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Above: A Yellow House Bat (Scotophilus dinganii) caught in the Pufuri area, Kruger National Park, South Africa.

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Research and Conservation Activities

By Rachael Cooper-Bohannon



Working together to secure a future for bats in southern Africa

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Observation, Discussions and Updates

Recent changes in African Bat Taxonomy (2013-2014). Part I

By Victor Van Cakenberghe^{1,2} and Ernest C.J. Seamark²

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Rhinolophus damarensis Roberts, 1946

Damara Horseshoe Bat

Analyses made by Jacobs et al. (2013) revealed that R. darlingi (sensu lato) is a paraphyletic taxon; eastern and western populations of *R. darlingi* are placed in two non-sister clades which diverged ~9.68 Mya. The eastern population of R. darlingi is nested within the classic fumigatus clade which includes R. fumigatus, R. hildebrandtii and R. eloquens. Since the type locality of R. darlingi is in Zimbabwe, they refer to this eastern population as R. darlingi. The second clade comprised of individuals sampled in the western regions of South Africa and Namibia, where Austin Roberts in 1941 collected a single Rhinolophus which he recognized as being different from R. darlingi darlingi and which he described as R. d. damarensis Roberts, 1946. Jacobs et al. (2013) elevate this subspecies to full species status to refer to the populations occurring in the western regions of South Africa and Namiba. What is also of interest is that within the new species of R. damarensis, there are two groups which separated about 4.8 Mya, and may represent two subspecies one occurring in the northern (R. d. damarensis) and the second in central Namibia and northwestern, south-western and central South Africa (the latter still remains undescribed).

Rhinolophus kahuzi Fahr and Kerbis Peterhans in Kerbis Peterhans *et al.*, 2013

Kahuzi Horseshoe Bat

This new species is a member of the *Rhinolophus maclaudi* species group, characterized by the large ears and the poorly

developed connecting process behind the sella. Within this group, it is distinguished by its large ears with 11 internal ear folds. The scientific name refers to Mt Kahuzi, and is used as a noun in apposition. This species is only known from the type locality (Western slope of Mt Kahuzi, Kahuzi-Biega National Park, South Kivu Province, and eastern Democratic Republic of the Congo) which is within a protected area; Kerbis Peterhans *et al.* (2013) suggest this species be listed as Data Deficient for IUCN Red List status.

Rhinolophus willardi Kerbis Peterhans and Fahr in Kerbis Peterhans *et al.*, 2013

Willard's Horseshoe Bat

The large ears and the poorly developed connecting process behind the sella also characterize *R. willardi* as a member of the *Rhinolophus maclaudi* species group. This new species is the smallest member within this species group and is distinguished from the other species by the presence of twelve internal ear folds. The scientific name honors Dr. David Willard (Collection Manager, Division of Birds, FMNH) in recognition of his unparalleled 35+ years of service to the Field Museum of Natural History. This species is only known from the type locality (Misotschi-Kabogo highlands, eastern Democratic Republic of the Congo) and one other (4 km SW of the village Talama, eastern Democratic Republic of the Congo) both of these sites being outside of protected areas. For these reasons, Kerbis Peterhans *et al.* (2013) suggest this species be listed as Data Deficient for IUCN Red List status.

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Miniopterus mossambicus Monadjem, Goodman, Stanley and Appleton, 2013

Mozambique Long-fingered Bat

Molecular techniques, cranio-dental characters and tragus shape were used in describing this species, which is different from morphologically similar M. natalensis, M. fraterculus and M. minor. This new species is named after the country Mozambigue, where the type series was collected on the outskirts of Nampula (town) in the Nampula Province, northern Mozambique.

Literature Cited

JACOBS, D.S., H. BABIKER, A. BASTIAN, T. KEARNEY, R. VAN EEDEN and J.M. BISHOP. 2013. Phenotypic convergence in genetically distinct lineages of a Rhinolophus species complex

(Mammalia, Chiroptera). PloS one 8(12): e82614. doi: 10.1371/ journal.pone.0082614

- KERBIS PETERHANS, J.C., J. FAHR, M.H. HUHNDORF, P. KALEME, A.J. PLUMPTRE, B.D. MARKS and R. KIZUNGU. 2013. Bats (Chiroptera) from the Albertine Rift, eastern Democratic Republic of Congo, with the description of two new species of the Rhinolophus maclaudi group. Bonner Zoological Bulletin 62(2): 186-202. www. zoologicalbulletin.de/BzB_Volumes/Volume_62_2/186_202_ <u>BzB62_2_Kerbis_JC_et_al.pdf</u>
- MONADJEM, A., S.M. GOODMAN, W.T. STANLEY and B. APPLETON. 2013. A cryptic new species of Miniopterus from south-eastern Africa based on molecular and morphological characters. Zootaxa 3746(1): 123-142. doi: 10.11646/zootaxa.3746.1.5.
- ROBERTS, A. 1946. Description of numerous new subspecies of mammals. Annals of the Transvaal Museum 20(4): 303-328.



