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Above: An adult female Blasius's Horseshoe Bat (*Rhinolophus blasii*) (TM 48451) caught at Gatkop Cave, Limpopo Province, South Africa, December 2011.

Inside this issue:

Observations, Discussions and Updates

Observation # 22 - First observation of the Trident Leaf-nosed Bat (*Cloeotis percivali*) from Kruger National Park, South Africa

Submitted by: Walter Jubber

Date of observation: 11 March 2010

Locality: Pufuri Camp, Makuleke Contractual Park, Kruger NP, South Africa

GPS (lat long): 22°25.256'S 31°13.770E

Photo credit: Walter Jubber

Primary observation:

Found a dead *Cloeotis percivali* (Trident Bat) this morning in the main lodge area. Hit by a ceiling fan left on over night.

Editorial Response:

This voucher of *Cloeotis percivali* was sent to the Ditsong National Museum of Natural History, Pretoria as part of the registered SANParks research project 'Inventory of bat species occurring at Pufuri (Makuleke Contractual Park), with a comparison of morphological and molecular identifications, and screening of voucher specimens for viruses', and the veterinarian export permit RB/2010/22. The skull was extracted and prepared, and the species identity confirmed. The voucher specimen is still to be returned to the Kruger National Park, where it will be accessioned in the Skukuza Biological Reference Collection. – **Teresa Kearney.**

Mendeley (www.mendeley.com) - African Chiroptera Working Group

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Of the nearly 10,000 journals surveyed over 90% are already "green" (i.e. they have already given official green light to author self-archiving: 62% for post prints, 29% for preprinted). Many of the remaining 9% "gray" journals will agree if the author asks.

AfricanBats has created a Mendeley group - African Chiroptera Working Group. The aim of this group is to collate information on bats mainly in Africa, with the express objective to assist in the conservation of Africa's bat diversity. Science can not be totally placed into a single defined block and various information form other areas and disciplines will also be included. Much of the papers contained in the reading list are papers that deal with bats from anywhere in the world. What bat researchers are undertaking in South America, Australia, Europe China, USA, all have a bearing on the science in Africa. Therefore I hope that more bat researchers from around the globe will join this group and share these papers as well as useful ideas and techniques that may assist those working for the understanding and the conservation of Africa's bats.

So come and join us on *www.mendeley.com* and join the *African Chiroptera Working Group*.

Scientific Contribution

First record and echolocation call of *Glauconycteris argentata* (Dobson, 1875) from Gabon

Daniel PEEREBOOM[1], Stefan VAN LIESHOUT[1], Kathryn J. JEFFERY[2,3,4] & Wim BERGMANS[5]

[1] Consultancy Bureau E.C.O. Logisch, P.O. Box 38, 2910 AA Nieuwerkerk aan den IJssel, The Netherlands. daniel@eco-logisch.com.
[2] Agence Nationale des Parcs Nationaux de Gabon, Batterie 4, Libreville, B.P.20379, Gabon. jefferykath@gmail.com.
[3] Institute de Recherche en Écologie Tropicale, B.P.13354, Libreville, Gabon.
[4] University of Stirling, Stirling, Scotland, FK9 4LA, UK.
[5] Pieter Pauwstraat 10-1, 1017 ZJ Amsterdam, The Netherlands. BergmansWim@kpnplanet.nl.

Key words: Chiroptera, *Glauconycteris argentata*, Lopé National Park, conservation, Gabon, echolocation.

Introduction

The insectivorous bat fauna of Gabon is still poorly known despite the detailed studies of Brosset in the Makokou and Bélinga regions (BROSSET, 1966, BROSSET, 1969). After Brosset several smaller studies on insectivoures bats were conducted, on species diversity in the Gamba protected area complex (RODRIGUEZ *et al*. 2006) and on bats and infectious diseases (POURRUT *et al*., 2007; TOWNER *et al*., 2007; POURRUT *et al*., 2009; MAGANGA *et al*., 2011). In total 37 species of insectivorous Chiroptera have been recorded for Gabon (BROSSET, 1966; AFRICAN CHIROPTERA REPORT, 2011). We carried out a bat study in a forest-savanna mosaic in northern Lopé National Park, central Gabon, from January to April 2010. The purpose of this study was to describe the calls of insectivorous bat species occurring in the Central African forest zone, thereby serving as a basis for acoustic bat surveys in this biome. Acoustic surveys can improve our knowledge of the distribution and ecology of insectivorous bats. This knowledge could help clarify their role as virus disperser to enable their inclusion in conservation schemes. Here we present a description of the echolocation calls of *Glauconycteris argentata* (Dobson, 1875) and the first record of this species for Gabon.

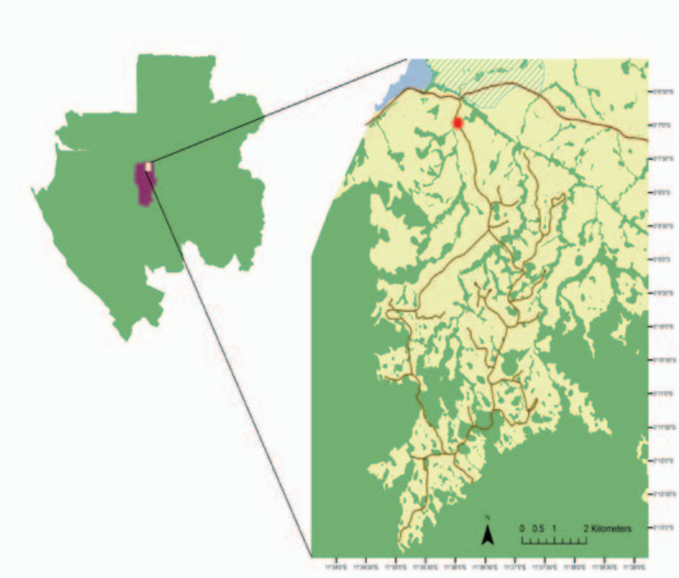

Figure 1: Map of Gabon with location of Lopé National Park (left) and detailed map of study area (right). Green areas denote forest, yellow savanna, blue the river Ogooué. Blue hatched lines indicate the location of Lopé village and brown lines are roads. The red spot indicates the location of the mist nets placed on the 2nd February 2010.

Materials and methods

The study was carried out in a 50 km^2 study area in northern Lopé National Park, central Gabon (see Figure 1). The park is characterized by a diversity of habitat types. While most of the park is covered by tropical lowland forest, the study area is dominated by savannas interspersed with natural forest fragments and gallery forests. Gabon's principal river, the Ogooué, flanks the northern boundary of the study area, and a chain of hills runs along the western side. A block of continuous forest flanks the western and southern boundaries. Bats were caught during 33 trapping sessions from January till April 2010. On the 2nd February 2010, two ground level mist-nets with dimensions of 12 x 4 meters and 18 x 4 meters were placed across and beside a stream in a gallery forest (11°36'00 E, 0°7'00 S) adjacent to a bridge (Figure 1). A third mist-net (9 x 4 m) was placed above the bridge at 3 meters above ground level. The nets were opened from 18.00 - 22.00 p.m. Captured bats were immediately removed from the nets and stored in holding bags for a maximum of 4 hours before being examined and measured. The following measurements were recorded: forearm length, from the elbow to the carpals with the wings folded; 3rd metacarpal: length of the metacarpal of the third digit; 1st and 2nd phalanx of third digit: length of the first and second phalanges of the third digit, respectively; tail length: from the tip of the tail to its base adjacent to the anus; tragus length: length from the base of the tragus to the tip; ear length: from the lower border of the external auditory meatus to the tip of the pinna; ear width: maximum width of the ear; rostrum width: width of rostrum across canines; tibia length: from the knee joint to the ankle; head-body length: maximum length from tip of the nose to base of the tail. All measurements are given in mm. In addition, photographs were taken for subsequent examination, droppings were collected and stored in RNA latter and one ectoparasite was collected. These samples are stored at the Agence Nationale des Parcs Nationaux de Gabon with field number 87. Echolocation calls were recorded using a Pettersson D240X bat detector with an Edirol R09 recorder during the few seconds after their release, at or close to their capture site. The recordings were made in a semi-open habitat on a savanna at approximately 30 meters from a forest edge. The echolocation calls were analysed by using Batsound v.3.3. software from Pettersson Electronics AB. The sampling rate was set at 44.1 kHz with a 16 bit resolution.

Results

189 Individuals of 29 species of insectivorous bats were caught and their echolocation calls were recorded and analyzed (PEEREBOOM *et al. in prep*). An adult female Silvery Butterfly Bat (*G. argentata)* was captured on the 2nd

Table 1. External measurements (in mm) of the female *G. argentata* with field number 87 captured in Lopé National Park, Gabon, in comparison with ranges of females given by PETERSON and SMITH (1973).

Measurement	Lopé NP	PETERSON and SMITH
forearm	42.6	40.0-43.7 (n=45)
3rd metacarpal	42	39.2-45.4 (n=45)
1st phalanx of 3rd digit	15.5	13.7-16.0 (n=45)
2nd phalanx of 3rd digit	28.7	21.5-25.1 (n=44)
tail	52.6	41-53 (n=42)
tragus	3.4	-
ear length	9.6	9-14 (n=42)
ear width	6	-
rostrum width	7.6	-
tibia	20.2	16.9-19.6 (n=41)
head-body	47.4	-

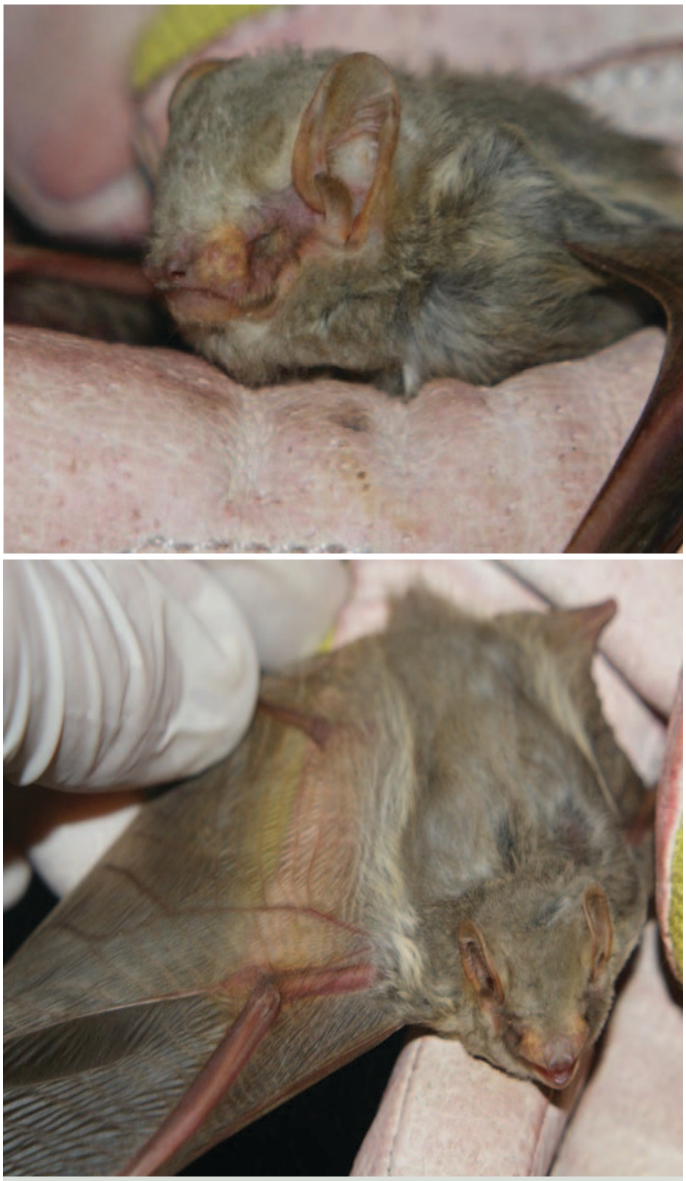

Figure 2 (top) and 3 (below). *Glauconycteris argentata* with field number 87 from Lopé NP. Clearly visible are the pale flanks, the general greyish colour, the slightly curved inner margin of the tragus and the absence of a strong reticulated pattern on the wings membrane.

Table 2. Echolocation parameters for the captured individual of *Glauconycteris argentata* with field number 87. The following call parameters were calculated from a total of 16 pulses: minimum frequency (Fmin), maximum frequency (Fmax), dominant frequency (domF), pulse duration (DUR), dominant frequency of the first harmonic (HARM), and interpulse interval (IPI).

	Mean	SD	min	max
Fmin (kHz)	31.59	1.48	28.42	34.45
Fmax (kHz)	89.16	7.11	77.95	101.60
DOMF (kHz)	43.96	1.8	40.26	47.14
DUR (ms)	2.4	0.31	2.0	3.0
HARM (kHz)	94.04	8.55	81.82	104.6
IPI (ms)	55	34	24	128

of February 2010 at 19:15 hours at 0.5 m above the water surface in the net positioned across the stream. The bat, with field number 87, was identified as *G. argentata* based on external measurements (Table 1), the pale wing membranes which lacked a strongly reticulated pattern on wings and tail membrane; grey ventral pelage and dull brown dorsal pelage with pale pelage on the flanks (see Figures 2 and 3). The tragus of our individual is sickle-shaped, with a strongly curved outer margin and a slightly curved inner margin (see Figure 2). The bat was not lactating or showing any other signs of reproduction.

Comparisons

Several similar-sized species of *Glauconycteris* occur in Africa. Compared to *Glauconycteris alboguttata* J. A. Allen, 1917, our individual lacks the seal brown pelage, dark wing membranes, the obvious shoulder spots and *G. abloguttata* is slightly smaller in size (EGER and SCHLITTER, 2001). *Glauconycteris beatrix* Thomas, 1901 and *Glauconycteris humeralis* J. A. Allen, 1917 have dark interfemoral membranes, lack the dorsolateral pale-coloured pelage and are smaller in size, with forearm under 40 mm (ROSEVEAR, 1965; EGER and SCHLITTER, 2001). *Glauconycteris curryae* Eger and Schlitter, 2001 is smaller in size (forearm 33.5 – 38.0 mm), lacks the dorsolateral pale-coloured pelage of *G. argentata* and differs in general colour (EGER and SCHLITTER, 2001). *Glauconycteris egeria* Thomas, 1913 is smaller in size (forearm 37 mm), has larger ears and a longer and narrower tragus (ROSEVEAR, 1965). *Glauconycteris gleni* Peterson and Smith, 1973 closely resembles *G. argentata* but lacks the characteristic dorsolateral pale-coloured pelage of *G. argentata*, the markings of venation of the interfemoral membrane are considerably darker and the interfemoral membrane wither (PETERSON and SMITH, 1973). *Glauconycteris kenyacola* Peterson, 1982 is similar in size to *G. argentata*, but with distinctive whitish facial markings on nose, chin and at the base of the ears (PETERSON, 1982). *Glauconycteris poensis* (Gray, 1842) is smaller in size with forearm under 40 mm and the colouration of the pelage averages much darker grey (ROSEVEAR, 1965; PETERSON, 1982). The tragus of *G. poensis* has strongly curved inner margins, where the tragus of *G. argentata* has a slightly curved inner margin. *Glauconycteris variegata* (Tomes,1861) resembles *G. argentata* in shape and size, but differs in the characteristic markings of veination of the interfemoral membrane in *G. variegata* and the shape of the inner margin of the tragus is straight in *G. variegata*.

