and Côte d’Ivoire (Ivory Coast) in West Africa and is situated in the transition zone between the tropical forest zone to the south and moist woodlands to the north. Mount Nimba supports an exceptional biodiversity, with a number of endemic plants, invertebrates and vertebrates restricted to the massif, including the bat *Hipposideros lamottei*. Previous surveys suggested a high bat richness of 41 species associated with the mountain. During a series of surveys conducted in 2008–2012, we found that the bat diversity in this region far surpasses earlier figures and currently is 59 species. At least one bat species is entirely restricted to the mountain, with several other near-endemics or Upper Guinea forest endemics. Three species are listed as threatened by the IUCN, including one Critically Endangered. Furthermore, the conservation statuses of nine taxa have yet to be evaluated by the IUCN, several of which are recently described species and are likely to be threatened. This study highlights the irreplaceability of Mount Nimba for the conservation of bat diversity on the African continent, and draws attention to its protection.

Nkrumah E. E., Vallo P., Klose S. M., Ripperger S. P., Badu E. K., Gloza-rausch F., Drosten C., Kalko E. K. V., Tschapka M. and Oppong S. K. 2016. Foraging behavior and habitat selection of Noack’s Round-Leaf Bat (*Hipposideros* aff. *ruber*) and conservation implications. *Tropical Conservation Science* 9(4): 1–11. doi: 10.1177/1940082916680428.

In sub-Saharan Africa, anthropogenic activities such as cocoa (*Theobroma cacao*) farming have replaced the natural forest vegetation, making agricultural environments more readily available to some species of bats. To augment bat conservation in such highly modified agro-environments, we evaluated the foraging decisions of the widely distributed Noack’s round-leaf bat (*Hipposideros* aff. *ruber*) in a Ghanaian agro-environment for two factors: (a) foraging durations and (b) habitat selection from radio telemetry data collected from 13 bats. We hypothesized that it opportunistically selects foraging habitats in proportion to its availability. Our compositional analysis revealed, however, a nonrandom use of habitats. A ranking matrix indicated *Hipposideros* aff. *ruber* uses all available habitats but strongly preferred seminatural habitats dominated by fallow lands. Cocoa farms were predominantly used as flight paths for commuting between roosts and other nearby habitats during foraging. We observed a mean foraging duration of 109 min (SD = 62 min) per night for the species. In conclusion, our data suggest that (a) they are flexible in selecting all habitat types in the agro-environment but strongly preferred fallow matrices, (b) the provision of canopy trees within the agro-environment serves as flight paths for commuting from roost to habitats offering higher prey densities, and (3) the maintenance of fallow matrices as conservation units in sub-Saharan agro-environments helps augment conservation efforts of the species.

Obame-Nkoghe J., Rahola N., Bourgarel M., Yangari P., Prugnolle F., Maganga G.D., Leroy E-M., Fontenille D., Ayala D. and Paupy C. 2016. Bat flies (Diptera: Nycteribiidae and Streblidae) infesting cave-dwelling bats in Gabon: diversity, dynamics and potential role in *Polychromophilus melanipherus* transmission. *Parasites & Vectors* 9: 333. doi: 10.1186/s13071-016-1625-z.

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 Djibilong 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 schmidlii 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, $F_{(4,75)} = 13.15$, $P < 0.001$) 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.

Omoleke S. A., Mohammed I. and Saidu Y. 2016. Ebola viral disease in West Africa: A threat to global health, economy and political stability. *Journal of Public Health in Africa* 7(1): 27–40. doi: 10.4081/jphia.2016.534.

Introduction: The West African sub-continent is currently experiencing, it's first, and ironically, largest and longest Ebola Viral Diseases (EVD) outbreak ever documented in modern medical history. The current outbreak is significant in several ways, including longevity, magnitude of morbidity and mortality, occurrence outside the traditional niches, rapid spread and potential of becoming a global health tragedy. The authors provided explicit insights into the current and historical background, driver of the epidemic, societal impacts, status of vaccines and drugs development and proffered recommendations to halt and prevent future occurrences.

Method: The authors drew or synthesized pieces of evidence from relevant literature and multiple data sources as well as experiences from public health practice in West Africa.

Result: There are strong indications that the EVD may have been triggered by human activities into the forest ecosystem spurred by increasing population and poverty-driven forest-dependent local economy. Containment efforts are being hampered by weak and fragile health systems including public health surveillance and weak governance, certain socio-anthropological factors, fast travels (improved transport systems) and globalization. The societal impacts of the EBV outbreak are grave-including economic shutdown, weakening of socio-political systems, psychological distress, and unprecedented consumption of scares health resources. The research and development pipeline for product against EBV seems to grossly insufficient.