Erratum for KEARNEY et al. (2010) – Chiroptera of Lufupa Camp, Kafue National Park, Zambia; with taxonomic notes on Epomophorus, Nycticeinops, Scotophilus and Scotoecus

By Teresa C. Kearney^{1,2}

Kruskop

cf. leucogaster (ECJS-12/2008 and ECJS-17/2008),

pointed out the error in KEARNEY et al. (2010). In

Figure 14 the incorrect species and individual information was associated with letters a) to e). It should have read: Figure 14. Baculae of a) N.

Sergei

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kindly Citation

KEARNEY, T. C., E.C.J. SEAMARK, C. MATEKE and D. HOOD. 2010. Chiroptera of Lufupa Camp, Kafue National Park, Zambia; with taxonomic notes on *Epomophorus*, *Nycticeinops*, *Scotophilus* and *Scotoecus*. *African Bat Conservation News* **23**: 7–31. *Download*

c) N. capensis (ECJS-33/2008), d) N. zuluensis (ECJS-44/2008), and e) Nyct. schlieffenii (ECJS-1/2008) from Lufupa in Zambia.

Museum accession numbers for voucher specimens from Namibia referred to by field number in MONADJEM et al. (2013) – A cryptic new species of *Miniopterus* from south-eastern Africa based on molecular and morphological characters

By Teresa C. Kearney^{1,2} and Ernest C.J. Seamark²

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MONADJEM et al. (2013) referred in Table 1 to field numbers for specimens from Namibia, when associating Genbank accession numbers for their Cytochrome b sequence results



at Evergreen Campsite, Erongo Mts, Namibia, lodged with the State Museum in Windhoek, under collectors number ECJS-90/2008

with the voucher specimens the tissue that was sequenced came from. The six specimens from Namibia were collected by Ernest C.J. Seamark and Teresa Kearney, under permit # 1318/2008 that was issued by the Namibian Ministry of Environment and Tourism. Additional information for these specimens, in relation to the sex, age, collection date, and a more precise description of the locality, and accession numbers for three of the specimens that were included in the collection at the Ditsong National Museum of Natural History (formally Transvaal Museum) in South Africa, are indicated in Table 1 below. The other specimens have yet to be returned to Namibia to be lodged in the State Museum in Windhoek, which is why they currently have no museum accession numbers.

Citation

MONADJEM, A., S.M. GOODMAN, W.T. STANLEY and B. APPLETON. 2013. A cryptic new species of Miniopterus from south-eastern Africa based on molecular and morphological characters. Zootaxa 3746(1): 123-142. doi: 10.11646/zootaxa.3746.1.5

Observations, Discussions and Updates

Table 1: Additional information for specimens of *Miniopterus natalensis* from Namibia, whose Cytochrome *b* sequence results were presented in MONADJEM *et al.* (2013). # = species identification and sequence accession numbers from MONADJEM *et al.* (2013); MusNr = Ditsong National Museum of Natural History (formerly Transvaal Museum) accession number; and ColDate = date of collection.

Field number	Genbank#	Species [#]	MusNr	Sex / age	ColDate		Locality		
ECJS-85/2008	KF709540	M. natalensis	-	♀ ad	19/09/2008	Namibia: Eronga 21.44618S 15.87924E.	Mountain,	Evergreen	Campsite;
ECJS-86/2008	KF709541	M. natalensis	TM 48687	onumber 2 ad	19/09/2008	Namibia: Eronga 21.44618S 15.87924E.	Mountain,	Evergreen	Campsite;
ECJS-88/2008	KF709542	M. natalensis	-	ੈ ad	19/09/2008	Namibia: Eronga 21.44618S 15.87924E.	Mountain,	Evergreen	Campsite;
ECJS-89/2008	KF709543	M. natalensis	TM 48688	$\stackrel{\circ}{_{ m p}}$ ad	19/09/2008	Namibia: Eronga 21.44618S 15.87924E.	Mountain,	Evergreen	Campsite;
ECJS-90/2008	KF709544	M. natalensis	-	ੈ ad	19/09/2008	Namibia: Eronga 21.44618S 15.87924E.	Mountain,	Evergreen	Campsite;
ECJS-91/2008	KF709545	M. natalensis	TM 48689	ੀ ad	19/09/2008	Namibia: Eronga 21.44618S 15.87924E.	Mountain,	Evergreen	Campsite;