This species was captured only once during 33 trapping sessions, which also yielded 24 other insectivorous species and 5 species of Pteropodidae (PEEREBOOM *et al. in prep*).

Glauconycteris argentata - Gabon *Scientific contributions* Peereboom *et al.* (2012)

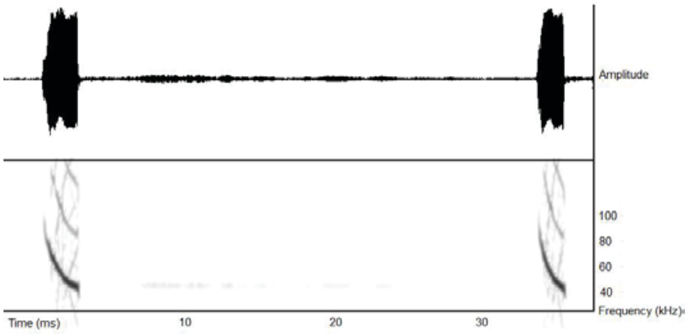

Figure 4. Waveform and spectrogram of two calls emitted by *G. argentata* with field number 87. The spectrogram was produced using Hanning window, FFT size 256.

Echolocation calls

The echolocation calls of this individual were frequency-modulated with a short quasi-constant frequency component (FM-qCF, see Figure 4). This type of call is often produced by vespertilionid bats that forage in semi-cluttered habitat close to trees, above clearings, or forest edges and trails (ALDRIDGE and RAUTENBACH, 1987). Our individual of *G. argentata* emitted echolocation calls with a dominant frequency around 44 kHz. The calls ranged in frequency from around 89 kHz to 32 kHz. A single harmonic was present in all pulses with a maximum energy around 94 kHz.

Discussion

This new record fills a gap in the known distribution of *G. argentata*, which is widespread in Central and East Africa (JACOBS *et al.*, 2008). The species is recorded from neighbouring countries Cameroon and Congo and is believed to be native but never before recorded from Gabon. *G. argentata* is associated with tropical forests and moist woodlands and has been recorded roosting in groups of up to 30 individuals in palm trees where they cling to the leaves near the midrib in groups (ROSEVEAR, 1965). During our inventory, nets were placed at potential flight paths and therefore potentially species-rich sites such as riverine forests, forest edges, or forest paths. Our single observation suggests that the species may be quite rare in northern Lopé. There is no data available on the foraging behaviour of *G. argentata*. The species might also be a high foraging species and our single observation could therefore also be caused by the limited amount of elevated mist nets during our survey.

This is the first description of the echolocation call of this species. The echolocation call parameters of this individual may not be representative for the species. More calls of different individuals, recorded in different habitats and regions within its distribution range need to be analysed for a comprehensive assessment of echolocation calls of this species. Our recordings of the echolocation call can also differ from normal foraging echolocation calls caused by stress in the animal from trapping and handling the individual.

Acknowledgements

We thank the Gabonese Government agencies for granting us permission to execute this research in their country, notably the Centre National de Recherche en Science et Téchnologie (CENAREST) and the Agence Nationale des Parcs Nationaux (ANPN) for research and park authorizations. Fieldwork was hosted by the Station d'Études des Gorilles et Chimpanzés, CIRMF, Lopé National Park, Gabon. Excellent technical and logistical assistance in the field was provided by Vianet Mihindou of the Ministère de l'Économie Forestière (MINEF). The Centre de Coordination Ouest pour l'Etude et la Protection des Chauves-souris in Genève was helpful by providing several publications.

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TOWNER, J. S., POURRUT, X., ALBARINO, C. G., NKOGUE, C. N., BIRD, B. H., GRARD, G., KSIAZEK, T. G., GONZALEZ, J.P., NICHOL, S. T. and LEROY, E. M., 2007. Marburg virus infection detected in a common African bat. *PLoS ONE* **2(8)**: e764.

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RECENT LITERATURE

PUBLISHED PAPERS

ADJEMIAN, J., FARNON, E. C., TSCHIOKO, F., WAMALA, J. F., BYARUHANGA, E., BWIRE, G. S., KANSIIME, E. K., AHIMBISIBWE, S. K., JEFFS, B., LUTWAMA, J. J., DOWNING, R., TAPPERO, J. W., FORMENTY, P., AMMAN, B., MANNING, C., TOWNER, J., NICHOL, S. T., and ROLLIN, P. E., 2011. Outbreak of Marburg hemorrhagic fever among miners in Kamwenge and Ibanda Districts, Uganda. *Journal of Infectious Diseases* 204(Suppl. 3): S796-S799. doi: 10.1093/infdis/jir312

Marburg hemorrhagic fever was detected among 4 miners in Ibanda District, Uganda, from June through September, 2007. Infection was likely acquired through exposure to bats or bat secretions in a mine in Kamwenge District, Uganda, and possibly human-to-human transmission between some patients. We describe the epidemiologic investigation and the health education response

AHMIM, M., and MOALI, A., 2011. The diet of the Maghrebian mouse-eared bat *Myotis punicus* (Mammalia, Chiroptera) in Kabylia, northern Algeria. *Ecologia Mediterranea* 37 (1): 45 - 51.

This paper describes the composition of the diet of the Maghrebian mouse-eared bat species *Myotis punicus* in the north of Algeria. The Maghrebian mouse-eared bat, *Myotis punicus* Felten, 1977 is classified by the IUCN Red List as a species of missing data and it is a species whose knowledge of hunting habitat and diet are virtually unknown in Algeria. In our contribution we have studied the diet of the specie in the area located in the region of Kabylia Babors, in wilayates (districts) of Bejaia and Jijel in Algeria between the months of March 2007 and January 2008. The protocol used consisted of a sampling of guano in the different sites used by the species and the identification of remains of insects under microscope. For analysis, samples of guano have been soaked at least one hour in 70% alcohol before being dissected using forceps under a binocular magnification 400x and the determination was made with a help of the identification key by Shiel et al. (1997). The results suggests that *Myotis punicus* in the studied sites of Algeria consumed prey belonging to three groups of arthropods: insects (frequence 96.06%), chilopods (2.82%) and spiders (1.12%)

ALI, R. A. M., 2011. Molecular phylogenetic relationship between and within the fruit bat (*Rousettus aegyptiacus*) and the lesser tailed bat (*Rhinopoma hardwickei*) deduced from RAPD-PCR analysis. *Journal of American Science* 7(10): 678-687.

The RAPD-PCR in the present study was used to determine the genetic variation within and among two Egyptian bat species, *Rousettus aegyptiacus* and *Rhinopoma hardwickei*. The animals were captured from one locality at Giza governorate, Egypt. A total of 39 bands were amplified by the three primers OPAO2, OPAO8 and OPCO3 with an average 13 bands per primer at molecular weights ranged from 1409 to 107 bp. The polymorphic loci between both species were 34 with percentage 87.18 %. The numbers of monomorphic bands in *Rousettus aegyptiacus aegyptiacus* and *Rhinopoma hardwickei arabium* were 14 and 9 bands, respectively. The two species are sharing 5 (12.8 %) monomorphic bands. The similarity coefficients value between the two bat species was ranged from 0.353 to 0.500 with an average of 0.404 (40.4%). Dendrogram showed that, the two bats genotypes are separated from each other into two clusters and more variation among members of *Rhinopoma hardwickei arabium* was observed in comparison to those of *Rousettus aegyptiacus aegyptiacus*. It is concluded that, the similarity coefficient value between the two bat species indicates that, the two bat species may have the same origin but are not identical and separated into two clusters.

ALLEGRINI, B., DURAND, G., DURAND, E., and PEYRE, O., 2011. On some bats recorded in the Adrar region, Mauitania. *African Bat Conservation News*, 26: 2-4.

ANDRIANAIVOARIVELO, R. A., ANDRIAFIDISON, D., RAHAINGONIRINA, C., RAHARIMBOLA, S., RAKOTOARIVELO, A. A., RAMILIJAONA, O. R., RACEY, P. A., and JENKINS, R. K. B., 2011. A conservation assessment of *Rousettus madagascariensis* (G. Grandidier, 1929, Pteropodidae) roosts in eastern Madagascar. *Madagascar Conservation & Development* 6(2): 78-82. doi: 10.4314/mcd.v6i2.6

We visited four cave roosts of the near threatened, and endemic, fruit bat *Rousettus madagascariensis* over a five year period and found major threats to the bats from hunting and deforestation. The conservation of this species is particularly challenging because it is legally hunted inside its cave roosts. Although provisional protected area status was obtained for two sites with community support, hunting continued. *R. madagascariensis* roosts were associated with humid forest and the loss of vegetation around caves rendered them unsuitable for the bats at two abandoned sites. A few individual hunters can have a rapid and destructive impact on *R. madagascariensis* roosts and future initiatives in this area should involve working with hunters to develop realistic solutions to reduce hunting. These efforts need to be supported by habitat protection measures.

BAMBINI, L., KOFOKY, A. F., MBOHOAHY, T., RALISATA, M., MANJOAZY, T., HOSKEN, D. J., and JENKINS, R. K. B., 2011. Do bats need trees? Habitat use of two Malagasy hipposiderid bats *Triaenops furculus* and *T. menamena* in the dry southwest. *Hystrix* (*n.s.*) 22(1): 81-92.

Habitat degradation and loss threaten the survival of many bat species. Recent studies in Madagascar however have found some species are present in areas of low forest cover even though their echolocation calls and wing morphology suggest they are able to forage in forests. The present study investigated habitat use and prey selection in two sympatric hipposiderid bats, *Triaenops* *furculus* and *T. menamena*, in the dry southwest of Madagascar. The study colony occupied a cave in limestone karst surrounded by intact spiny bush and several secondary or degraded habitats. We used bat detectors and radiotracking to determine habitat use, and faecal analysis and invertebrate sampling to assess prey selection. Spiny bush, the dominant habitat type in the study area, was used less than predicted from its availability, based on satellite imagery and ground-based habitat mapping. Areas containing large trees were used by radiotracked bats in approximate proportion to their availability and acoustic sampling revealed highest bat activity in this habitat. The radio-tracked individuals used agricultural land more than expected from its availability. A significant difference was found in the proportion of Lepidoptera in the faeces of the two species, with *T. furculus* showing a preference for moths. *Triaenops furculus* also selected Coleoptera, whereas *T. menamena* preferred mainly Hemiptera. While this study did not identify a strong association with forested habitats in *T. furculus* or *T. menamena*, it remains to be established whether the bats forage in a sub-optimal habitat due to their preference for roosting in the nearby karst caves.

BANYARD, A. C., HAYMAN, D. T. S., JOHNSON, N., MCELHINNEY, L., and FOOKS, A. R., 2011. *Bats and lyssaviruses*. 239-289pp. *Advances in Virus Research*, 79: 46. doi: 10.1016/B978-0-12-387040-7.00012-3.

Numerous bat species have been identified as important reservoirs of zoonotic viral pathogens. Rabies and rabies-related viruses constitute one of the most important viral zoonoses and pose a significant threat to public health across the globe. Whereas rabies virus (RABV) appears to be restricted to bats of the New World, related lyssavirus species have not been detected in the Americas and have only been detected in bat populations across Africa, Eurasia, and Australia. Currently, 11 distinct species of lyssavirus have been identified, 10 of which have been isolated from bat species and all of which appear to be able to cause encephalitis consistent with that seen with RABV infection of humans. In contrast, whereas lyssaviruses are apparently able to cause clinical disease in bats, it appears that these lyssaviruses may also be able to circulate within bat populations in the absence of clinical disease. This feature of these highly encephalitic viruses, alongside many other aspects of lyssavirus infection in bats, is poorly understood. Here, we review what is known of the complex relationship between bats and lyssaviruses, detailing both natural and experimental infections of these viruses in both chiropteran and nonchiropteran models. We also discuss potential mechanisms of virus excretion, transmission both to conspecifics and spill-over of virus into nonvolant species, and mechanisms of maintenance within bat populations. Importantly, we review the significance of neutralizing antibodies reported within bat populations and discuss the potential mechanisms by which highly neurovirulent viruses such as the lyssaviruses are able to infect bat species in the absence of clinical disease.

BENDA, P., AL-JUMAILY, M. M., REITER, A., and NASHER, A. K., 2011. Noteworthy records of bats from Yemen with description of a new species from Socotra. *Hystrix (n.s.)* 22(1): 23-56.

New records of some previously rarely found bat species from Yemen are presented. *Epomophorus labiatus* and *Neoromicia guineensis* were recorded in Yemen for the first time, both species occur solely in the westernmost part of the country. The most important and/or numerous records were made for *Rousettus aegyptiacus*, *Eptesicus nasutus*, *Hypsugo ariel*, *Scotophilus dinganii*, *Plecotus* cf. *balensis*, *Miniopterus natalensis*, *Tadarida aegyptiaca* and *Chaerephon nigeriae*. Additional distribution data are given also for *Hipposideros tephrus*, *Taphozous perforatus*, *Coleura afra*, *Nycticeinops schlieffenii* and *Chaerephon pumilus*. *Rousettus aegyptiacus* was found in 15 new localities throughout the Yemeni mainland. *Eptesicus nasutus*, *Plecotus* cf. *balensis* and *Chaerephon nigeriae* had been known from only one Yemeni site each. The first two species were recorded in one new locality each, while *C. nigeriae* was found in three new sites in western Yemen. Five new sites in Hadramaut and easternmost Yemen are reported for *Hypsugo ariel*. The Socotran population previously attributed to the latter species was found to be distinct in several morphological characters and is here described as a separate species, *Hypsugo lanzai* sp. nov.

BIESOLD, S. E., RITZ, D., GLOZA-RAUSCH, F., WOLLNY, R., DREXLER, J. F., CORMAN, V. M., KALKO, E. K. V., OPPONG, S., DROSTEN, C., and MÜLLER, M. A., 2011. Type I Interferon reaction to viral infection in interferon-competent, immortalized cell lines from the African fruit bat *Eidolon helvum*. *PLoS ONE* 6(11): e28131. doi: 10.1371/journal.pone.0028131

Bats harbor several highly pathogenic zoonotic viruses including Rabies, Marburg, and henipaviruses, without overt clinical symptoms in the animals. It has been suspected that bats might have evolved particularly effective mechanisms to suppress viral replication. Here, we investigated interferon (IFN) response, -induction, -secretion and -signaling in epithelial-like cells of the relevant and abundant African fruit bat species, *Eidolon helvum* (*E. helvum*). Immortalized cell lines were generated; their potential to induce and react on IFN was confirmed, and biological assays were adapted to application in bat cell cultures, enabling comparison of landmark IFN properties with that of common mammalian cell lines. *E. helvum* cells were fully capable of reacting to viral and artificial IFN stimuli. *E. helvum* cells showed highest IFN mRNA induction, highly productive IFN protein secretion, and evidence of efficient IFN stimulated gene induction. In an Alphavirus infection model, O'nyong-nyong virus exhibited strong IFN induction but evaded the IFN response by translational rather than transcriptional shutoff, similar to other Alphavirus infections. These novel IFN-competent cell lines will allow comparative research on zoonotic, bat-borne viruses in order to model mechanisms of viral maintenance and emergence in bat reservoirs.