Conclusion: The outbreak of Ebola and the seeming difficulty to contain the epidemic is simply a reflection of the weak health systems, surveillance and emergency preparedness/response in many Sub-Sahara African countries, poverty and disconnect between the government and the people. Although interventions by the UN and other international development agencies could eventually halt the epidemic, local communities must be engaged to build trust and create demand for the public health interventions being implemented in the Ebola-ravaged populations. In the intermediate and long term, Post-Ebola rehabilitation should focus on strengthening of health systems, improving awareness about zoonosis and health behaviour, alleviating poverty and mitigating the impact of triggering factors. Finally, huge and sustained investments to spur research and development of disease control tools for emerging and pernicious infectious diseases (not only EVD).

Perkins S. L. and Schaer J. 2016. A modern menagerie of mammalian malaria. *Trends in Parasitology* 32(10): 772–782. doi: 10.1016/j.pt.2016.06.001.

Malaria parasites belong to the diverse apicomplexan order Haemospororida and use a variety of vertebrate and dipteran hosts worldwide. Recently, the utilization of molecular methods has resulted in a burst of newly discovered and rediscovered taxa infecting mammalian hosts, particularly in apes, ungulates, and bats. Additional study of these diverse mammal-infecting taxa is crucial for better understanding the evolutionary history of malaria parasites, especially given that most previous comparative phylogenetic analyses have tended to use both limited taxon sampling and a small set of genetic loci, resulting in weakly supported (and sometimes hotly contested) hypotheses. The ability to generate genomic data from these mammalian parasites, even from subpatent infections, will open up exciting prospects for research on malaria parasites.

Philips T. K., DeWildt C. S., Davis H. and Anderson R. S. 2016. Survey of the terrestrial arthropods found in the caves of Ghana. *Journal of Cave and Karst Studies* 78(2): 128–137. doi: 10.4311/2015LSC0120.

The first biological inventory of the caves of Ghana was conducted during January 2006 with some subsequent work in June 2007 and July 2008. Seventy species or morphospecies of insects, as well as amblypigids, phalangids, and diplopods were discovered in sixteen caves. All taxa appear to be either troglophilic or accidental and the most abundant and richest insect faunas were found in caves with resident bat populations. Insect diversity in caves consists mainly of species of cockroaches, cave crickets, tenebrionid beetles, reduviid assassin bugs, and ants. All caves surveyed are briefly described, coordinates documented, and a list of all the arthropods discovered is also given.

Popa E. M., Anthwal N. and Tucker A. S. 2016. Complex patterns of tooth replacement revealed in the fruit bat (*Eidolon helvum*). *Journal of Anatomy* 229(6): 847–856. doi: 10.1111/joa.12522.

How teeth are replaced during normal growth and development has long been an important question for comparative and developmental anatomy. Non-standard model animals have become increasingly popular in this field due to the fact that the canonical model laboratory mammal, the mouse, develops only one generation of teeth (monophyodonty), whereas the majority of mammals possess two generations of teeth (diphyodonty). Here we used the straw-coloured fruit bat (*Eidolon helvum*), an Old World megabat, which has two generations of teeth, in order to observe the development and replacement of tooth germs from initiation up to mineralization stages. Our morphological study uses 3D reconstruction of histological sections to uncover differing arrangements of the first and second-generation tooth germs during the process of tooth replacement. We show that both tooth germ generations develop as part of the dental lamina, with the first generation detaching from the lamina, leaving the free edge to give rise to a second generation. This separation was particularly marked at the third premolar locus, where the primary and replacement teeth become positioned side by side, unconnected by a lamina. The position of the replacement tooth, with respect to the primary tooth, varied within the mouth, with replacements forming posterior to or directly lingual to the primary tooth. Development of replacement teeth was arrested at some tooth positions and this appeared to be linked to the timing of tooth initiation and the subsequent rate of development. This study adds an additional species to the growing body of non-model species used in the study of tooth replacement, and offers a new insight into the development of the diphyodont condition.

Prat Y., Taub M. and Yovel Y. 2016. Everyday bat vocalizations contain information about emitter, addressee, context, and behavior. *Scientific Reports* 6: 39419. doi: 10.1038/srep39419.