Recent Literature

Books and Reports



Atlas d'une sélection de vertébrés terrestres de Madagascar / Atlas of selected land vertebrates of Madagascar

Editors: Steven M. Goodman and Marie Jeanne Raherilalao

Association Vahatra has recently published a bilingual (French-English) book entitled, "Atlas d'une sélection de vertébrés terrestres de Madagascar / Atlas of selected land vertebrates of Madagascar." The book is edited by Steven M. Goodman and Marie Jeanne Raherilalao and with contributions from a number of Malagasy field biologists. This large format volume of near A3 format and with 290 pages and 446 color plates-photos, is the product of more than 20 years of work. The Atlas brings together information from numerous sources, including data gathered during extensive biological inventories in some of the most remote forests of the island, from specimens in natural history museums around the world, and from the relevant literature, to present distributional maps on a range of taxa as well as descriptive text that interprets associated patterns and, for most taxa, provides potential habitat models. The groups covered include two families of reptiles, forest-dwelling birds, and all native small mammals (rodents, tenrecs, bats, and Carnivora).

One of the largest islands in the world, Madagascar is home to an astonishing array of endemic vertebrate biodiversity. While recent decades have seen numerous publications on the subject—ranging from technical papers to species descriptions and field guides no detailed atlas exists. The Atlas will be an important reference for all students, researchers, naturalists, and conservationists interested in the land vertebrates of Madagascar, one of the most extraordinary and threatened biodiversity hotspots on Earth.

To place an order contact associatvahatra@moov.mg.

Papers

Ahmim, M. and A. Moali. 2013. The diet of four species of horseshoe bat (Chiroptera: Rhinolophidae) in a mountainous region of Algeria: evidence for gleaning. *Hystrix, Italian Journal of Mammalogy* 24(2): 174-176. doi: <u>10.4404/hystrix-24.2-8728</u>.

We analyzed the diet of four rhinolophids (*Rhinolophus ferrumequinum*, *R. hipposideros*, *R. euryale* and *R. blasii*) in the region of Kabylia Babors, in northern Algeria. Between March 2007 and January 2008 we sampled droppings at ten sites and carried out a morphological identification of prey remains. Three main groups of Arthropoda (Insecta, Chilopoda and Araneida) were preyed upon but frequencies varied across species. The insect prey most frequently preyed upon by *R. ferrumequinum* are Diptera (34.56%), mainly including Culicidae (10.40%), Chironomidae/Ceratopogonidae (10.94%) and Tipulidae (4.28%), and also Lepidoptera (24.13%). In *R. hipposideros* droppings we found Diptera (41.58%), Chironomidae/Ceratopogonidae (9.68%) and Tipulidae (6.45%). Also common were Lepidoptera (moths; 21.14%) and Hemiptera (11.68%). *R. euryale* ate mainly Diptera (29.00%), Chironomidae/Ceratopogonidae (7.14%) and Tipulidae (5.71%). The order Lepidoptera (moths) was also well represented (19.08%). *R. blasii* preyed on two groups of Arthropoda: Insecta (96.87%) and Chilopoda (4.34%). The most consumed insect prey was Diptera (37.50%), mainly Chironomidae/Ceratopogonidae (9.38%), Culicidae, Anisopodidae and Sphaeroceridae (6.25%). The order Trichoptera was also well represented in its diet (15.63%) and Lepidoptera accounted for 12.50%. The most interesting aspect of this study was that Chilopoda appeared in the diet of all species and that, albeit rarely, *R. ferrumequinum* also ate spiders. This result suggests that all

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species could glean prey from substrate, most probably as a strategy to better exploit the open habitats typical of the study area.