CANUTI, M., EIS-HUEBINGER, A. M., DEIJS, M., DE VRIES, D., DREXLER, J. F., OPPONG, S. K., MÜLLER, M. A., KLOSE, S. M., WELLINGHAUSEN, N., COTTONTAIL, V. M., KALKO, E. K. V., DROSTEN, C., and VAN DER HOEK, L., 2011. Two novel parvoviruses in frugivorous New and Old World bats. *PLoS ONE* 6(12): e29140. doi: 10.1371/journal.pone.0029140

Bats, a globally distributed group of mammals with high ecological importance, are increasingly recognized as natural reservoir hosts for viral agents of significance to human and animal health. In the present study, we evaluated pools of blood samples obtained from two phylogenetically distant bat families, in particular from flying foxes (Pteropodidae), *Eidolon helvum* in West Africa, and from two species of New World leaf-nosed fruit bats (Phyllostomidae), *Artibeus jamaicensis* and *Artibeus lituratus* in Central America. A sequence-independent virus discovery technique (VIDISCA) was used in combination with high throughput sequencing to detect two novel parvoviruses: a PARV4-like virus named Eh-BtPV-1 in *Eidolon helvum* from Ghana and the first member of a putative new genus in *Artibeus jamaicensis* from Panama (Aj-BtPV-1). Those viruses were circulating in the corresponding bat colony at rates of 7-8%. Aj-BtPV-1 was also found in *Artibeus lituratus* (5.5%). Both viruses were detected in the blood of infected animals at high concentrations: up to 10E8 and to 10E10 copies/ml for Aj-BtPV-1 and Eh-BtPV-1 respectively. Eh-BtPV-1 was additionally detected in all organs collected from bats (brain, lungs, liver, spleen, kidneys and intestine) and spleen and kidneys were identified as the most likely sites where viral replication takes place. Our study shows that bat parvoviruses share common ancestors with known parvoviruses of humans and livestock. We also provide evidence that a variety of Parvovirinae are able to cause active infection in bats and that they are widely distributed in these animals with different geographic origin, ecologies and climatic ranges.

CÉSAR, J., BOUYER, J., GRANJON, L., AKOUDJIN, M., and LOUPPE, D., 2011. Les relictes forestières de la falaise de Banfora: Les dégradations au voisinage de Bobo-Dioulasso, Burkina Faso. *Bois et Forêts des Tropiques* 65/308(2): 5-19.

Vegetation monitoring and inventories of animal, micro-mammal and insect bioindicators were used to assess environmental degradation in three villages close to the town of Bobo-Dioulasso. The damage that appeared most severe resulted from tree felling for fuelwood and from sand and gravel extraction for building. Both activities are a consequence of urban development. Environmental degradation due to crop and livestock farming seems less severe. However, all of these human pressures are damaging Koro's market gardens as well as the Koua protected forest. The monitoring and inventory work now underway to deepen understanding of human-induced environmental changes shows that animal species are reacting to the disruption of their habitats, which is worsened by frequent erosion. The study concludes with proposals for protective measures and reforestation to curb erosion in crop fields and along river banks. The extraction of building materials also needs to be organised to reduce its impact on the environment, but this is likely to be problematical as long as individual interests take priority over collective needs.

CHINNASAMY, K., PITCHAMUTHU, M., SWAMI DOSS, D. P., MARIMUTHU, G., and EMMANUVEL RAJAN, K., 2011. Genetic diversity and population structure of leaf-nosed bat *Hipposideros speoris* (Chiroptera: Hipposideridae) in Indian subcontinent. *African Journal of Biotechnology* 10(8): 1320-1328.

Genetic variation and population structure of the leaf-nosed bat *Hipposideros speoris* were estimated using 16S rRNA sequence and microsatellite analysis. Twenty seven distinct mitochondrial haplotypes were identified from 186 individuals, sampled from eleven populations. FST test revealed significant variations between populations in the overall pairwise estimation ($FST = 0.710$; $p < 0.001$). In addition, haplotype network and analysis of molecular variation analysis (AMOVA) consistently suggest the prevalence of genetic structure in the sampled populations. However, the mtDNA data was not significantly different in few closely located urban populations, but significant difference has been observed with the use of microsatellite data. The Bayesian clustering analysis identified eight clusters among the populations; the clustering pattern also corresponded to the haplotype networks. Overall, the present study suggests a "macrogeographic genetic isolation-by-distance" and possibility of gene flow among closely located populations.

COPELAND, R. S., KIRK-SPRIGGS, A. H., MUTETI, S., BOOTH, W., and WIEGMANN, B. M., 2011. Rediscovery of the "terrible hairy fly", *Mormotomyia hirsuta* Austen (Diptera: Mormotomyiidae), in eastern Kenya, with notes on biology, natural history, and genetic variation of the Ukasi Hill population. *African Invertebrates* 52(2): 363-390.

Sixty-two years since last observed alive, *Mormotomyia hirsuta* Austen, the "terrible hairy fly", was found inside and outside a large, cave-like cleft boulder at the summit of Ukasi Hill in eastern Kenya, the type locality of the species. Adults were observed climbing the walls of the boulder and walking on thick layers of bat guano, in which larvae and puparia were also discovered. Large numbers of *M. hirsuta* were observed on and at the base of the northern side of the boulder, which at the time of capture experienced continuous shade during daylight hours. Only three individuals were observed at the southern opening, exposed to direct sunlight and hot, dry conditions. A collection of vertebrate bones and skulls from layers of guano both inside and outside the cleft revealed several vertebrate associates, including two species of Chiroptera, *Chaerephon* cf. *bivittatus* (Heuglin) and *Tadarida aegyptiaca* (E. Geoffroy), which are probably the two major guano-producing species responsible for the larval breeding medium. Male-biased sexual size dimorphism was pronounced in adult *M. hirsuta*, with seven body-part measurements, including legs, larger by 33-61% in males than females. Males demonstrated isometric growth while female growth was allometric. In contrast to males, female head and thorax lengths did not increase proportionally with leg length. Estimates of genetic diversity in the Ukasi population show higher than expected allelic diversity and indicate possible gene flow and frequent population bottlenecks. To promote the conservation of this endangered species, a joint effort has been initiated between the International Centre of Insect Physiology and Ecology, Nairobi and the National Museums of Kenya, Nairobi, to gazette the Ukasi hill area as a protected site.

DALHOUMI, R., AISSA, P., and AULAGNIER, S., 2011. Taxonomie et répartition des chiroptères de Tunisie. *Rev. suisse Zool.* 118(2): 265-292.

An extensive review of the published and unpublished literature resulted in an updated list of 19 bat species for Tunisia. Provisional distribution was mapped for all of them. The family Vespertilionidae (six genera, ten species) is the most diversified, beyond Rhinolophidae (one genus, five species). Only one species each of Hipposideridae, Rhinopomatidae, Molossidae and Miniopteridae have been recorded so far. Some species are widely distributed over the country (Mediterranean species), when others are restricted to the northern part (Palaearctic species) and some are only distributed in the southern desert areas (Saharo-Sindian species). Three species are classified as vulnerable and five species are classified as near threatened according to the I.U.C.N. redlist; they should benefit conservation measures.

DECHER, J., NORRIS, R. W., and FAHR, J., 2010. Small mammal survey in the upper Seli River valley, Sierra Leone. *Mammalia* 74(2): 163-176. doi: 10.1515/MAMM.2010.026

In 2006 an inventory of small mammals was conducted on the upper Seli River in central Sierra Leone on the southwestern fringe of the Loma-Man portion of the Guinea Highlands as part of the baseline surveys conducted for the Bumbuna Hydroelectric Project (BHP). We recorded a total of 35 mammal species, including three shrews (Soricomopha), 19 bats (Chiroptera), 11 rodents (Rodentia), one primate, and one carnivore. New, or first well-documented species for Sierra Leone are the shrew *Crocidura nigeriae*, the bats *Myonycteris torquata*, *Rhinolophus denti knorri*, and the rare horseshoe bat *Rhinolophus ziama* endemic to Upper Guinea. Also reported are two bat specimens apparently representing an undescribed species of *Neoromicia* related to *N. nana*. We support the creation of a protected area as an offset for areas lost to the inundation of the BHP reservoir.

DELL, L. A., KRUGER, J. L., BHAGWANDIN, A., JILLANI, N. E., PETTIGREW, J. D., and MANGER, P. R., 2010. Nuclear organization of cholinergic, putative catecholaminergic and serotonergic systems in the brains of two megachiropteran species. *Journal of Chemical Neuranatomy* 40(2): 177-195. doi: 10.1016/j.jchemneu.2010.05.008

The nuclear organization of the cholinergic, putative catecholaminergic and serotonergic systems within the brains of the megachiropteran straw-coloured fruit bat (*Eidolon helvum*) and Wahlberg's epauletted fruit bat (*Epomophorus wahlbergi*) were identified following immunohistochemistry for cholineacetyl- transferase, tyrosine hydroxylase and serotonin. The aim of the present study was to investigate possible differences in the nuclear complement of the neuromodulatory systems of these species in comparison to previous studies on megachiropterans, microchiropterans and other mammals. The nuclear organization of these systems is identical to that described previously for megachiropterans and shows many similarities to other mammalian species, especially primates; for example, the putative catecholaminergic system in both species presented a very compact nucleus within the locus coeruleus (A6c) which is found only in megachiropterans and primates. A cladistic analysis of 38 mammalian species and 82 characters from these systems show that megachiropterans form a sister group with primates to the exclusion of other mammals, including microchiropterans. Moreover, the results indicate that megachiropterans and microchiropterans have no clear phylogenetic relationship to each other, as the microchiropteran systems are most closely associated with insectivores. Thus a diphyletic origin of Chiroptera is supported by the present neural findings.

DORNBURG, A., COLOSI, J. G., MASER, C., REESE, A. T., and WATKINS-COLWELL, G. J., 2011. A survey of the Yale Peabody Museum collection of Egyptian mammals collected during construction of the Aswan High Dam, with an emphasis on material from the 1962-1965 Yale University Prehistoric Expedition to Nubia. *Bulletin of the Peabody Museum of Natural History* 52(2): 255-272. doi: 10.3374/014.052.0206

Zoological collections housing Egyptian specimens that pre-date the construction of the Aswan High Dam are of unique historical importance. Before the construction of the High Aswan Dam, Yale University organized three archeological salvage expeditions, between 1962 and 1965, to the Nile River Valley south of Aswan as part of an international UNESCO-organized salvage mission. Although the focus of these expeditions was the recovery of archeological artifacts, team leaders also included collection of zoological specimens in their operations. These efforts resulted in the collection of 448 species spanning 16 families of Egyptian mammals that were subsequently deposited in the Yale Peabody Museum of Natural History. Our re-survey of these collections revealed that almost two-thirds had been misidentified or only identified to "order" level taxonomic ranks. Many of the specimens collected were from sites now submerged beneath Lake Nasser and so provide a unique temporal snapshot of a region whose biodiversity was significantly restructured by human engineering. Our inventory identified several specimens now threatened with extinction or already extinct in Egypt, and also significantly expands the contemporary range of larger rat-tailed bats (*Rhinopoma microphyllum*).

EVIN, A., HORÁČEK, I., and HULVA, P., 2011. Phenotypic diversification and island evolution of pipistrelle bats (*Pipistrellus pipistrellus* group) in the Mediterranean region inferred from geometric morphometrics and molecular phylogenetics. *Journal of Biogeography* 38: 2091-2105.

Aim The Mediterranean Basin is a centre of radiation for numerous species groups. To increase our understanding of the mechanisms underlying speciation and radiation events in this region, we assessed the phenotypic variability within the *Pipistrellus pipistrellus-pygmaeus-hanaki* species complex. Although bats form the second largest mammalian order, studies of insular evolution in this group are scarce. We approached this problem from a microevolutionary perspective and tested for the recurrence of the insular syndrome. **Location** The Mediterranean Basin, with a special focus on isolated populations from Corsica, the Maghreb, Cyprus, Cyrenaica and Crete. ***Methods*** Phenotypic variability was assessed by cranial morphometrics using the coordinates of 41 3D landmarks and associated geometric-morphometric methods. We analysed 125 specimens representing all of the lineages in the species complex. Differences between taxa and between insular and continental populations in cranial size, shape, form and allometries were tested using analyses of variance and visualized using boxplots and canonical variate analysis. Relationships between molecular data from a previous study (cytochrome *b* sequences) and morphometric data were tested with co-inertia analyses (RV test) and multivariate regressions. ***Results*** The three species were relatively well differentiated in cranial size and shape, and each species showed a significant amount of inter-population variability. Comparisons of pairs of insular versus continental populations revealed heterogeneities in cranial patterns among island phenotypes, suggesting no recurrent insular syndrome. Molecular and phenotypic traits were correlated, except for molecular and lateral cranium shape. **Main conclusions** The *Pipistrellus pipistrellus-pygmaeus-hanaki* species complex exhibits phenotypic variability as a result of the fragmentation of its distribution (especially on islands), its phylogenetic and phylogeographic history and, most probably, other evolutionary factors that were not investigated in this study. We found no recurrent pattern of evolution on islands, indicating that site- specific factors play a prevailing role on Mediterranean islands. The correlation between molecular and phenotypic data is incomplete, suggesting that factors other than phylogenetic relationships, potentially connected with feeding ecology, have played a role in shaping cranial morphology in this species complex.

FAHR, J., 2011. *Bats - History of research, current knowledge, and future prospects*. 196-201 pp. *In* KONATÈ, S. and KAMPMANN, D. (Eds). *Biodiversity Atlas of West Africa, Volume III: Côte d'Ivoire*. Abidjan & Frankfurt/Main. 526 pp.

FAHR, J., 2011. *Bats of West Africa*. 110-117 pp. *In* SINSIN, B., THIOMBIANO, A., KONATÈ, S., and KAMPMANN, D. (Eds). *Biodiversity Atlas of West Africa, Volume I-III*. Cotonou, Ouagadougou, Abidjan & Frankfurt/Main. 526 pp.