Animal vocal communication is often diverse and structured. Yet, the information concealed in animal vocalizations remains elusive. Several studies have shown that animal calls convey information about their emitter and the context. Often, these studies focus on specific types of calls, as it is rarely possible to probe an entire vocal repertoire at once. In this study, we continuously monitored Egyptian fruit bats for months, recording audio and video around-the-clock. We analyzed almost 15,000 vocalizations, which accompanied the everyday interactions of the bats, and were all directed toward specific individuals, rather than broadcast. We found that bat vocalizations carry ample information about the identity of the emitter, the context of the call, the behavioral response to the call, and even the call's addressee. Our results underline the importance of studying the mundane, pairwise, directed, vocal interactions of animals.

Raharimihaja T. E. A., Rakotoarison J. L. M., Racey P. A. and Andrianaivoarivelo R. A. 2016. A comparison of the effectiveness of methods of deterring Pteropodid bats from feeding on commercial fruit in Madagascar. *Journal of Threatened Taxa* 8(13): 9512–9524. doi: 10.11609/jott.2688.8.13.9512-9524.

We compared the effectiveness of methods of deterring *Pteropus rufus* from feeding on commercial fruit in east central and southeastern Madagascar in 2012–2013 during the *Litchi chinensis* harvest. Two of the three methods used, installing plastic flags and ringing bells in the trees, were derived from those used by litchi growers in the southeast. We improved and standardized these methods and compared their effectiveness with an organic product made from dried blood and vegetable oil (Plantskydd®) with a taste and odour aimed at deterring mammal feeding. The bats damaged from 440–7,040 g of litchi fruits per tree and two of the three methods reduced the fruit lost to bats: the plastic flags and the organic deterrent. There were significant differences in the damage levels between the study sites and between our three methods of deterrence. The plastic flags and bell ringing methods were significantly less effective in reducing the fruit bat damage compared to the taste deterrent. The latter was most effective when it had enough time to dry and adhere to the fruits after spraying and before rain. Its effectiveness was further demonstrated in flight cage experiments during which *Rousettus madagascariensis* avoided litchis treated with Plantskydd®. Analysis of bat faecal samples revealed no feeding preference but the collected samples contained large numbers of *Ficus* seeds, suggesting that the bats feed extensively on *Ficus* fruits rather than on fruit of economic importance. Apart from fruit ripeness, tree productivity or other phenological factors did not affect the amount of fruit eaten by the bats. More fruits were damaged by birds than bats at both study sites.

Ravel A., Adaci M., Bensalah M., Charruault A-L., Essid E. M., AMmar H. K., Marzougui W., Mahboubi M., Mebrouk F., Merzeraud G., Vianey-Liaud M., Tabuce R. and Marivaux L. 2016. Origine et radiation initiale des chauves-souris modernes: nouvelles découvertes dans l'Éocène d'Afrique du Nord. *Geodiversitas* 38(3): 355–434. doi: 10.5252/g2016n3a3.

Origin and radiation of modern bats: new discoveries in the Eocene of North Africa. This study focuses on new fossil faunas of bats discovered in North Africa following several field campaigns. The fossiliferous localities include those from the Early to Middle Eocene of Tunisia (Chambi) and Algeria (Glib Zegdou). Systematic and cladistic analyses carried out on the fossil material, primarily including isolated teeth, allow us to highlight the modalities of the radiation of the first modern microbats. These new faunas include eight well-identified new taxa belonging to five modern families: one Necromantidae (?*Necromantis fragmentum* Ravel, n. sp.), two Hipposideridae Miller, 1907 (?*Palaeophyllophora tunisiensis* Ravel, n. sp. and *Hipposideros* [*Pseudorhinolophus*] *africanum* Ravel, n. sp.), three Emballonuridae Gervais in de Castelnau, 1855 (*Vespertiliavus kasserinensis* Ravel, n. sp., ?*Vespertiliavus aenigma* Ravel, n. sp., and *Pseudovespertiliavus parva* Ravel, n. gen., n. sp.), one Nycteridae (*Khoufechia gunnelli* Ravel, n. gen., n. sp.) and an undetermined Vespertilionidae. Two other taxa are identified (*Chambinycteris pusilli* Ravel, n. gen., n. sp. and *Drakonycteris glibzegdouensis* Ravel, n. gen., n. sp.), but they show an original dental pattern which precludes a family attribution. Two cladistic analyses allow to clarify the phylogenetic position of the best documented taxa. The results highlight for Hipposideridae and Emballonuridae chiropterans a major dispersal axis from North Africa towards South Europe during the Middle Eocene.