Albariño, C.G., L.S. Uebelhoer, J.P. Vincent, M.L. Khristova, A.K. Chakrabarti, A. McElroy, S.T. Nichol and J.S. Towner. 2013. Development of a reverse genetics system to generate recombinant Marburg virus derived from a bat isolate. *Virology* 446(1/2): 230–237. doi: <u>10.1016/j.virol.2013.07.038</u>.

Recent investigations have shown the Egyptian fruit bat (*Rousettus aegyptiacus*) to be a natural reservoir for marburgviruses. To better understand the life cycle of these viruses in the natural host, a new reverse genetics system was developed for the reliable rescue of a Marburg virus (MARV) originally isolated directly from a *R. aegyptiacus* bat (371Bat). To develop this system, the exact terminal sequences were first determined by 5' and 3' RACE, followed by the cloning of viral proteins NP, VP35, VP30 and L into expression plasmids. Novel conditions were then developed to efficiently replicate virus mini-genomes followed by the construction of full-length genomic clones from which recombinant wild type and GFP-containing MARVs were rescued. Surprisingly, when these recombinant MARVs were propagated in primary human macrophages, a dramatic difference was found in their ability to grow and to elicit anti-viral cytokine responses.

Ammerman, L.K., W.A. Brashear and S.N. Bartlett. 2013. Further Evidence for the Basal Divergence of Cheiromeles (Chiroptera: Molossidae). Acta Chiropterologica 15(2): 307–312. doi: <u>10.3161/150811013X678946</u>.

The earliest diverging lineages in the subfamily Molossinae have not been well established. The genera *Cheiromeles* and *Mormopterus* have been found in separate studies to be the oldest lineage, however no previous studies using a molecular approach have included an analysis of sequence data from *Cheiromeles* and *Mormopterus* together in the same study. The objective of this study was to test the hypothesis that recombination activating gene 2 (Rag2) sequence data support the basal divergence of *Cheiromeles* in the Molossinae subfamily. Bayesian and Maximum Likelihood analyses of Rag2 sequences from 64 molossid bats (representing 13 genera, 31 species) and five outgroup taxa (*Antrozous pallidus, Myotis daubentoni, M. velifer, M. yumanensis,* and *Natalus stramineus*) obtained from GenBank resulted in the placement of *Cheiromeles* as the most basal lineage within a monophyletic Molossinae. *Mormopterus* was placed as sister to the rest of Molossinae (excluding *Cheiromeles*).

Andriamandimby, S.F., J.-M. Héraud, R. Ramiandrasoa, M. Ratsitorahina, J.H. Rasambainarivo, L. Dacheux, A. Lepelletier, S.M. Goodman, J.-M. Reynes, and H. Bourhy. 2013. Surveillance and control of rabies in La Reunion, Mayotte, and Madagascar. *Veterinary Research* 44(77). doi: <u>10.1186/1297-9716-44-77</u>.

Mayotte and La Reunion islands are currently free of animal rabies and surveillance is performed by the French Human and Veterinary Public Health Services. However, dog rabies is still enzootic in Madagascar with 4 to 10 confirmed human cases each year. The number of antirabies medical centres in Madagascar is still scarce to provide easy access to the local population for post-exposure rabies prophylaxis. Furthermore, stray dog populations are considerable and attempts to control rabies by mass campaigns of dog vaccination have not received sufficient attention from the national health authorities. To address these challenges, an expanded program to control rabies needs to be initiated by the Malagasy authorities.

Anthony, S.J., J.H. Epstein, K.A. Murray, I. Navarrete-Macias, C.M. Zambrana-Torrelio, A. Solovyov, R. Ojeda-Flores, N.C. Arrigo, A. Islam, S.A. Khan, P. Hosseini, T.L. Bogich, K.J. Olival, M.D. Sanchez-Leon, W.B. Karesh, T. Goldstein, S.P. Luby, S.S. Morse, J.A.K. Mazet, P. Daszak and W.I. Lipkin. 2013. A strategy to estimate unknown viral diversity in mammals. *mBio* 4(5): e00598–13. doi: <u>10.1128/mBio.00598-13</u>.