FAHR, J., and KALKO, E. K. V., 2011. Biome transitions as centres of diversity: Habitat heterogeneity and diversity patterns of West African bat assemblages across spatial scales. *Ecography* 34(2): 177-195. doi: *10.1111/j.1600-0587.2010.05510.x*

It is widely accepted that species diversity is contingent upon the spatial scale used to analyze patterns and processes. Recent studies using coarse sampling grains over large extents have contributed much to our understanding of factors driving global diversity patterns. This advance is largely unmatched on the level of local to landscape scales despite being critical for our understanding of functional relationships across spatial scales. In our study on West African bat assemblages we employed a spatially explicit and nested design covering local to regional scales. Specifically, we analyzed diversity patterns in two contrasting, largely undisturbed landscapes, comprising a rainforest area and a forest-savanna mosaic in Ivory Coast, West Africa. We employed additive partitioning, rarefaction, and species richness estimation to show that bat diversity increased significantly with habitat heterogeneity on the landscape scale through the effects of beta diversity. Within the extent of our study areas, habitat type rather than geographic distance explained assemblage composition across spatial scales. Null models showed structure of functional groups to be partly filtered on local scales through the effects of vegetation density while on the landscape scale both assemblages represented random draws from regional species pools. We present a mixture model that combines the effects of habitat heterogeneity and complexity on species richness along a biome transect, predicting a unimodal rather than a monotonic relationship with environmental variables related to water. The bat assemblages of our study by far exceed previous figures of species richness in Africa, and refute the notion of low species richness of Afrotropical bat assemblages, which appears to be based largely on sampling biases. Biome transitions should receive increased attention in conservation strategies aiming at the maintenance of ecological and evolutionary processes

FOOD AND AGRICULTURE ORGANISATION OF THE UNITED NATIONS. 2011. *Investigating the role of bats in emerging zoonoses: Balancing ecology, conservation and public health interest.* NEWMAN, S.H., FIELD, H., EPSTEIN, J., DE JONG, C. (Eds). FAO Animal Production and Health Manual No. 12: i - xii; 1 - 169.

GERLACH, J., 2011. Conservation of the Seychelles sheath-tailed bat *Coleura seychellensis* from 1997-2011 and future prospects. *Phelsuma* 19: 54-68.

The Critically Endangered Seychelles sheath-tailed bat *Coleura seychellensis* has been the subject of conservation activity on Silhouette Island since 1997, in addition research into its status has been carried out on Mahé island. The species was more abundant in the past and many known roosts have been abandoned. The causes of decline have been speculated to include disturbance and predation but studies of the roosts suggest that habitat change may be the most significant factor. The species occupies small caves in boulder fields in lowland woodland which has been extensively invaded by introduced plants. These plants support reduced numbers of insects, especially Coleoptera. Lepidoptera and Coleoptera dominate the diet with a strong preference for the latter before and during the breeding season. Habitat management on Silhouette has removed alien plants from around the roosts and improved foraging conditions for the bat resulting in an increase in breeding activity. The population at La Passe on Silhouette has increased from 14-25 individuals in the 1990s to 40 in 2009. In 2010 this colony fragmented with 18-20 individuals leaving to start a second colony at Anse Lascars. The forced closure of the conservation project in March 2011 means that all conservation action for the species has ceased. In the absence of Seychelles government commitment to support conservation of this Critically Endangered species its future prospects do not look promising.

GRARD, G., BIEK, R., MUYEMBE TAMFUM, J. J., FAIR, J., WOLFE, N., FORMENTY, P., PAWESKA, J., and LEROY, E., 2011. Emergence of divergent Zaire Ebola virus strains in Democratic Republic of the Congo in 2007 and 2008. *Journal of Infectious Diseases* 204(Suppl. 3): S776-S784. doi: *10.1093/infdis/jir364*

Background. Zaire ebolavirus was responsible for 2 outbreaks in Democratic Republic of the Congo (DRC), in 1976 and 1995. The virus reemerged in DRC 12 years later, causing 2 successive outbreaks in the Luebo region, Kasai Occidental province, in 2007 and 2008. ***Methods***. Viruses of each outbreak were isolated and the full-length genomes were characterized. Phylogenetic analysis was then undertaken to characterize the relationships with previously described viruses. **Results**. The 2 Luebo viruses are nearly identical but are not related to lineage A viruses known in DRC or to descendants of the lineage B viruses encountered in the Gabon-Republic of the Congo area, with which they do, however, share a common ancestor. ***Conclusions***. Our findings strongly suggest that the Luebo 2007 outbreak did not result from viral spread from previously identified foci but from an independent viral emergence. The previously identified epidemiological link with migratory bat species known to carry Zaire ebolavirus RNA support the hypothesis of viral spillover from this widely dispersed reservoir. The high level of similarity between the Luebo2007 and Luebo2008 viruses suggests that local wildlife populations (most likely bats) became infected and allowed local viral persistence and reemergence from year to year.

GUNNELL, G. F., 2010. *Chiroptera*. 587-603pp. *In* WERDELIN, L. and SANDERS, W. L. (Eds). *Cenozoic mammals of Africa*. Univ. of California Press, Berkeley. xxi + 986 pp.

HAYMAN, D. T. S., WANG, L. F., BARR, J., BAKER, K. S., SUU-IRE, R., BRODER, C. C., CUNNINGHAM, A. A., and WOOD, J. L. N., 2011. Antibodies to Henipavirus or Henipa-like viruses in domestic pigs in Ghana, West Africa. *PLoS ONE* 6(9): e25256. doi:*10.1371/journal.pone.0025256*

Henipaviruses, Hendra virus (HeV) and Nipah virus (NiV), have pteropid bats as their known natural reservoirs. Antibodies against henipaviruses have been found in *Eidolon helvum*, an Old World fruit bat species, and henipavirus-like nucleic acid has been detected in faecal samples from *E. helvum* in Ghana. The initial outbreak of NiV in Malaysia led to over 265 human encephalitis cases, including 105 deaths, with infected pigs acting as amplifier hosts for NiV during the outbreak. We detected non-neutralizing antibodies against viruses of the genus Henipavirus in approximately 5% of pig sera (N = 97) tested in Ghana, but not in a small sample of other domestic species sampled under a *E. helvum* roost. Although we did not detect neutralizing antibody, our results suggest prior exposure of the Ghana pig population to henipavirus(es). Because a wide diversity of Henipavirus-like nucleic acid sequences have been found in Ghanaian *E. helvum*, we hypothesise that these pigs might have been infected by henipavirus(es) sufficiently divergent enough from HeVor NiV to produce cross-reactive, but not cross-neutralizing antibodies to HeV or NiV.

HULVA, P., FORNŮSKOVÁ, A., CHUDÁRKOVÁ, A., EVIN, A., ALLEGRINI, B., BENDA, P., and BRYJA, J., 2010. Mechanisms of radiation in a bat group from the genus *Pipistrellus* inferred by phylogeography, demography and population genetics. *Molecular Ecology* 19(24): 5417-5431. doi: *10.1111/j.1365-294X.2010.04899.x*

Here, we present a study of the *Pipistrellus pipistrellus* species complex, a highly diversified bat group with a radiation centre in the Mediterranean biodiversity hotspot. The study sample comprised 583 animals from 118 localities representatively covering the bat's range in the western Palearctic. We used fast-evolving markers (the mitochondrial D-loop sequence and 11 nuclear microsatellites) to describe the phylogeography, demography and population structure of this model taxon and address details of its diversification. The overall pattern within this group includes a mosaic of phylogenetically basal, often morphologically distant, relatively small and mostly allopatric demes in the Mediterranean Basin, as well as two sympatric sibling species in the large continental part of the range. The southern populations exhibit constant size, whereas northern populations show a demographic trend of growth associated with range expansion during the Pleistocene climate oscillations. There is evidence of isolation by distance and female philopatry in *P. pipistrellus sensu stricto*. Although the northern populations are reproductively isolated, we detected introgression events among several Mediterranean lineages. This pattern implies incomplete establishment of reproductive isolating mechanisms in these populations as well as the existence of a past reinforcement stage in the continental siblings. The occurrence of reticulations in the radiation centre among morphologically and ecologically derived relict demes suggests that adaptive unequal gene exchange within hybridizing populations could play a role in speciation and adaptive radiation within this group.

HUME, J., and MIDDLETON, G., 2011. A preliminary vertebrate palaeontological cave survey of the Comoros Islands. *Phelsuma* 19: 27-40.

The results of a reconnaissance palaeontological cave survey are described, with an island by island review of potential fossil localities within the Comoros Archipelago. Lava cave localities were examined and details recorded. The first lava caves on Anjouan were recorded, including new native bat roosts. In general the cave localities were too eroded, lacked any substantial sediment deposits or were geochemically unsuitable for the long-term preservation of fossil material; hence the lack of success in finding a single preserved fossil or subfossil bone.

JENKINS, R. K. B., KEANE, A., RAKOTOARIVELO, A. R., RAKOTOMBOAVONJY, V., RANDRIANANDRIANINA, F. H., RAZAFIMANAHAKA, H. J., RALAIARIMALALA, S. R., and JONES, J. P. G., 2011. Analysis of patterns of bushmeat consumption reveals extensive exploitation of protected species in eastern Madagascar. *PLoS ONE* 6(12): e27570. doi: *10.1371/journal.pone.0027570*

Understanding the patterns of wild meat consumption from tropical forests is important for designing approaches to address this major threat to biodiversity and mitigate potential pathways for transmission of emerging diseases. Bushmeat consumption has been particularly poorly studied in Madagascar, one of the world's hottest biodiversity hotspots. Studying bushmeat consumption is challenging as many species are protected and researchers must consider the incentives faced by informants. Using interviews with 1154 households in 12 communes in eastern Madagascar, as well as local monitoring data, we investigated the importance of socio-economic variables, taste preference and traditional taboos on consumption of 50 wild and domestic species. The majority of meals contain no animal protein. However, respondents consume a wide range of wild species and 95% of respondents have eaten at least one protected species (and nearly 45% have eaten more than 10). The rural/urban divide and wealth are important predictors of bushmeat consumption, but the magnitude and direction of the effect varies between species. Bushmeat species are not preferred and are considered inferior to fish and domestic animals. Taboos have provided protection to some species, particularly the Endangered Indri, but we present evidence that this taboo is rapidly eroding. By considering a variety of potential influences on consumption in a single study we have improved understanding of who is eating bushmeat and why. Evidence that bushmeat species are not generally preferred meats suggest that projects which increase the availability of domestic meat and fish may have success at reducing demand. We also suggest that enforcement of existing wildlife and firearm laws should be a priority, particularly in areas undergoing rapid social change. The issue of hunting as an important threat to biodiversity in Madagascar is only now being fully recognised. Urgent action is required to ensure that heavily hunted species are adequately protected.

KALKO, E. K. V., and FAHR, J., 2011. *Sampling bats*. 540-545 pp. *In* SINSIN, B., THIOMBIANO, A., KONATÈ, S., and KAMPMANN, D. (Eds). *Biodiversity Atlas of West Africa, Volume I-III.* Cotonou, Ouagadougou, Abidjan & Frankfurt/Main.

KAMINS, A. O., RESTIF, O., NTIAMOA-BAIDU, Y., SUU-IRE, R., HAYMAN, D. T. S., CUNNINGHAM, A. A., WOOD, J. L. N., and ROWCLIFFE, J. M., 2011. Uncovering the fruit bat bushmeat commodity chain and the true extent of fruit bat hunting in Ghana, West Africa. *Biological Conservation* 144(12): 3000-3008. doi: 10.1016/j.biocon.2011.09.003

Harvesting, consumption and trade of bushmeat are important causes of both biodiversity loss and potential zoonotic disease emergence. In order to identify possible ways to mitigate these threats, it is essential to improve our understanding of the mechanisms by which bushmeat gets from the site of capture to the consumer's table. In this paper we highlight the previously unrecognized scale of hunting of the African straw-colored fruit bat, *Eidolon helvum*, a species which is important in both ecological and public health contexts, and describe the commodity chain in southern Ghana for its trade. Based on interviews with 551 Ghanaians, including bat hunters, vendors and consumers, we estimate that a minimum of 128,000 *E. helvum* bats are sold each year through a commodity chain stretching up to 400 km and involving multiple vendors. Unlike the general bushmeat trade in Ghana, where animals are sold in both specialized bushmeat markets and in restaurants, *E. helvum* is sold primarily in marketplaces; many bats are also kept by hunters for personal consumption. The offtake estimated in this paper raises serious conservation concerns, while the commodity chain identified in this study may offer possible points for management intervention. The separation of the *E. helvum* commodity chain from that of other bushmeat highlights the need for species-specific research in this area, particularly for bats, whose status as bushmeat is largely unknown.

KANGOYÉ, M. N., GUENDA, W., THIOMBIANO, A., KALKO, E. K. V., and FAHR, J., 2011. *Small mammals: Bats*. 288-291 pp. *In* THIOMBIANO, A. and KAMPMANN, D. (Eds). *Biodiversity Atlas of West Africa, Volume I-III.* Ouagadougou & Frankfurt/Main. 592 pp.

KEARNEY, T. C., and TAYLOR, P. J., 2011. Selection of cranial and mandible measurements for traditional morphometric analyses of southern African vesper bats of the genera *Eptesicus*, *Hypsugo*, *Neoromicia*, and *Pipistrellus* (Mammalia: Chiroptera: Vespertilionidae). *Annals of the Ditsong National Museum of Natural History* 1: 53-61.

Univariate and multivariate statistical procedures were used to select 12 statistically problem-free and redundancy-reduced cranial and mandible measurements from a larger suite of 52 measurements made on *Neoromicia nana*. Specimens from three additional vesper species (*Neoromicia capensis*, *Neoromicia zuluensis* and *Pipistrellus hesperidus*) were used in an R-mode PCA to identify the measurements that best distinguish the different species. This selection process was followed to select meaningful measurements used in a traditional morphometric analysis to assess inter-generic as well as intra- and inter-specific variation in southern African vesper bats from the genera *Eptesicus*, *Hypsugo*, *Neoromicia*, and *Pipistrellus*.

KEARNEY, T. C., and SEAMARK, E. C. J., 2011. Report for Botswana Ministry of Environment, Wildlife and Tourism. Bat fieldwork at three different areas in the Okavango Delta in 2009. *AfricanBats Technical Report,* 01/2011: i-iv+1-66pp.