Razafimanahaka J. H., Ralisata M., Randrianandrianina F., Jenkins R. K. B., Ratsirarson J. and Racey P. A. 2016. Habitat use by the endemic Malagasy bat *Hipposideros commersoni* in a littoral forest. *Acta Chiropterologica* 18(2): 423–431. doi: 10.3161/15081109ACC2016.18.2.009.

We investigated habitat use by the endemic Malagasy bat *Hipposideros commersoni* in evergreen littoral rainforest during the wet season in 2006, in order to better inform conservation guidelines. We used radio tracking to locate roosting and foraging sites. Roosts, typically 5.4 ± 0.2 m from the ground, were always occupied by single bats and were found on branches of trees with a diameter at breast height of 8.2 ± 0.7 cm. Home range size was 31.8 ± 9.2 ha for males and 41.7 ± 12.9 ha for females. Roosts were always located within the foraging areas and only five (5.4%) of the 91 located were situated outside the sheltered littoral forest. Foraging bats made greatest use of natural, sheltered littoral forest and relatively few foraging sorties occurred beyond the forest edge. Females were not trapped during January and may undergo local movements at that time. There are no known caves in the vicinity of the study area and *H. commersoni* roosted only on trees. Previous studies in Madagascar have highlighted the importance of caves for bats and we now extend this to include tree roosts, within the evergreen rainforest.

Riccucci M. 2016. Play in bats: general overview, current knowledge and future challenges. *Vespertilio* 18: 91–97.
Although virtually all young mammals play, this particular behaviour is still poorly studied. So far little is known about play in bats. As reported in Leen & Novick (1969) the young of the free-tailed bats, *Tadarida brasiliensis*, "all joint together for the greater part of the day or night to play and tussle". Neuweiler (1969) gives an account of a mother-offspring play in *Pteropus medius*. Some social play has been reported in vampire bats (*Desmodus rotundus*). The occurrence of babbling in some species attests to the humanlike development of audio-vocal communication in bats, as found in *Saccopteryx bilineata*. From a neural and functional perspective, babbling may be equivalent to play behaviour. A few personal observations are mentioned: on *Pteropus seychellensis* in Praslin, Seychelles; on *Pteropus medius* in Viharamahadevi Park, Colombo (Sri Lanka); on *Pteropus rodricensis* on Rodrigues (Mauritius, Indian Ocean). It could be helpful to study bat play in captivity, even during periods of rehabilitation.

Rougeron V., Suquet E., Maganga G. D., Jiolle D., Mombo I. M., Bourgarel M., Motsch P., Arnathau C., Durand P., Drexler F., Drosten C., Renaud F., Prugnolle F. and Leroy E. M. 2016. Characterization and phylogenetic analysis of new bat astroviruses detected in Gabon, Central Africa. *Acta Virologica* 60(4): 386–392. doi: 10.4149/av_2016_04_386.
Astroviruses are emerging RNA viruses that cause enteropathogenic infections in humans and in other mammals. The identification of astroviruses in a wide range of animals highlights the zoonotic importance of these viruses. Bats can harbor many different viruses, among which some are highly pathogenic for humans (for instance, Nipah, Ebola and SARS coronavirus), and also several astroviruses. As some RNA viruses can be directly transmitted from bats to humans, it is crucial to collect data about their frequency, genetic diversity and phylogenetic characterization. In this study, we report the molecular identification of 44 new astroviruses (with a detection rate of 4.5%) in 962 apparently healthy bats that belong to five different species and that were captured in different caves in North-East Gabon, Central Africa. Our results show that bat astroviruses form a group that is genetically distinct from astroviruses infecting other mammals. Moreover, these astroviruses showed an important genetic diversity and low host restriction in bat species.

Rulli M. C., Santini M., Hayman D. T. S. and D'Odorico P. 2017. The nexus between forest fragmentation in Africa and Ebola virus disease outbreaks. *Scientific Reports* 7: 41613. doi: 10.1038/srep41613.
Tropical forests are undergoing land use change in many regions of the world, including the African continent. Human populations living close to forest margins fragmented and disturbed by deforestation may be particularly exposed to zoonotic infections because of the higher likelihood for humans to be in contact with disease reservoirs. Quantitative analysis of the nexus between deforestation and the emergence of Ebola virus disease (EVD), however, is still missing. Here we use land cover change data in conjunction with EVD outbreak records to investigate the association between recent (2004–2014) outbreaks in West and Central Africa, and patterns of land use change in the region. We show how in these EVD outbreaks the index cases in humans (i.e. spillover from wildlife reservoirs) occurred mostly in hotspots of forest fragmentation.