The majority of emerging zoonoses originate in wildlife, and many are caused by viruses. However, there are no rigorous estimates of total viral diversity (here termed "virodiversity") for any wildlife species, despite the utility of this to future surveillance and control of emerging zoonoses. In this case study, we repeatedly sampled a mammalian wildlife host known to harbor emerging zoonotic pathogens (the Indian Flying Fox, *Pteropus giganteus*) and used PCR with degenerate viral family-level primers to discover and analyze the occurrence patterns of 55 viruses from nine viral families. We then adapted statistical techniques used to estimate biodiversity in vertebrates and plants and estimated the total viral richness of these nine families in *P. giganteus* to be 58 viruses. Our analyses demonstrate proof-of-concept of a strategy for estimating viral richness and provide the first statistically supported estimate of the number of undiscovered viruses in a mammalian host. We used a simple extrapolation to estimate that there are a minimum of 320,000 mammalian viruses awaiting discovery within these nine families, assuming all species harbor a similar number of viruses, with minimal turnover between host species. We estimate the cost of discovering these viruses to be ~\$6.3 billion (or ~\$1.4 billion for 85% of the total diversity), which if annualized over a 10-year study time frame would represent a small fraction of the cost of many pandemic zoonoses.

Baker, K.S., R. Suu-Ire, J. Barr, D.T.S. Hayman, C.C. Broder, D.L. Horton, C. Durrant, P.R. Murcia, A.A. Cunningham and J.L.N. Wood. 2013. Viral antibody dynamics in a chiropteran host. *The Journal of Animal Ecology*, 83: 415–428. doi: <u>10.1111/1365-2656.12153</u>.

Bats host many viruses that are significant for human and domestic animal health, but the dynamics of these infections in their natural reservoir hosts remain poorly elucidated. In these, and other, systems, there is evidence that seasonal life-cycle events drive infection dynamics, directly impacting the risk of exposure to spillover hosts. Understanding these dynamics improves our ability to predict zoonotic spillover from the reservoir hosts. To this end, we followed henipavirus antibody levels of >100 individual *E. helvum* in a closed, captive, breeding population over a 30-month period, using a powerful novel antibody quantitation method. We demonstrate the presence of maternal antibodies in this system and accurately determine their longevity. We also present evidence of population-level persistence of viral infection and demonstrate periods of increased horizontal virus transmission associated with the pregnancy/lactation period. The novel findings of infection persistence and the effect of pregnancy on viral transmission, as well as an accurate quantitation of chiropteran maternal antibiody half-life, provide fundamental baseline data for the continued study of viral infections in these important reservoir hosts.

Bates, P.J.J., K. Cameron, M.J. Pearch and B. Hayes. 2013. A review of the bats (Chiroptera) of the Republic of Congo, including eight species new to the country. *Acta Chiropterologica* 15(2): 313–340. doi: <u>10.3161/150811013X678955</u>.

In July–August, 2012, a small collection of bats was made in the Republic of Congo. These 24 specimens represent 14 species, of which eight (belonging to the Hipposideridae, Vespertilionidae and Miniopteridae), are new records for the country. The current paper briefly describes the specimens, illustrates diagnostic characters to assist with future identifications, and provides insights into their taxonomy. In addition, it reviews the literature records and provides distribution data for all 43 bat species, which are included now on the country's faunal checklist. Published collecting localities for bats in Congo are mapped and discussed both in terms of their geographical distribution and in relation to the variety of habitats that have been sampled in the past. Based on the literature, predictions are made about how many species of bat may be present in Congo. Recommendations are made for future bat research and conservation in the country.

Cebesoy, S. and M. Karakas. 2013. Histochemical Determination of muscle fiber types in primary flight muscles of *Miniopterus schreibersi*. *Journal of Animal and Veterinary Advances* 12(3): 382–386. doi: <u>10.3923/</u><u>javaa.2013.382.386</u>.

Two primary flight muscles of *Miniopterus schreibersi* were studied using morphological and histochemical analysis. All animals were killed with an overdose of sodium pentabarbital administered intraperitoneally. Muscles were dissected free, cleaned of excess fasia, blotted dry and weighed. Their proximal and distal portions were mounted in gum tragacanth on cork, quick-frozen by immersionin isopentane cooled to about -160°C. Transverse serial sections (10-12 µm thickness) were obtained with a freezing cryostat sections from each muscle were stained with Nicotinamide Adenine Dinucleotide Tetrazolium Reductase (NADH-TR) to assess oxidative capacity. The method was used demonstate Succinate Dehydrogenase (SDH) activity. Sections of each muscle were stained using myosin Adenosine Triphosphatase (mATPase). Two fast twitch fiber types are histochemically identified in pectoralis muscles of *M. schreibersi*. These were classified as type IIa and b according to glycine-calcium-formalin preincubation staining protocol for myosin ATPase. The primary flight muscles, serratus ventalis included type I, IIa and b fibers. Type I fibers in serratus ventralis were highly oxidative as stained darkly for NADH-TR. All type IIa fibers exhibited relatively intense staining properties for NADH-TR and SDH suggesting a intermediate oxidative capacity. In *M. schreibersi* for the pectoral muscle are fiber type IIa 87% and fiber type IIb 13%. Fiber ratios for serratus ventralis arefiber type I 14%, fiber type IIa 70% and fiber type IIb 16%.