KORINE, C., SÁNCHEZ, F., and PINSHOW, B., 2011. Effects of ethanol on food consumption and skin temperature in the Egyptian fruit bat (*Rousettus aegyptiacus*). *Integrative & Comparative Biology* 51(3): 432-440. doi: 10.1093/icb/icr012

Since mammalian frugivores generally choose to eat ripe fruit in which ethanol concentration ([EtOH]) increases as the fruit ripens, we asked whether ethanol acts as an appetitive stimulant in the Egyptian fruit bat, *Rousettus aegyptiacus*, and also studied the effects of ethanol on their skin temperature (Ts). We hypothesized that the responses of fruit bats to dietary ethanol are concentration dependent and tested the predictions that the bats' response is positive, i.e., they eat more when [EtOH] in the food is in the range found in naturally ripe fruit, while it negatively affects them at higher concentrations. We also tested the prediction that in winter, even when availability of fruit is low and thermoregulatory costs are high, ingestion of ethanol by fruit bats is low because assimilated ethanol reduces shivering thermogenesis and peripheral vasodilation; these, alone or together, are detrimental to the maintenance of body temperature (Tb). In summer, captive bats offered food containing 0.1% ethanol significantly increased consumption over food with no ethanol; they did not change consumption when food contained 0.01, 0.3, or 0.5% ethanol; but significantly decreased consumption at higher levels of ethanol [EtOH], i.e., 1 and 2%. In winter, captive bats ate significantly less when their food contained 0.1% ethanol than when it contained 0, 0.3, or 0.5%. During summer, freshly caught bats ate significantly more ethanol-containing food than freshly caught bats in winter. Skin temperature (Ts) in Egyptian fruit bats decreased significantly at an ambient temperature (Ta) of 12°C (winter conditions) after gavage with liquid food containing 1% ethanol. The effect was clearly temperature-dependent, since ethanol did not have the same effect on bats gavaged with food containing 1% or no ethanol at a Ta of 25°C (summer conditions). In conclusion, ethanol may act as an appetitive stimulant for Egyptian fruit bats at low concentrations, but only in summer. Bats are deterred by food containing [EtOH] corresponding to that in overripe, unpalatable fruit (1 and 2%). Furthermore, during winter, Egyptian fruit bats are deterred by ethanol-rich fruit, possibly due to the potential thermoregulatory consequences of ethanol consumption.

KÜHL, A., HOFFMANN, M., MÜLLER, M. A., MUNSTER, V. J., GNIRβ, K., KIENE, M., TSEGAYE, T. S., BEHRENS, G., HERRLER, G., FELDMANN, H., DROSTEN, C., and PÖHLMANN, S., 2011. Comparative analysis of Ebola virus glycoprotein interactions with human and bat cells. *Journal of Infectious Diseases* 204(Suppl. 3): S840-S849. doi: 10.1093/infdis/jir306

Infection with Ebola virus (EBOV) causes hemorrhagic fever in humans with high case-fatality rates. The EBOV-glycoprotein (EBOV-GP) facilitates viral entry and promotes viral release from human cells. African fruit bats are believed not to develop disease upon EBOV infection and have been proposed as a natural reservoir of EBOV. We compared EBOV-GP interactions with human cells and cells from African fruit bats. We found that susceptibility to EBOV-GP-dependent infection was not limited to bat cells from potential reservoir species, and we observed that GP displayed similar biological properties in human and bat cells. The only exception was GP localization, which was to a greater extent intracellular in bat cells as compared to human cells. Collectively, our results suggest that GP interactions with fruit bat and human cells are similar and do not limit EBOV tropism for certain bat species.

KUZMIN, I. V., BOZICK, B., GUAGLIARDO, S. A., KUNKEL, R., SHAK, J. R., TONG, S., and RUPPRECHT, C. E., 2011. Bats, emerging infectious diseases, and the rabies paradigm revisited. *Emerging Health Threats Journal* 4: 7159. doi: 10.3402/ehtj.v4i0.7159

The significance of bats as sources of emerging infectious diseases has been increasingly appreciated, and new data have been accumulated rapidly during recent years. For some emerging pathogens the bat origin has been confirmed (such as lyssaviruses, henipaviruses, coronaviruses), for other it has been suggested (filoviruses). Several recently identified viruses remain to be “orphan” but have a potential for further emergence (such as Tioman, Menangle and Pulau viruses). In the present review we summarize information on major bat-associated emerging infections; discuss specific characteristics of bats as carriers of pathogens (from evolutionary, ecological, and immunological positions). We also discuss drivers and forces of an infectious disease emergence, and describe various existing and potential approaches for control and prevention of such infections at individual, populational, and societal levels.

KUZMIN, I. V., TURMELLE, A. S., AGWANDA, B., MARKOTTER, W., NIEZGODA, M., BREIMAN, R. F., and RUPPRECHT, C. E., 2011. Commerson’s Leaf-Nosed Bat (*Hipposideros commersoni*) is the Likely Reservoir of Shimoni Bat Virus. *Vector-Borne and Zoonotic Diseases* 11(11): 1465-1470. doi: 10.1089/vbz.2011.0663

In this study we attempted to identify whether Commerson’s leaf-nosed bat (*Hipposideros commersoni*) is the reservoir of Shimoni bat virus (SHIBV), which was isolated from a bat of this species in 2009. An alternative explanation is that the isolation of SHIBV from *H. commersoni* was a result of spill-over infection from other species, particularly from the Egyptian fruit bats (*Rousettus aegyptiacus*), which frequently sympatrically roost with *H. commersoni* and are known as the reservoir of the phylogenetically related Lagos bat virus (LBV). To evaluate these hypotheses, 769 bats of at least 17 species were sampled from 18 locations across Kenya during 2009-2010. Serum samples were subjected to virus neutralization tests against SHIBV and LBV. A limited amount of cross-neutralization between LBV and SHIBV was detected. However, *H. commersoni* bats demonstrated greater seroprevalence to SHIBV than to LBV, and greater virus-neutralizing titers to SHIBV than to LBV, with a mean difference of 1.16 log10 (95% confidence intervals [CI]: 0.94-1.40; $p < 0.001$). The opposite pattern was observed for sera of *R. aegyptiacus* bats, with a mean titer difference of 1.06 log10 (95% CI: 0.83-1.30; $p < 0.001$). Moreover, the seroprevalence in *H. commersoni* to SHIBV in the cave where these bats sympatrically roosted with *R. aegyptiacus* (and where SHIBV was isolated in 2009) was similar to their seroprevalence to SHIBV in a distant cave where no *R. aegyptiacus* were present (18.9% and 25.0%, respectively). These findings suggest that *H. commersoni* is the host species of SHIBV. Additional surveillance is needed to better understand the ecology of this virus and the potential risks of infection to humans and other mammalian species.

LAVRENCHENKO, L. A., KRUSKOP, S. V., BEKELE, A., BELAY, G., MOROZOV, P. N., IVLEV, Y. F., and WARSHAVSKY, A. A., 2010. Mammals of the Babille Elephant Sanctuary (Eastern Ethiopia). *Russian Journal of Theriology* 9(2): 47-60.

The paper presents the results of a first attempt to document the mammals of the Babille Elephant Sanctuary (Eastern Ethiopia). Four species (*Nycteris thebaica*, *Lavia frons*, *Mus tenellus*, *Helogale parvula*) were documented for the first time in the Sanctuary, two species (*Rhinolophus fumigatus*, *Mastomys awashensis*) were found new for eastern Ethiopia and the presence of another species (*Neoromicia zuluensis*) was confirmed for the first time within the limits of Ethiopia. Moreover, genetic and chromosomal characteristics of two rodents (*Acomys* sp. and *Gerbilliscus* cf. *robustus*) suggested new undescribed species. In total, according to our current estimate based on original data and previously published literature, the mammal fauna of the Sanctuary includes 59 species belonging to 11 orders, 30 families and 51 genera. The Babille Elephant Sanctuary has significant conservation value due to its high mammal species diversity and complex structure of the fauna including elements with different zoogeographic affinities

LE GRANGE, A., VAN DER MERWE, M., and BESTER, M., 2011. Reproductive strategy of the Egyptian free-tailed bat, *Tadarida aegyptiaca*, from a subtropical latitude (25°S) in South Africa. *African Zoology* 46(1): 169-175. doi: 10.3377/004.046.0107

Free-tailed bats (Molossidae) are widely distributed in Africa and exhibit considerable reproductive flexibility. The Egyptian free-tailed bat, *Tadarida aegyptiaca*, is one of the most widespread of the molossids and is therefore an excellent model to study the variation in reproduction through latitudinal changes. Bats were collected during 2008 and 2009 from Pretoria (25°S), South Africa. In males, spermatogenesis was already underway in January (summer) and spermatozoa were first noted in the epididymis during May (late autumn), where they are stored until the end of September. From September, the testes showed little spermatogenic activity and possibly remained quiescent until early summer. In females, follicular development started prior to January with large Graafian follicles present in June. Ovulation, copulation and subsequent fertilization occurred in late August (spring). When compared to the same species from a low temperate latitude (33°S) it is apparent that spermatogenesis and follicular development were initiated earlier in the year at 25°S. We propose that the seasonal monoestry displayed by *T. aegyptiaca* at 25°S may be the norm throughout their distributional range and that a latitudinal difference of just eight degrees could influence the timing of events in the reproductive cycle of a free-tailed bat.

LEROY, E. M., GONZALEZ, J. P., and BAIZE, S., 2011. Ebola and Marburg haemorrhagic fever viruses: Major scientific advances, but a relatively minor public health threat for Africa. *Clinical Microbiology and Infection* 17(7): 964-976. doi: *10.1111/j.1469-0691.2011.03535.x*

Ebola and Marburg viruses are the only members of the Filoviridae family (order Mononegavirales), a group of viruses characterized by a linear, non-segmented, single-strand negative RNA genome. They are among the most virulent pathogens for humans and great apes, causing acute haemorrhagic fever and death within a matter of days. Since their discovery 50 years ago, filoviruses have caused only a few outbreaks, with 2317 clinical cases and 1671 confirmed deaths, which is negligible compared with the devastation caused by malnutrition and other infectious diseases prevalent in Africa (malaria, cholera, AIDS, dengue, tuberculosis ...). Yet considerable human and financial resourses have been devoted to research on these viruses during the past two decades, partly because of their potential use as bioweapons. As a result, our understanding of the ecology, host interactions, and control of these viruses has improved considerably.

MACDONALD, D. W., JOHNSON, P. J., ALBRECHTSEN, L., DUTTON, A., SEYMOUR, S., DUPAIN, J., HALL, A., and FA, J. E., 2011. Association of body mass with price of bushmeat in Nigeria and Cameroon. *Conservation Biology* 25(6): 1220-1228. doi: *10.1111/j.1523-1739.2011.01741.x*

Spatially extensive patterns of bushmeat extraction (and the processes underlying these patterns) have not been explored. We used data from a large sample (n= 87) of bushmeat trading points in urban and rural localities in Nigeria and Cameroon to explore extraction patterns at a regional level. In 7,594 sample days, we observed 61,267 transactions involving whole carcasses. Rural and urban trading points differed in species for sale and in meat condition (fresh or smoked). Carcass price was principally associated with body mass, with little evidence that taxonomic group (primate, rodent, ungulate, or mammalian carnivore) affected price. Moreover, meat condition was not consistently associated with price. However, some individual species were more expensive throughout the region than would be expected for their size. Prices were weakly positively correlated with human settlement size and were highest in urban areas. Supply did not increase proportionally as human settlement size increased, such that per capita supply was significantly lower in urban centers than in rural areas. Policy options, including banning hunting of more vulnerable species (those that have low reproductive rates), may help to conserve some species consumed as bushmeat because carcass prices indicate that faster breeding, and therefore the more sustainable species, may be substituted and readily accepted by consumers.

MAGANGA, G. D., BOURGAREL, M., EBANG ELLA, G., DREXLER, J. F., GONZALEZ, J. P., DROSTEN, C., and LEROY, E. M., 2011. Is Marburg virus enzootic in Gabon? *Journal of Infectious Diseases* 204(Suppl. 3): S800-S803. doi: *10.1093/infdis/jir358*

Marburg virus (MARV) nucleic acid was detected in *Rousettus aegyptiacus* bats in 2005 and 2006 in the midwest and southeast of Gabon. In this study we used MARV-specific real-time reverse-transcription polyermase chain reaction (RT-PCR) and MARV-specific nested RT-PCR assay to screen 1257 bats caught during July 2009, December 2009, and June 2010 in 3 caves situated in northern Gabon. Nine specimens tested positive by the real-time assay, with cycle threshold values ranging from 35 to 39, of which only 1 *R. aegyptiacus* specimen collected in 2009 was positive in the nested VP35 RT-PCR assay. Together with MARV-positive bats in the south and west found in 2005 and 2006, confirmation of phylogenetically closely related MARV-positive bats 5 years later and in northern Gabon suggests that MARV is now enzootic in Gabon and emphasizes the importance of long-term monitoring of bat populations and human-bat interfaces.

MCKECHNIE, A. E., and MZILIKAZI, N., 2011. Heterothermy in Afrotropical mammals and birds: A review. *Integrative and Comparative Biology* 51(3): 349-363. doi: *10.1093/icb/icr035*

Recent years have seen a rapid increase in the number of Afrotropical endotherms known to avoid mismatches between energy supply and demand by using daily torpor and/or hibernation. Among mammals, heterothermy has been reported in 40 species in six orders, namely Macroscelidea, Afrosoricida, Rodentia, Eulipotyphla, Primates and Chiroptera. These species span a range in body mass of 7-770 g, with minimum heterothermic body temperatures ranging from 1-27°C and bout length varying from 1 h to 70 days. Daily torpor is the most common form of heterothermy, with true hibernation being observed in only seven species, *Graphiurus murinus*, *Graphiurus ocularis*, *Atelerix frontalis*, *Cheirogaleus medius*, *Cheirogaleus major*, *Microcebus murinus* and *Microcebus griseorufus*. The traditional distinction between daily torpor and hibernation is blurred in some species, with free-ranging individuals exhibiting bouts of >24 h and body temperatures <16°C, but none of the classical behaviours associated with hibernation. Several species bask in the sun during rewarming. Among birds, heterothermy has been reported in 16 species in seven orders, and is more pronounced in phylogenetically older taxa. Both in mammals and birds, patterns of heterothermy can vary dramatically among species occurring at a particular site, and even among individuals of a single species. For instance, patterns of heterothermy among cheirogalid primates in western Madagascar vary from daily torpor to uninterrupted hibernation for up to seven months. Other examples of variation among closely-related species involve small owls, elephant shrews and vespertilionid bats. There may also be variation in terms of the ecological correlates of torpor within a species, as is the case in the freckled nightjar *Caprimulgus tristigma*.

MEGALI, A., YANNIC, G., and CHRISTE, P., 2011. Disease in the dark: Molecular characterization of *Polychromophilus murinus* in temperate zone bats revealed a worldwide distribution of this malaria-like disease. *Molecular Ecology* 20(5): 1039-1048. doi: *10.1111/j.1365-294X.2010.04905.x*

For a better understanding of the complex coevolutionary processes between hosts and parasites, accurate identification of the actors involved in the interaction is of fundamental importance. Blood parasites of the Order Haemosporidia, responsible for malaria, have become the focus of a broad range of studies in evolutionary biology. Interestingly, molecular-based studies on avian malaria have revealed much higher species diversity than previously inferred with morphology. Meanwhile, studies on bat haemosporidian have been largely neglected. In Europe, only one genus (*Polychromophilus*) and two species have been morphologically described. To evaluate the presence of potential cryptic species and parasite prevalence, we undertook a molecular characterization of *Polychromophilus* in temperate zone bats. We used a nested-PCR approach on the cytochrome *b* mitochondrial gene to detect the presence of parasites in 237 bats belonging to four different species and in the dipteran bat fly *Nycteribia kolenatii*, previously described as being the vector of *Polychromophilus*. *Polychromophilus murinus* was found in the four bat species and in the insect vector with prevalence ranging from 4% for *Myotis myotis* to 51% for *M. daubentoni*. By sequencing 682 bp, we then investigated the phylogenetic relationships of *Polychromophilus* to other published malarial lineages. Seven haplotypes were found, all very closely related, suggesting the presence of a single species in our samples. These haplotypes formed a well-defined clade together with Haemosporidia of tropical bats, revealing a worldwide distribution of this parasite mostly neglected by malarial studies since the 1980s.