Sasaki M., Orba Y., Sasaki S., Gonzalez G., Ishii A., Hang'ombe B. M., Mweene A. S., Ito K. and Sawa H. 2016. Multi-reassortant G3P[3] group a rotavirus in a horseshoe bat in Zambia. *Journal of General Virology* 97(10): 2488–2493. doi: 10.1099/jgv.0.000591.
Group A rotavirus is a major cause of diarrhoea in humans, especially in young children. Bats also harbour group A rotaviruses, but the genetic backgrounds of bat rotavirus strains are usually distinct from those of human rotavirus strains. We identified a new strain of group A rotavirus in the intestinal contents of a horseshoe bat in Zambia. Whole genome sequencing revealed that the identified virus, named RVA/Bat-wt/ZMB/LUS12-14/2012/G3P[3], possessed the genotype constellation G3-P[3]-I3-R2-C2-M3-A9-N2-T3-E2-H3. Several genome segments of LUS12-14 were highly similar to those of group A rotaviruses identified from humans, cows and antelopes, indicating interspecies transmission of rotaviruses between bats and other mammals with possible multiple genomic reassortment events.

Schuh A. J., Amman B. R., Jones M. E. B., Sealy T. K., Uebelhoer L. S., Spengler J. R., Martin B. E., Coleman-McCray J. A. D., Nichol S. T. and Towner J. S. 2017. Modelling filovirus maintenance in nature by experimental transmission of Marburg virus between Egyptian rousette bats. *Nature Communications* 8: 14446. doi: 10.1038/ncomms14446.
The Egyptian rousette bat (ERB) is a natural reservoir host for Marburg virus (MARV); however, the mechanisms by which MARV is transmitted bat-to-bat and to other animals are unclear. Here we co-house MARV-inoculated donor ERBs with naive contact ERBs. MARV shedding is detected in oral, rectal and urine specimens from inoculated bats from 5–19 days post infection. Simultaneously, MARV is detected in oral specimens from contact bats, indicating oral exposure to the virus. In the late study phase, we provide evidence that MARV can be horizontally transmitted from inoculated to contact ERBs by finding MARV RNA in blood and oral specimens from contact bats, followed by MARV IgG antibodies in these same bats. This study demonstrates that MARV can be horizontally transmitted from inoculated to contact ERBs, thereby providing a model for filovirus maintenance in its natural reservoir host and a potential mechanism for virus spillover to other animals.

Schuh A. J., Amman B. R. and Towner, J. S. 2017. Filoviruses and bats. *Microbiology Australia*: 12-16. doi: 10.1071/MA17005.
While Reston and Lloviu viruses have never been associated with human disease, the other filoviruses cause outbreaks of hemorrhagic fever characterised by person-to-person transmission and high case fatality ratios. Cumulative evidence suggests that bats are the most likely reservoir hosts of the filoviruses. Ecological investigations following Marburg virus disease outbreaks associated with entry into caves inhabited by *Rousettus aegyptiacus* bats led to the identification of this bat species as the natural reservoir host of the marburgviruses. Experimental infection of *R. aegyptiacus* with Marburg virus has provided insight into the natural history of filovirus infection in bats that may help guide the search for the reservoir hosts of the ebolaviruses.

Smith A., Schoeman M. C., Keith M., Erasmus B. F. N., Monadjem A., Moilanen A. and Di Mini E. 2016. Synergistic effects of climate and land-use change on representation of African bats in priority conservation areas. *Ecological Indicators* 69: 276-383. doi: 10.1016/j.ecolind.2016.04.039.

Bats are considered important bioindicators and deliver key ecosystem services to humans. However, itis 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.

Tapanes E., Detwiler K. M. and Cords M. 2016. Bat predation by *Cercopithecus* monkeys: Implications for zoonotic disease transmission. *EcoHealth* 13(2): 405–409. doi: 10.1007/s10393-016-1121-0.

The relationship between bats and primates, which may contribute to zoonotic disease transmission, is poorly documented. We provide the first behavioral accounts of predation on bats by *Cercopithecus* monkeys, both of which are known to harbor zoonotic disease. We witnessed 13 bat predation events over 6.5 years in two forests in Kenya and Tanzania. Monkeys sometimes had prolonged contact with the bat carcass, consuming it entirely. All predation events occurred in forest-edge or plantation habitat. Predator–prey relations between bats and primates are little considered by disease ecologists, but may contribute to transmission of zoonotic disease, including Ebolavirus.