MEYER, C. F. J., AGUIAR, L. M. S., AGUIRRE, L. F., BAUMGARTEN, J., CLARKE, F. M., COSSON, J. F., ESTRADA VILLEGAS, S., FAHR, J., FARIA, D., FUREY, N., HENRY, M., HODGKISON, R., JENKINS, R. K. B., JUNG, K. G., KINGSTON, T., KUNZ, T. H., MACSWINEY GONZALEZ, M. C., MOYA, I., PONS, J. M., RACEY, P. A., REX, K., SAMPAIO, E. M., STONER, K. E., VOIGT, C. C., VON STADEN, D., WEISE, C. D., and KALKO, E. K. V., 2011. Accounting for detectability improves estimates of species richness in tropical bat surveys. *Journal of Applied Ecology* 48(3): 777-787. doi: 10.1111/j.1365-2664.2011.01976.x

1. Species richness is a state variable of some interest in monitoring programmes but raw species counts are often biased due to imperfect species detectability. Therefore, monitoring programmes should quantify detectability for target taxa to assess whether it varies over temporal or spatial scales. We assessed the potential for tropical bat monitoring programmes to reliably estimate trends in species richness. 2. Using data from 25 bat assemblages from the Old and New World tropics, we estimated detectability for all species in an assemblage (mean proportion of species detected per sampling plot) and for individual species (species-specific detectability). We further assessed how these estimates of detectability were affected by external sources of variation relating to time, space, survey effort and biological traits. 3. The mean proportion of species detected across 96 sampling plots was estimated at 0.76 (range 0.57-1.00) and was significantly greater for phytophagous than for animalivorous species. Species-averaged detectability for phytophagous species was influenced by the number of surveys and season, whereas the number of surveys and sampling methods [ground- or canopy-level mist nets, harp traps and acoustic sampling (AS)] most strongly affected estimates of detectability for animalivorous bats. Species-specific detectability averaged 0.4 and was highly heterogeneous across 232 species, with estimates ranging from 0.03 to 0.84. Species-level detectability was influenced by a range of external factors such as location, season, or sampling method, suggesting that raw species counts may sometimes be strongly biased. 4. Synthesis and applications. Due to generally high species-specific detection probabilities, Neotropical aerial insectivorous bats proved to be well suited for monitoring using AS. However, for species with low detectability, such as most gleaning animalivores or nectarivores, count data obtained in bat monitoring surveys must be corrected for detection bias. Our results indicate that species-averaged detection probabilities will rarely approach 1 unless many surveys are conducted. Consequently, long-term bat monitoring programmes need to adopt an estimation scheme that corrects for variation in detectability when comparing species richness over time and when making regional comparisons. Similar corrections will be needed for other species-rich tropical taxa.

NEGREDO, A., PALACIOS, G., VÁZQUEZ-MORÓN, S., GONZÁLEZ, F., DOPAZO, H., MOLERO, F., JUSTE, J., QUETGLAS, J., SAVJI, N., CRUZ MARTÍNEZ, M., HERRERA, J. E., PIZARRO, M., HUTCHISON, S. K., ECHEVARRÍA, J. E., LIPKIN, W. I., and TENORIO, A., 2011. Discovery of an Ebolavirus-like filovirus in Europe. *PLoS Pathogens* 7(10): e1002304. doi: 10.1371/journal.ppat.1002304

A novel filovirus, provisionally named Lloviu virus (LLOV), was detected during the investigation of *Miniopterus schreibersii* die-offs in Cueva del Lloviu in southern Europe. LLOV is genetically distinct from other marburgviruses and ebolaviruses and is the first filovirus detected in Europe that was not imported from an endemic area in Africa. Filoviruses, amongst the most lethal of primate pathogens, have only been reported as natural infections in sub-Saharan Africa and the Philippines. Infections of bats with the ebolaviruses and marburgviruses do not appear to be associated with disease. Here we report identification of genetically distinct filovirus in dead insectivorous bats in caves in Spain.

NESI, N., NAKOUNÉ, E., CRUAUD, C., and HASSANIN, A., 2011. DNA barcoding of African fruit bats (Mammalia, Pteropodidae). The mitochondrial genome does not provide a reliable discrimination between *Epomophorus gambianus* and *Micropteropus pusillus*. *Comptes Rendus Biologies* 331(7): 544-554. doi: 10.1016/j.crvi.2011.05.003

Sequences of the mitochondrial cytochrome c oxidase subunit I (*COI*) gene have been shown to be useful for species identification in various groups of animals. However, the DNA barcoding approach has never been tested on African fruit bats of the family Pteropodidae (Mammalia, Chiroptera). In this study, the *COI* gene was sequenced from 120 bats collected in the Central African Republic and belonging to either *Epomophorus gambianus* or *Micropteropus pusillus*, two species easily diagnosed on the basis of morphological characters, such as body size, skull shape and palatal ridges. Two additional molecular markers were used for comparisons: the complete mitochondrial cytochrome *b* gene and the intron 7 of the nuclear β-fibrinogen (*FGB*) gene. Our results reveal an unexpected discordance between mitochondrial and nuclear genes. The nuclear *FGB* signal agrees with our morphological identifications, as the three alleles detected for *E. gambianus* are divergent from the fourteen alleles found for *M. pusillus*. By contrast, this taxonomic distinction is not recovered with the analyses of mitochondrial genes, which support rather a polyphyletic pattern for both species. The conflict between molecular markers is explained by multiple mtDNA introgression events from *M. pusillus* into *E. gambianus* or, alternatively, by incomplete lineage sorting of mtDNA haplotypes associated with positive selection on *FGB* alleles of *M. pusillus*. Our work shows the failure of DNA barcoding to discriminate between two morphologically distinct fruit bat species and highlights the importance of using both mitochondrial and nuclear markers for taxonomic identification.

NKOGHE, D., PADILLA, C., BECQUART, P., WAUQUIER, N., MOUSSAVOU, G., AKUÉ, J. P., OLLOMO, B., POURRUT, X., SOURIS, M., KAZANJI, M., GONZALEZ, J. P., and LEROY, E., 2011. Risk factors for Zaire ebolavirus-specific IgG in rural Gabonese populations. *Journal of Infectious Diseases* 204(Suppl. 3): S768-S775. doi: 10.1093/infdis/jir344

Background. In Gabon, several Ebolavirus outbreaks have occurred exclusively in the northeastern region. We conducted a large serosurvey to identify areas and populations at risk and potential demographic, clinical, and behavioral risk factors. ***Methods***. Blood samples and clinical and sociodemographic data were collected from 4349 adults and 362 children in a random sample of 220 villages in the 9 provinces of Gabon. An enzyme-linked immunosorbent assay was used to detect Zaire ebolavirus (ZEBOV)-specific IgG, and thin blood smears were used to detect parasites. Logistic regression was implemented using Stata software (Stata), and a probability level of <.05 was considered to be statistically significant. **Results**. The prevalence of ZEBOV-specific IgG was 15.3% overall, increasing to 32.4% (P< .001) in forest areas. No sociodemographic risk factors were found, but the antibody prevalence increased linearly up to 20 years of age. Chronic arthralgia and amicrofilaremia were the only factors associated with ZEBOV seropositivity. ***Conclusions***. These findings confirm the endemicity of ZEBOV in Gabon and its link to the ecosystem. Human antibody positivity would appear to be to the result of exposure to contaminated fruits.

O'BRIEN, J., 2011. Bats of the Western Indian Ocean islands. *Animals* 1(3): 259-290. doi: 10.3390/ani1030259

The natural colonisation of many remote oceanic islands by bats, including those of the western Indian Ocean, has been facilitated by their unique capability among mammals for powered flight. In the western Indian Ocean region, only the Malagasy islands of Madagascar and the Comoros archipelago have been naturally colonised by non-volant mammals. Despite their greater potential for inter-island dispersal, and thus gene transfer, endemicity of Chiroptera in the western Indian Ocean islands is high. Given their vulnerability to stochastic and anthropogenic disturbances, greater focus needs to be placed on investigating the demographic and ecological history of bats on Western Indian Ocean islands to safeguard not only their future, but also the ecosystem functioning on these islands, for which they are undoubtedly such an integral part. Here, I summarise the taxonomic and life history information available on bats from Western Indian Ocean islands and highlight knowledge gaps and conservation issues that threaten the continued persistence of some species.

PANYUTINA, A. A., PUZACHENKO, A. Y., and SOLDATOVA, I. B., 2011. Morphological diversity of wings in rhinolophoid bats (Chiroptera). *Zoologičeskij žurnal* 90(11): 206-222. [in Russian with English summary]

The paper presents the results of studying the morphological diversity in the structure of the wing in horseshoe bats (Rhinolophoidea) related to the ecological differentiation within the superfamily. Various wing elements are shown to form several groups of mutually correlated attributes. Major groups unite characters that reflect the size and play a definite role in the formation of the outer contours of the wing. The distribution of signs shows that they describe different aspects of the variability and can give a fairly complete picture of the morphological and ecological structure of the superfamily. The results obtained using the multidimensional scaling and clustering methods primarily reflect the ecological types, and only then the taxonomic relationship. The variability of design features of the wing shape in rhinolophoids revealed that the same wing shape in different families might be represented by different ratios of finger elements, especially of the lengths of distal and proximal phalanges of III-IV fingers.

RALISATA, M., ANDRIAMBOAVONJY, F. R., RAKOTONDRAVONY, D., RAVOAHANGIMALALA, O. R., RANDRIANANDRIANINA, F. H., and RACEY, P. A., 2010. Monastic *Myzopoda*: the foraging and roosting ecology of a sexually segregated Malagasy endemic bat. *Journal of Zoology*: 1-10. doi: 10.1111/j.1469-7998.2010.00724.x

We studied the social organization, use of foraging habitat, roost switching and diet of the sucker-footed bat *Myzopoda aurita* in south-eastern Madagascar. All 138 bats caught were males, 18 of which were selected for radio-tracking. The areas individual bats used for foraging varied between 7 and 108 ha (100% minimum convex polygon). Bats foraged close the roost for the first hour after emergence, then travelled up to 1.8 km away. Compositional analysis revealed that they selected coffee plantations, degraded humid forest and wooded grassland more than any other habitats. All 133 roosts located consisted of the partially unfurled leaves of *Ravenala madagascariensis* and housed between nine and 51 individuals. Bats changed roosts every 1-5 days. Their diet comprised mainly of Lepidoptera and Coleoptera. No ectoparasites were observed. *Myzopoda aurita* is one of the few mammals endemic to Madagascar that uses disturbed patches of vegetation and is not therefore threatened by deforestation, although it may be affected by loss of roosts for building materials. The search for females continues.

RAMASINDRAZANA, B., GOODMAN, S. M., SCHOEMAN, M. C., and APPLETON, B., 2011. Identification of cryptic species of *Miniopterus* bats (Chiroptera: Miniopteridae) from Madagascar and the Comoros using bioacoustics overlaid on molecular genetic and morphological characters. *Biological Journal of the Linnean Society* 104: 284-302. doi: 10.1111/j.1095-8312.2011.01740.x

The number of *Miniopterus* bat species on Madagascar and the nearby Comoros islands (Malagasy region) has risen from four to 11. These recently described cryptic taxa have been differentiated primarily based on molecular markers and associated a posteriori morphological characters that corroborate the different clades. Members of this Old World genus are notably conservative in morphology across their range. Several sites on Madagascar hold up to four small-bodied taxa of this genus that are morphologically similar to one another, although they can be distinguished based on the tragus, an ear structure associated with echolocation. *Miniopterus* often emit species-specific calls. In the present study, we analyze the bioacoustics of the 11 species of *Miniopterus* currently recognized from the Malagasy region, with an initial identification of the 87 recorded and collected individuals based on molecular markers and certain morphological characters. In most cases, bioacoustic parameters differentiate species and have taxonomic utility. *Miniopterus griveaudi* populations, which occur on three islands (Madagascar, Anjouan, and Grande Comore), showed no significant differences in peak echolocation frequencies. After running a discriminant function analysis based on five bioacoustic parameters, some mismatched assignments of Malagasy species were found, which include allopatric sister-taxa and sympatric, phylogenetically not closely-related species of similar body size. Because the peak echolocation frequencies of two species (*Miniopterus sororculus* and *Miniopterus aelleni*) were independent of body size, they were acoustically distinguishable from cryptic sympatric congeners. The small variation around the allometric relationship between body size and peak echolocation frequency of Malagasy *Miniopterus* species suggests that intraspecific communication rather than competition or prey detection may be the driver for the acoustic divergence of these two species. Our well-defined echolocation data allow detailed ecological work to commence aiming to test predictions about the relative roles of competition, prey availability, and social communication on the evolution of echolocation in Malagasy *Miniopterus* species.

RAZGOUR, O., KORINE, C., and SALTZ, D., 2011. Does interspecific competition drive patterns of habitat use in desert bat communities? *Oecologia* 167(2): 493-502. doi: 10.1007/s00442-011-1995-z

Bodies of water are a key foraging habitat for insectivorous bats. Since water is a scarce and limiting resource in arid environments, bodies of open water may have a structuring effect on desert bat communities, resulting in temporal or spatial partitioning of bat activity. Using acoustic monitoring, we studied the spatial and temporal activity patterns of insectivorous bats over desert ponds, and hypothesised that sympatric bat species partition the foraging space above ponds based on interspecific competitive interactions. We used indirect measures of competition (niche overlap and competition coefficients from the regression method) and tested for differences in pond habitat selection and peak activity time over ponds. We examined the effect of changes in the activity of bat species on their potential competitors. We found that interspecific competition affects bat community structure and activity patterns. Competing species partitioned their use of ponds spatially, whereby each species was associated with different pond size and hydroperiod (the number of months a pond holds water) categories, as well as temporally, whereby their activity peaked at different hours of the night. The drying out of temporary ponds increased temporal partitioning over permanent ponds. Differences in the activity of species over ponds in response to the presence or absence of their competitors lend further support to the role of interspecific competition in structuring desert bat communities. We suggest that habitat use and night activity pattern of insectivorous bats in arid environments reflect the trade-offs between selection of preferred pond type or activity time and constraints posed by competitive interactions.

ROEHRS, Z. P., LACK, J. B., and VAN DEN BUSSCHE, R. A., 2011. A molecular phylogenetic reevaluation of the tribe Nycticeiini (Chiroptera: Vespertilionidae). *Acta Chiropterologica* 13(1): 17-31. doi: 10.3161/150811011X578598

Monophyly of the tribe Nycticeiini (*Baeodon*, *Nycticeinops*, *Nycticeius*, *Otonycteris*, *Rhogeessa*, *Scoteinus* [= *Scoteanax* and *Scotorepens*], *Scotoecus*, *Scotomanes*, and *Scotophilus*) has been challenged by new datasets over the last two decades including baculum morphology, cytogenetics, and mitochondrial ribosomal sequence data. These studies have resulted in new classifications for the *Nycticeius*-like bats, but only one study has empirically tested Nycticeiini monophyly. In this study, a suite of nuclear markers including both exon (APOB, DMP1, RAG2) and intron (PRKCI, STAT5A, THY) gene regions were used with previously studied mtDNA sequences (12S rRNA, tRNAVal, 16S rRNA) to test Nycticeiini monophyly and develop new hypotheses for relationships of *Nycticeius*-like bats within Vespertilioninae. Although results of these phylogenetic analyses did not fully resolve phylogenetic relationships for all taxa historically included in Nycticeiini, they did reject the validity of Nycticeiini. Taxa historically circumscribed in this tribe were found scattered throughout generated phylogenies, with *Scotoecus* aligning basal to *Pipistrellus-Nyctalus*, *Nycticeinops* with the Hypsugine group, *Scotomanes* with *Eptesicus*, and *Rhogeessa* with *Antrozous*.

RUSSO, D., MAGLIO, G., RAINHO, A., MEYER, C. F. J., and PALMEIRIM, J. M., 2011. Out of the dark: Diurnal activity in the bat *Hipposideros ruber* on São Tomé island (West Africa). *Mammalian Biology* 76(6): 701-708. doi: 10.1016/j.mambio.2010.11.007

Geographical areas historically characterized by a lower risk of diurnal avian predation should in theory allow bats to be active in daytime too, especially to forage. Oceanic islands are ideal for studying temporal niche shifts in bats since they often feature depauperate avian assemblages with fewer birds of prey. We report on the second case of diurnal activity known for an insular insectivorous bat, *Hipposideros ruber* on the island of São Tomé (Gulf of Guinea). We present observations of daylight flights made at several sites on the island in six months (from July to November and in January). We also carried out daytime (09h00-16h00) emergence counts at three roosts. In this time interval, bats were continuously active, although activity rates changed: bats tended to return to roosts in early afternoon and, at two sites, to decrease emergence rate under intense light probably to reduce the risk of hyperthermia. At one roost, we observed that heavy rain caused abrupt daytime returns of large numbers of bats. In daytime bats did forage and kept echolocating. Social interactions (chases) were also frequently observed. In daytime adult males were significantly more frequent than females, while the opposite was noticed at night, an intersexual segregation possibly leading to temporal niche partitioning.

SALICINI, I., IBÁÑEZ, C., and JUSTE, J., 2011. Multilocus phylogeny and species delimitation within the Natterer's bat species complex in the Western Palearctic. *Molecular Phylogenetics and Evolution* 61(3): 888-898. doi:10.1016/j.ympev.2011.08.010

Delimiting species is a crucial issue for many biological disciplines and is of primary importance for designing effective conservation plans. Traditional taxonomy based on morphological characters can be misled by the presence of phenotypic plesiomorphism or adaptative convergence. The use of multiple locus genetic data appears thus as a powerful tool for recognizing species boundaries. In this study, we used six nuclear introns and two mitochondrial markers to conduct a phylogenetic study of the *Myotis nattereri* species complex in the Western Palearctic. We combined tree-based and non-tree-based analyses, and also used concatenated phylogenetic methods of the separated nuclear and mitochondrial dataset as well as a recent coalescence-based multilocus approach. The strong concordance between the results of the analyses conducted confirms that *M. nattereri* is a paraphyletic group that is composed of four well-differentiated lineages in the study area. In the framework of the unified species concept, these four clades can be confidently considered as four valid species. This recognition of new cryptic species in the Western Mediterranean region shows that the biodiversity of this well- studied area is still not fully understood.

SAYED, N. H. M., 2011. Phylogenetic relationship between the fruit bat (*Rousettus aegyptiacus*) and lesser tailed bat (*Rhinopoma hardwickei*) inferred from G-banded chromosomes and electrophoretic protein pattern analysis. *Journal of American Science* 7(10): 656-669.

The present work is an attempt to find out both the genetic similarities and the divergences between the fruit bat (*Rousettus aegytiacus*) and lesser tailed bat (*Rhinopoma hardwickei*) by using G-banding technique for bone marrow metaphase chromosomes and sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) for liver protein. The diploid chromosome number (2n) for each of these two species is 36 chromosomes and NFa is 68 arms. The chromosomes of both two species are grouped in 17 pairs, in addition to the sex chromosomes. The relative lengths of the X chromosome and the Y chromosome are 5.6 % and 6.4 % in the fruit bat respectively and The relative lengths of the X chromosome and the Y chromosome are 0.7 % and 1.2% in the lesser tailed bat respectively. The G-banding displays obvious alternations of white and dark bands; this facilitates ideogram construction. The sequence of banding pattern of chromosomes of the 2 species display fairly similar and different pictures. SDS-PAGE for soluble muscle protein showed 23 and 19 protein bands in the, *Rousettus aegytiacus* and *Rhinopoma hardwickei* respectively. The two species have 2 common bands. The molecular weight of the bands ranges from 118-26 kDa and from 118-24 kDa in the *Rousettus aegytiacus* and *Rhinopoma hardwickei*, respectively. Bands of molecular weight 70,60,50,42,36,31,29 and 27 kDa are characteristic to the *Rousettus aegytiacus* and are missed in the *Rhinopoma hardwickei*. Also, bands of molecular weight 113,105, 65 and 24 KDa are characteristic to the *Rhinopoma hardwickei*. Moreover, the unique band at molecular weight 113 is characteristic to the *Rhinopoma hardwickei*. The statistical analysis showed that the degree of similarity between the two species is 0.095(9.5%). As a conclusion, the fruit bat (*Rousettus aegytiacus*) and the lesser tailed bat (*Rhinopoma hardwickei*) are not identical and separated species.

SCHOEMAN, M. C., and JACOBS, D. S., 2011. The relative influence of competition and prey defences on the trophic structure of animalivorous bat ensembles. *Oecologia* 166(2): 493-506. doi: 10.1007/s00442-010-1854-3

Deterministic filters such as competition and prey defences should have a strong influence on the community structure of animals like animalivorous bats which have life histories characterized by low fecundity, low predation risk, long life expectancy and stable populations. We investigated the relative influence of these two deterministic filters on the trophic structure of animalivorous bat assemblages in South Africa. We used null models to test if patterns of dietary overlap were significantly different from patterns expected by chance and multivariate analyses to test the correlations between diet and phenotype (body size, wing morphology and echolocation). We found little evidence that competition structured the trophic niche of coexisting bats. Contrary to predictions from competition, dietary overlap between bats of ensembles and functional groups (open-air, clutter-edge, and clutter foragers) were significantly higher than expected by chance. Instead, we found support for the predictions of the allotonic frequency hypothesis: there were significant relationships between peak echolocation frequency and the proportion of moths in the diets of bats at local and regional scales, and peak echolocation frequency was the best predictor of diet even after we controlled for the influence of body size and phylogeny. These results suggest that echolocation frequency and prey hearing exert more influence on the trophic structure of sympatric animalivorous bats than competition. Nonetheless, differential habitat use and sensory bias may also be major determinants of trophic structure because these are also correlated with frequencies of bat calls.

SCHOEMAN, M. C., and WADDINGTON, K. J., 2011. Do deterministic processes influence the phenotypic patterns of animalivorous bat ensembles at urban rivers? *African Zoology* 46(2): 288-301. doi: 10.3377/004.046.0208

Although urbanization is perhaps the most damaging, persistent, and rapidly expanding form of anthropogenic pressure on natural ecosystems, data on the patterns and processes of sympatric bat species in urban landscapes are relatively scant. We quantified the packing and dispersion of sympatric animalivorous bats based on flight and echolocation parameters at two urban rivers in Durban, South Africa. We used null models to test if the observed phenotypic patterns deviated significantly from the random patterns expected in the absence of competition or prey defences at ensemble and functional group scales. As we predicted, species packing increased in the species-rich ensemble comprising many morphologically similar species that grouped together, with a few morphologically distinct species dispersed further away. Furthermore, we found evidence that competition influenced flight patterns of the open-air bats at the species-rich river ensemble, and prey defences influenced echolocation patterns of coexisting bats at the ensemble and functional group scales. However, non-deterministic processes such as habitat structure and the physics of sound and flight probably mediated these deterministic processes to influence the phenotypic structure of sympatric bats in urban landscapes.

SEAMARK, E. C. J., KEARNEY, T. C., and WATSON, J., 2012. An updated distribution map and additional museum voucher specimens of the genus *Cistugo* (Chiroptera: Cistugonidae), with a review of the distinction between *Cistugo seabrae* Thomas, 1912 and *C. lesueuri* Roberts, 1919, and aspects concerning their allopatric distribution. *Annals of the Ditsong National Museum of Natural History* 2: 111-119.

While recent work focused on resolution at the family level, and led to the suggestion of a new family for the genus *Cistugo*, the validity of *Cistugo lesueuri* still remains unresolved. We provide a review of the classification of *C. lesueuri* and *C. seabrae*, and an updated distribution map for the genus including new localities for each species. Two measurements initially provided to distinguish the species are revisited, and suggest the distributions of *C. lesueuri* and *C. seabrae* may not be allopatric, as had previously been assumed.

STANLEY, W. T., and GOODMAN, S. M., 2011. Small mammal inventories in the East and West Usambara and South Pare Mountains, Tanzania. 3. Chiroptera. *Fieldiana: Life and Earth Sciences* 4: 34-52.

Whereas the terrestrial mammal fauna of the East and West Usambara Mountains have been the subject of numerous investigations, the local bat fauna remains poorly documented, as is the case for bats of the South Pare Mountains. During mammal surveys of these three massifs, we used mist nets to collect local bats, documenting 20 bat species in total. In the Usambara Mountains, 161 individual bats representing 19 species were documented during the three years of the survey between 1991 and 1993. In the East and West Usambara Mountains, 17 and 12 species, respectively, were recorded. Most animals were taken in net sets placed outside or at the edge of forested habitats. In the South Pare Mountains, 67 bats representing six species were collected during the two surveys, including 62 bats of six species at 1100 m (surveyed 17-29 July 1993) and five bats representing three species at 2000 m (surveyed 19-28 August 2004). Based on our morphological studies, no evidence of undescribed taxa in these collections exists. Species common across all three massifs include two pteropodids (*Epomophorus wahlbergi* and *Lissonycteris angolensis*), one rhinolophid (*Rhinolophus clivosus*), and one vespertilionid (*Neoromicia capensis*). Taxa only captured on a single massif include *Rousettus lanosus* and *Rhinolophus simulator* (South Pare, 10% of total captures), *Myonycteris relicta* and *Nycteris thebaica* (West Usambara, 10% of total captures), and *Rousettus aegyptiacus*, *Rhinolophus deckenii*, *R. fumigatus*, *R. swinnyi*, *Nycteris grandis*, *Myotis bocagei*, and *Scotophilus viridis* (East Usambara, 35% of total captures). Comparisons of capture rates and species richness between these three montane sites to more lowland forest sites indicate a notable reduction in species richness and density with increasing elevation. Our preliminary surveys are at best rough estimates of patterns of species diversity and richness in the montane portions of these massifs; more fieldwork and associated taxonomic work are clearly needed to have more in-depth knowledge of the local bat fauna.

STANLEY, W. T., GOODMAN, S. M., and NEWMARK, W. D., 2011. Small mammal inventories in the East and West Usambara Mountains, Tanzania. 1. Study areas, methodologies, and general results. *Fieldiana: Life and Earth Sciences* 4: 1-17.

The Eastern Arc Mountains of southeastern Kenya and Tanzania hold a rich and unique biodiversity. The most celebrated of these mountains are the East and West Usambaras. Although these massifs have been the subjects of biological study for over a century, little is known about the shrews, bats, and rodents occurring in the montane forests. Using pitfall buckets, small mammal traps, and mist-nets, between 1991 and 1993, we surveyed the small mammals in the Amani area in the East Usambara and Ambangulu area in the West Usambara to document the natural history of the local fauna. These surveys were conducted during the dry season annually between early July and early September. In this chapter, we outline the study sites, methodologies, capture rates, and other trapping details. A total of 18,563 sample-nights was accrued over the three-year study, and on these two massifs, we documented 12 crocidurine shrew, one macroscelidid elephant shrew, 19 bat, and 14 rodent species. Species accumulation curves suggest that additional trapping effort may be required in the East Usambara Mountains to have a more complete view of the local small mammal fauna. There was no significant difference in the number of individuals captured or measures of species diversity in the pitfall and trap lines that were installed in the same location during the course of this study, suggesting that repeated sampling did not negatively affect the small mammal fauna of the study areas.

TOUSSAINT, D. C., MCKECHNIE, A. E., and VAN DER MERWE, M., 2010. Heterothermy in free-ranging male Egyptian Free-tailed bats (*Tadarida aegyptiaca*) in a subtropical climate. *Mammalian Biology* 75(5): 466-470. doi: 10.1016/j.mambio.2009.06.001

TSOAR, A., NATHAN, R., BARTAN, Y., VYSSOTSKI, A., DELL'OMO, G., and ULANOVSKY, N., 2011. Large-scale navigational map in a mammal. *PNAS* 108(37): e718-e724. doi: 10.1073/pnas.1107365108

Navigation, the ability to reach desired goal locations, is critical for animals and humans. Animal navigation has been studied extensively in birds, insects, and some marine vertebrates and invertebrates, yet we are still far from elucidating the underlying mechanisms in other taxonomic groups, especially mammals. Here we report a systematic study of the mechanisms of long-range mammalian navigation. High-resolution global positioning system tracking of bats was conducted here, which revealed high, fast, and very straight commuting flights of Egyptian fruit bats (*Rousettus aegyptiacus*) from their cave to remote fruit trees. Bats returned to the same individual trees night after night. When displaced 44 km south, bats homed directly to one of two goal locations familiar fruit tree or cave ruling out beaconing, route-following, or path-integration mechanisms. Bats released 84 km south, within a deep natural crater, were initially disoriented (but eventually left the crater toward the home direction and homed successfully), whereas bats released at the crater-edge top homed directly, suggesting navigation guided primarily by distal visual landmarks. Taken together, these results provide evidence for a large-scale cognitive map that enables navigation of a mammal within its visually familiar area, and they also demonstrate the ability to home back when translocated outside the visually familiar area.