Tsagkogeorga G., Müller S., Dessimoz C. and Rossiter S. J. 2017. Comparative genomics reveals contraction in olfactory receptor genes in bats. *Scientific Reports* 7: 259. doi: 10.1038/s41598-017-00132-9.

Gene loss and gain during genome evolution are thought to play important roles in adaptive phenotypic diversification. Among mammals, bats possess the smallest genomes and have evolved the unique abilities of powered flight and laryngeal echolocation. To investigate whether gene family evolution has contributed to the genome downsizing and phenotypic diversification in this group, we performed comparative evolutionary analyses of complete proteome data for eight bat species, including echolocating and nonecholocating forms, together with the proteomes of 12 other laurasiatherian mammals. Our analyses revealed extensive gene loss in the most recent ancestor of bats, and also of carnivores (both >1,000 genes), although this gene contraction did not appear to correlate with the reduction in genome size in bats. Comparisons of highly dynamic families suggested that expansion and contraction affected genes with similar functions (immunity, response to stimulus) in all laurasiatherian lineages. However, the magnitude and direction of these changes varied greatly among groups. In particular, our results showed contraction of the Olfactory Receptor (OR) gene repertoire in the last common ancestor of all bats, as well as that of the echolocating species studied. In contrast, non-echolocating fruit bats showed evidence of expansion in ORs, supporting a "trade-off" between sensory modalities.

Urbanowicz R. A., McClure C. P., Sakuntabhai A., Sall A. A., Kobinger G., Müller M. A., Holmes E. C., Rey F. A., Simon-Loriere E. and Ball J. K. 2016. Human adaptation of Ebola virus during the West African outbreak. *Cell* 167(4): 1079–1087. e5. doi: 10.1016/j.cell.2016.10.013.

The 2013-2016 outbreak of Ebola virus (EBOV) in West Africa was the largest recorded. It began following the cross-species transmission of EBOV from an animal reservoir, most likely bats, into humans, with phylogenetic analysis revealing the co-circulation of several viral lineages. We hypothesized that this prolonged human circulation led to genomic changes that increased viral transmissibility in humans. We generated a synthetic glycoprotein (GP) construct based on the earliest reported isolate and introduced amino acid substitutions that defined viral lineages. Mutant GPs were used to generate a panel of pseudoviruses, which were used to infect different human and bat cell lines. These data revealed that specific amino acid substitutions in the EBOV GP have increased tropism for human cells, while reducing tropism for bat cells. Such increased infectivity may have enhanced the ability of EBOV to transmit among humans and contributed to the wide geographic distribution of some viral lineages.

Vallo P., Nkrumah E. E., Tehoda P., Benda P., Badu E. K. and Decher, J. 2016. Nutlet is a little nut: disclosure of the phylogenetic position of Robbins' house bat *Scotophilus nucella* (Vespertilionidae). *Folia Zool*. 65(4): 302–309.

Evolutionary parallelism complicates taxonomy of the bat genus *Scotophilus*. This implies the necessity for a careful examination of morphologically similar species. Robbins' – or "nutlet" – house bat *Scotophilus nucella* is an insufficiently known taxon of the African rainforest zone based on just a handful of recorded specimens previously included in the nut-coloured house bat *S. nux*. Because its phylogenetic relationship to *S. nux* and other congeneric species is unknown, it was assessed using analysis of DNA sequences of single mitochondrial and nuclear genes. Based on the mitochondrial cytochrome b sequences, *S. nucella* was placed in sister position to *S. nux*. A genetic divergence of 7.8-9.4 % between them supports the recognition of *S. nucella* as a distinct species. Analysis of partial sequences of the nuclear zinc finger protein gene on the Y-chromosome corroborated the sister relationship of *S. nucella* and *S. nux*, while showing sufficient differences to consider them as two species. Mitochondrial genetic diversity in *S. nucella* was low, whereas *S. nux* showed a rather complex genetic structure over a large geographic area, despite limited sampling. The origin of the forest group of *Scotophilus* could be dated to the Miocene-Pliocene transition and the split leading to the contemporary species *S. nucella* and *S. nux* to the Pliocene-Pleistocene transition. Both time periods are characterized by an arid climate that led to the retreat of forest environment, which likely promoted speciation in forest refugia. Mid-Pleistocene diversification in led to a separate lineage from Guinea, West Africa, for which a subspecific status may be considered, as it differs 3.4-4.5 % from other African populations.

Weier S. M., Linden V. M. G., Gaigher I., White P. J. C. and Taylor P. J. 2017. Changes of bat species composition over altitudinal gradients on northern and southern aspects of the Soutpansberg mountain range, South Africa. *Mammalia* 81(1): 49-60. doi: 10.1515/mammalia-2015-0055.

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

Wilson L. A. B., Hand S. J., López-Aguirre C., Archer M., Black K. H., Beck R. M. D., Armstrong K. N. and Wroe S. 2016. Cranial shape variation and phylogenetic relationships of extinct and extant Old World leaf-nosed bats. *Alcheringa: An Australasian Journal of Palaeontology* 40(4): 509–524. doi: 10.1080/03115518.2016.1196434.

The leaf-nosed bats in Hipposideridae and Rhinonycteridae currently have an Old World tropical to subtropical distribution, with a fossil record extending back to the middle Eocene of Europe. The Riversleigh World Heritage fossil site in northwestern Queensland constitutes a particularly rich archive of faunal diversity for Old World leaf-nosed bats, having yielded more than 20 species. We used 2D geometric morphometrics to quantify cranial shape in hipposiderids and rhinonycterids, with the aim of referring unallocated fossil species, particularly from Riversleigh, to each family within a phylogenetic framework, and using a quantitative approach to reconstruct cranial shape for key clades in these Old World radiations. Our sample comprised 21 extant hipposiderids and rhinonycterids, 1 megadermatid and 1 rhinolophid, in which 31 landmarks were placed in lateral and ventral views, and five measurements were taken in dorsal view. The phylogeny used as the framework for this study was based on an analysis of 64 discrete morphological characters from the dentition, cranium and postcranium scored for 42 extant and fossil hipposiderids and rhinonycterids and five outgroup taxa (rhinolophids and megadermatids). The phylogenetic analysis was conducted using maximum parsimony, with relationships among selected extant taxa constrained to match the results of recent comprehensive molecular studies. Our phylogenetic results suggest that the Riversleigh leaf-nosed bats probably do not represent an endemic Australian radiation, with fossil species spread throughout the tree and several with sister-group relationships with non-Australian taxa. Discriminant analyses (DA) conducted separately on each dataset resulted in cross-validated classification success ranging from 61.9% for ventral landmarks to 71.4% for lateral landmarks. Classification of the original grouped cases resulted in success of 81% for each dataset. Of the eight fossil taxa included as unknowns in the DA, six were found to be assigned to the same group as recovered by the phylogenetic analysis. From our results, we assign the Riversleigh Miocene species *Archerops annectens*, *Brachipposideros watsoni*, *Brevipalatus mcculloughi*, *Rhinonicteris tedfordi* and *Xenorhinos halli* to Rhinonycteridae, and *Riversleigha williamsi* and *Hipposideros bernardsigei* to Hipposideridae. Our results support *Pseudorhinolophus bouziguensis*, from the early Miocene of Bouzigues in southern France, as belonging to Hipposideridae, and probably *Hipposideros*. The reconstructed ancestor of hipposiderids was distinguished from that of the rhinonycterids by having a shorter rostrum, and less of a distinction between the rostrum and braincase.

Yinda C. K., Zeller M., Conceição-Neto N., Maes P., Deboutte W., Beller L., Heylen E., Ghogomu S. M., Van Ranst M. and Matthijnssens J. 2016. Novel highly divergent reassortant bat rotaviruses in Cameroon, without evidence of zoonosis. *Scientific Reports* 6: 34209. doi: 10.1038/srep34209.

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

Yinda C. K., Zell R., Deboutte W., Zeller M., Conceição-Neto N., Heylen E., Maes P., Knowles N. J., Ghogomu, S. M., Van Ranst M. and Matthijnssens J. 2017. Highly diverse population of Picornaviridae and other members of the Picornavirales, in Cameroonian fruit bats. *BMC Genomics* 18: 249. doi: 10.1186/s12864-017-3632-7.

Background: The order *Picornavirales* represents a diverse group of positive-stranded RNA viruses with small nonenveloped icosahedral virions. Recently, bats have been identified as an important reservoir of several highly pathogenic human viruses. Since many members of the Picornaviridae family cause a wide range of diseases in humans and animals, this study aimed to characterize members of the order *Picornavirales* in fruit bat populations located in the Southwest region of Cameroon. These bat populations are frequently in close contact with humans due to hunting, selling and eating practices, which provides ample opportunity for interspecies transmissions.