TSOAR, A., SHOHAMI, D., and NATHAN, R., 2011. A movement ecology approach to study seed dispersal and plant invasion: An overview and application of seed dispersal by fruit bats. 103-119pp. *In* RICHARDSON, D. M. (Ed). *Fifty years of invasion ecology: The legacy of Charles Elton*. Wiley-Blackwell, Oxford. xix+432 pp, DOI: 10.1002/9781444329988.ch9

This chapter contains sections titled:
* Biological Invasions and Dispersal Processes
* Overview of The Concepts and Methods Applied to Quantify Seed Dispersal Patterns and Understand their Underlying Mechanisms
* Seed Dispersal and Movement Ecology of Invasive Species
* Fruit Bats as Long - Distance Seed Dispersers of Both Native and Alien Species
* Conclusions
* References

VALLO, P., BENDA, P., and REITER, A., 2011. Yellow-bellied or white-bellied? Identity of Arabian house bats (Vespertilionidae: *Scotophilus*) revealed from mitochondrial DNA and morphology. *African Zoology* 46(2): 350-361.

The yellow-bellied *Scotophilus dinganii* is the only African house bat species reported to occur in the Arabian Peninsula. Formerly, the Arabian house bats were referred to similar-looking white-bellied *S. leucogaster*, which differs from *S. dinganii* mainly by the colour of ventral pelage. We reassessed the taxonomic status of house bats from southwestern Yemen using genetic and morphological analyses. The Yemeni specimens clustered within two distantly related mitochondrial lineages of African *Scotophilus*: East African *S.* aff. *dinganii*, which is a paraphyletic group to *S. dinganii s.str.* from South Africa, and West African *S. leucogaster*. This taxonomic assignation was based on published sequences of reference museum specimens. Differences in external and cranial measurements also indicated the presence of two distinct taxa in Yemen. The Yemeni and comparative Ethiopian populations of *S.* aff. *dinganii* showed close morphological similarity to the type specimen of *S. nigrita colias* from Kenya. Because the Yemeni and Ethiopian yellow-bellied house bats cannot be synonymized with *S. dinganii*, the designation *S. colias* is tentatively suggested for this particular East African and Yemeni lineage of the *S. dinganii* complex. However, final correspondence of this name with the respective populations or applicability of some of other available names must yet be explored. Based on environmental differences of the Yemeni localities of origin, *S. colias* appears to be ecologically delimited to mountainous habitats, while *S. leucogaster* to harsh lowland deserts. This is consistent with known habitats of African populations of both species.

VEITH, M., MUCEDDA, M., KIEFER, A., and PIDINCHEDDA, E., 2011. On the presence of pipistrelle bats (*Pipistrellus* and *Hypsugo*; Chiroptera: Vespertilionidae) in Sardinia. *Acta Chiropterologica* 13(1): 89-99. doi: *10.3161/150811011X578642*

Islands are biodiversity hotspots, often containing numerous endemic species. This makes them also hotspots for conservation. Within the Mediterranean region, Sardinia is known for its comparatively high degree of endemism, including cryptic diversity. In this paper we aim to elucidate the variability of pipistrelles (*Pipistrellus* and *Hypsugo*) on Sardinia. More specifically, we ask which species occur on Sardinia and we describe the geographic affiliations of these evolutionary lineages. We sequenced ca. 560 bp of the 16S rRNA gene from 36 pipistrelle specimens representing 17 localities from all major parts of Sardinia. For comparison we added samples from the entire Mediterranean region as well as sequences stored at GenBank. We constructed Bayesian phylogenetic trees and minimum spanning networks to identify which species occur on Sardinia and to infer their genetic affiliation to lineages occurring throughout the Mediterranean and the Canary Islands. We identified five pipistrelle lineages on Sardinia: *Pipistrellus pipistrellus* (haplolineage II), *P. pygmaeus*, *P. kuhlii/desertii*, *Hypsugo savii s. str*. and *H.* cf. *darwinii*. Colonization of Sardinia occurred at different times from different geographical sources, namely Europe and Africa. Some lineages may have invaded Sardinia recently. The Sardinian *H.* cf. *darwinii* may be endemic to the island. Our results highlight the importance of Sardinia as a major Mediterranean hotspot for bat biodiversity. The island harbours a pipistrelle diversity that is higher than that on any other Mediterranean island. Lying geographically at the interface between Europe and Africa, Sardinia combines elements from both continents.

VENDITTI, C., MEADE, A., and PAGEL, M., 2011. Multiple routes to mammalian diversity. *Nature* 479(7373): 393-396. doi: *10.1038/nature10516*

The radiation of the mammals provides a 165-million-year test case for evolutionary theories of how species occupy and then fill ecological niches. It is widely assumed that species often diverge rapidly early in their evolution, and that this is followed by a longer, drawn-out period of slower evolutionary fine-tuning as natural selection fits organisms into an increasingly occupied niche space. But recent studies have hinted that the process may not be so simple. Here we apply statistical methods that automatically detect temporal shifts in the rate of evolution through time to a comprehensive mammalian phylogeny and data set of body sizes of 3,185 extant species. Unexpectedly, the majority of mammal species, including two of the most speciose orders (Rodentia and Chiroptera), have no history of substantial and sustained increases in the rates of evolution. Instead, a subset of the mammals has experienced an explosive increase (between 10- and 52-fold) in the rate of evolution along the single branch leading to the common ancestor of their monophyletic group (for example Chiroptera), followed by a quick return to lower or background levels. The remaining species are a taxonomically diverse assemblage showing a significant, sustained increase or decrease in their rates of evolution. These results necessarily decouple morphological diversification from speciation and suggest that the processes that give rise to the morphological diversity of a class of animals are far more free to vary than previously considered. Niches do not seem to fill up, and diversity seems to arise whenever, wherever and at what- ever rate it is advantageous.

VOIGT, F. A., FARWIG, N., and JOHNSON, S. D., 2011. Interactions between the invasive tree *Melia azedarach* (Meliaceae) and native frugivores in South Africa. *Journal of Tropical Ecology* 27(4): 355-363. doi: *10.1017/S0266467410000702*

The spread of many invasive plants is facilitated through seed dispersal by frugivorous animals. The effectiveness of various frugivores as dispersers of the seeds of *Melia azedarach*, a highly invasive alien tree species, was evaluated in South Africa in savanna and bushveld vegetation. During 264 h of observation, seven bird species and one bat species were recorded foraging on fruiting trees of *M. azedarach*. The most common visitors were the dark-capped bulbul (*Pycnonotus barbatus*) followed by Wahlberg's epauletted fruit bat (*Epomophorus wahlbergi*), but both species dropped nearly as many seeds as they dispersed. Knysna turaco (*Tauraco corythaix*) dispersed the highest number of fruits per minute, but occurred in low abundance in our study sites. Seed germination differed significantly between de-pulped fruits and untreated fruits after 2 mo, but was similar after 4 mo. Germination success did not differ between animal-handled and hand-depulped fruits. In contrast to the high germination success in the greenhouse, seedlings showed very low recruitment in the field. Thus, *M. azedarach* seems likely to benefit from frugivores (particularly dark-capped bulbul and Wahlberg's epauletted fruit bat) dispersing seeds to suitable microsites.

VOLLETH, M., YANG, F., and MÜLLER, S., 2011. High-resolution chromosome painting reveals the first genetic signature for the chiropteran suborder Pteropodiformes (Mammalia: Chiroptera). *Chromosome Research* 19(4): 507-519. doi: 10.1007/s10577-011-9196-5

Up to now, the composition of synteny-conserved segments in chiropteran karyotypes was studied by cross-species chromosome painting with probes derived from whole human (HSA) or chiropteran chromosomes only. Here, painting probes from the vespertilionid bat *Myotis myotis* were hybridized, for the first time, onto human metaphase chromosomes. The segmental composition of bat karyotypes was further refined by cross-species painting with probes derived from flow-sorted chromosomes of *Tupaia belangeri* and *Eulemur macaco* - two species with highly rearranged karyotypes. The use of such probes has led to the generation of higher resolution maps between human chromosomes 1, 3, 4, 5, 6, 11 and 15 and their counterparts in Vespertilionidae and the pteropodid species *Eonycteris spelaea*. Interestingly, the order of four sub-regions within the largest homologous segment delimited by human chromosome 4 painting probe in *Eonyceris* was found to be different from that found in vespertilionids. A subsequent survey across all major chiropteran families demonstrated that a paracentric inversion within this HSA 4 homologous segment could represent a synapomorphic character for the suborder Pteropodiformes

WEISS, S., WITKOWSKI, P. T., AUSTE, B., NOWAK, K., WEBER, N., FAHR, J., MOMBOULI, J. V., WOLFE, N. D., DREXLER, J. F., DROSTEN, C., KLEMPA, B., LEENDERTZ, F. H., and KRUGER, D. H., 2012. Hantavirus in bat, Sierra Leone. *Emerging Infectious Diseases* 18(1): 159-161. doi: 10.3201/eid1801.111026

WEYENETH, N., GOODMAN, S. M., APPLETON, B., WOOD, R., and RUEDI, M., 2011. Wings or winds: Inferring bat migration in a stepping-stone archipelago. *Journal of Evolutionary Biology* 24(6): 1298-1306. doi: 10.1111/j.1420-9101.2011.02262.x

Eocene ocean currents and prevailing winds correlate with over-water dispersals of terrestrial mammals from Africa to Madagascar. Since the Early Miocene (about 23 Ma), these currents flowed in the reverse direction, from the Indian Ocean towards Africa. The Comoro Islands are equidistant between Africa and Madagascar and support an endemic land vertebrate fauna that shares recent ancestry predominantly with Madagascar. We examined whether gene flow in two *Miniopterus* bat species endemic to the Comoros and Madagascar correlates with the direction of current winds, using uni- and bi-parentally inherited markers with different evolutionary rates. Coalescence-based analyses of mitochondrial matrilines support a Pleistocene (approximately 180 000 years ago) colonization event from Madagascar west to the Comoros (distance: 300 km) in the predicted direction. However, nuclear microsatellites show that more recent gene flow is restricted to a few individuals flying against the wind, from Grande Comore to Anjouan (distance: 80 km)

WEYENETH, N., GOODMAN, S. M., and RUEDI, M., 2011. Do diversification models of Madagascar's biota explain the population structure of the endemic bat *Myotis goudoti* (Chiroptera : Vespertilionidae)? *Journal of Biogeography* 38(1): 44-54. doi: 10.1111/j.1365-2699.2010.02393.x

Aim Three mechanisms have been proposed to explain the adaptive radiations and species diversifications of Madagascar's biota: the ecogeographical constraint, the riverine barrier and the micro-endemism models. On the intraspecific level, each model predicts different patterns of gene flow across the island's physical and ecological features. To evaluate these models, phylogeographical analyses were conducted on a widespread and endemic species of bat, *Myotis goudoti* (Vespertilionidae). ***Location*** Madagascar. ***Methods*** In order to reconstruct the phylogeographical history of *M. goudoti*, the mitochondrial D-loop and the cytochrome *b* gene were sequenced for 195 bats from 41 localities. Phylogenetic reconstructions and a minimum spanning tree were used to infer haplotype relationships. The effect of barriers on gene flow was evaluated using analyses of molecular variance and pairwise population differentiation. Mismatch distribution and coalescence-based estimates were conducted to infer the demographic history of *M. goudoti*. **Results** The sequenced individuals showed 159 distinct D-loop haplotypes, most of them being unique to a single location. Populations were significantly structured (FST = 0.170, P < 0.001) across Madagascar, but only a minor part of the overall genetic variance was explained by any of the three models. Shared ancestry of lineages across most physical or ecological barriers was common, whereas the uncovered genetic differences between southern and central-northern populations were unexpected. ***Main conclusions*** Major barriers predicted by the three biogeographical models do not explain the segregation of mitochondrial lineages of *M. goudoti* across Madagascar. This is not simply attributable to the high dispersal ability of this species, as populations are notably structured. The genetic contrast between southern and central-northern populations, separated by a zone of admixture, suggests that these areas currently support populations that expanded during the Late Pleistocene. This latitudinal differentiation of populations has been observed in less vagile animals, such as geckos and lemurs, suggesting that climate fluctuations of the Pleistocene had an impact across several groups and resulted in northern and southern refugia in Madagascar.

WOOD, R., WEYENETH, N., and APPLETON, B., 2011. Development and characterisation of 20 microsatellite loci isolated from the large bent-wing bat, *Miniopterus schreibersii* (Chiroptera: Miniopteridae) and their cross-taxa utility in the family Miniopteridae. *Molecular Ecology Resources* 11(4): 675-695. doi: 10.1111/j.1755-0998.2011.02994.x

The large bent-wing bat, *Miniopterus schreibersii* (Kuhl 1819), has a long history of taxonomic uncertainty and many populations are known to be in a state of decline. Microsatellite loci were developed for the taxonomic and population genetic assessment of the Australian complex of this species. Of the 33 primer sets designed for this research, seven (21%) were deemed suitably polymorphic for population-level analyses of the Australian taxa, with five (71%) of these loci revealing moderate to high levels of polymorphism (PIC = 0.56 to 0.91). The cross-taxa utility of the *M. schreibersii* microsatellite markers was assessed in the microbat (Chiroptera) family Miniopteridae. Sub-species and species covering the Miniopteridae's global distribution (with the exception of the Middle East) were selected, numbering 25 taxa in total. Amplification was successful for 26 loci, of which 20 (77%) were polymorphic. High cross-taxa utility of markers was observed with amplification achieved for all taxa for between four (20%) and 20 (100%) loci, and polymorphism was considered moderate to high (PIC = 0.47-0.91) for 12 (60%) of these loci. The high cross-taxa utility of the microsatellites reported herein reveal versatile and cost-effective molecular markers, contributing an important genetic resource for the research and conservation of Miniopteridae species worldwide.

YOVEL, Y., FALK, B., MOSS, C. F., and ULANOVSKY, N., 2011. Active control of acoustic field-of-view in a biosonar system. *PLoS Biol* 9(9): e1001150. doi: *10.1371/journal.pbio.1001150*

Active-sensing systems abound in nature, but little is known about systematic strategies that are used by these systems to scan the environment. Here, we addressed this question by studying echolocating bats, animals that have the ability to point their biosonar beam to a confined region of space. We trained Egyptian fruit bats to land on a target, under conditions of varying levels of environmental complexity, and measured their echolocation and flight behavior. The bats modulated the intensity of their biosonar emissions, and the spatial region they sampled, in a task dependant manner. We report here that Egyptian fruit bats selectively change the emission intensity and the angle between the beam axes of sequentially emitted clicks, according to the distance to the target, and depending on the level of environmental complexity. In so doing, they effectively adjusted the spatial sector sampled by a pair of clicks-the “field-of-view.” We suggest that the exact point within the beam that is directed towards an object (e.g., the beam’s peak, maximal slope, *etc.*) is influenced by three competing task demands: detection, localization, and angular scanning where the third factor is modulated by field-of-view. Our results suggest that lingual echolocation (based on tongue clicks) is in fact much more sophisticated than previously believed. They also reveal a new parameter under active control in animal sonar the angle between consecutive beams. Our findings suggest that acoustic scanning of space by mammals is highly flexible and modulated much more selectively than previously recognized.

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