Results: Fecal samples from 87 fruit bats (*Eidolon helvum* and *Epomophorus gambianus*), were combined into 25 pools and analyzed using viral metagenomics. In total, *Picornavirales* reads were found in 19 pools, and (near) complete genomes of 11 picorna-like viruses were obtained from 7 of these pools. The picorna-like viruses possessed varied genomic organizations (monocistronic or dicistronic), and arrangements of gene cassettes. Some of the viruses belonged to established families, including the Picornaviridae, whereas others clustered distantly from known viruses and most likely represent novel genera and families. Phylogenetic and nucleotide composition analyses suggested that mammals were the likely host species of bat sapelovirus, bat kunsagivirus and bat crohivirus, whereas the remaining viruses (named bat iflavirus, bat posalivirus, bat fisalivirus, bat cripavirus, bat felisavirus, bat dicibavirus and bat badiciviruses 1 and 2) were most likely diet-derived.

Conclusion: The existence of a vast genetic variability of picorna-like viruses in fruit bats may increase the probability of spillover infections to humans especially when humans and bats have direct contact as the case in this study site. However, further screening for these viruses in humans will fully indicate their zoonotic potential.

Zehender G., Sorrentino C., Veo C., Fiaschi L., Gioffrè S., Ebranati E., Tanzi E., Ciccozzi M., Lai A. and Galli M. 2016. Distribution of Marburg virus in Africa: An evolutionary approach. *Infection, Genetics and Evolution* 44: 8–16. doi: 10.1016/j.meegid.2016.06.014.

The aim of this study was to investigate the origin and geographical dispersion of Marburg virus, the first member of the Filoviridae family to be discovered. Seventy-three complete genome sequences of Marburg virus isolated from animals and humans were retrieved from public databases and analysed using a Bayesian phylogeographical framework. The phylogenetic tree of the Marburg virus data set showed two significant evolutionary lineages: Ravn virus (RAVV) and Marburg virus (MARV). MARV divided into two main clades; clade A included isolates from Uganda (five from the European epidemic in 1967), Kenya (1980) and Angola (from the epidemic of 2004-2005); clade B included most of the isolates obtained during the 1999-2000 epidemic in the Democratic Republic of the Congo (DRC) and a group of Ugandan isolates obtained in 2007-2009. The estimated mean evolutionary rate of the whole genome was 3.3 - 10-4 substitutions/site/year (credibility interval 2.0-4.8). The MARV strain had a mean root time of the most recent common ancestor of 177.9 years ago (YA) (95% highest posterior density 87-284), thus indicating that it probably originated in the mid-XIX century, whereas the RAVV strain had a later origin dating back to a mean 33.8 YA. The most probable location of the MARV ancestor was Uganda (state posterior probability, spp = 0.41), whereas that of the RAVV ancestor was Kenya (spp = 0.71). There were significant migration rates from Uganda to the DRC (Bayes Factor, BF = 42.0) and in the opposite direction (BF = 5.7). Our data suggest that Uganda may have been the cradle of Marburg virus in Africa.

Notice Board

Conferences

14th European Bat Research Symposium

To be held in: Donostia, Spain, 1 - 5 August 2017.
Further information: http://ebrs2017.eus/.

4th Conference on Wind Energy and Wildlife Impacts

To be held in: Estoril, Portugal, 6 - 8 September 2017.
Further information: http://cww2017.pt/.

Southern African Bat Conference

To be held in: Cape Town, South Africa, 4 - 6 October 2017.
Further information: www.batswithoutborders.org.

NASBR 47th Annual Symposium on Bat Research

To be held in: Knoxville, Tennessee, USA, 18 - 21 October 2017.
Further information: https://www.holohil.com/event/nasbr-46th-annual-symposium-on-bat-research/

Future events

NASBR 48th Annual Symposium on Bat Research - Puerto Vallarta, Jalisco, Mexico (24 - 27 October 2018).

NASBR 49th Annual Symposium on Bat Research - Grand Rapids, Michigan, USA (29 October - 2 November 2019)

15th European Bat Research Symposium - Turku, Finland (3 -7 August 2020

11th European Bat Detector Workshop - Finland (7 - 11 August 2020)

Call for contributions

African Bat Conservation News is divided into two main parts: peer reviewed and non peer reviewed articles.
The non peer reviewed part is further subdivided into a two sections:

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

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

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

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

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

African Bat Conservation News Project Cycle

Issues will be published Quarterly (January, April, July, October).
Deadlines for scientific contributions (1 November, 1 February, 1 May, 1 August).
Deadlines for non-scientific contributions (1 December, 1 March, 1 June, 1 September).
Non scientific contributions should be sent to the Editor while scientific contributions should be sent to the Scientific Editor.
Download notes to authors from www.africanbats.org.