Çoraman, E., A. Furman, A. Karataş and R. Bilgin. 2013. Phylogeographic analysis of Anatolian bats highlights the importance of the region for preserving the Chiropteran mitochondrial genetic diversity in the Western Palaearctic. Conservation Genetics 14(6): 1205–1216. doi: <u>10.1007/s10592-013-0509-4</u>.

Identification of intraspecific conservation units and incorporating the distribution of genetic diversity into management plans are crucial requirements for assessing effective protection strategies. This study investigates the phylogeographic structures of 33 bat species present in the Near East in order to evaluate the conservation implications of their intraspecific genetic diversity both at regional and large-scale levels. To compare Anatolian populations with the European ones, we utilized two commonly used mitochondrial markers, Cytb and ND1, and analysed them together with the available sequences from GenBank. The management requirements of the identified clades and their taxonomical relations were evaluated by analysing their distributions and the levels of their genetic differentiations. In 12 species and the large *Myotis* complex, we identified a total of 15 genetically distinct populations found in the Near East, some of which might represent biologically distinct taxa. Comparing the phylogeographic patterns of different taxa indicates that three regions, the Balkans, the Caucasus, and the southern Anatolia, harbour genetically divergent populations and should have higher priority in conservation practices. Considering that Turkey has one of the richest bat fauna in the Mediterranean region and the Anatolian populations of various species are genetically distinct, protecting populations in Turkey is critically important for preserving the genetic diversity of the bats in the Western Palaearctic. Both regional and large-scale conservation strategies, which incorporate the distribution of genetic diversity, should be assessed and further ecological studies are needed to clarify the taxonomic relations of the identified clades.

Dell, L.-A., J.-L. Kruger, J.D. Pettigrew and P.R. Manger. 2013. Cellular location and major terminal networks of the orexinergic system in the brain of two megachiropterans. *Journal of Chemical Neuroanatomy* 53: 64–71. doi: <u>10.1016/j.jchemneu.2013.09.001</u>.

The present study describes the distribution of orexin-A immunoreactive neurons and their terminal networks in the brains of two species of megachiropterans. In general the organization of the orexinergic system in the mammalian brain is conserved across species, but as one of two groups of mammals that fly and have a high metabolic rate, it was of interest to determine whether there were any specific differences in the organization of this system in the megachiropterans. Orexinergic neurons were limited in distribution to the hypothalamus, and formed three distinct clusters, or nuclei, a main cluster with a perifornical location, a zona incerta cluster in the dorsolateral hypothalamus and an optic tract cluster in the ventrolateral hypothalamus. The nuclear parcellation of the orexinergic system in the megachiropterans was similar to that seen in many mammals, but differs from the microchiropterans where the optic tract cluster is absent. The terminal networks of the orexinergic neurons in the megachiropterans was similar to that seen in a range of mammalian species, with significant terminal networks being found in the hypothalamus, cholinergic pedunculopontine and laterodorsal tegemental nuclei, the noradrenergic locus coeruleus complex, all serotonergic nuclei, the paraventricular nuclei of the epithalamus and adjacent to the habenular nuclei. While the megachiropteran orexinergic system is typically mammalian in form, it does differ from that reported for microchiropterans, and thus provides an additional neural character arguing for independent evolution of these two chiropteran suborders.

Drexler, J.F., V.M. Corman and C. Drosten. 2014. Ecology, evolution and classification of bat coronaviruses in the aftermath of SARS. *Antiviral Research* 101: 45–56. doi: <u>10.1016/j.antiviral.2013.10.013</u>.

In 2002/2003, a novel coronavirus (CoV) caused a pandemic, infecting more than 8000 people, of whom nearly 10% died. This virus, termed *severe acute respiratory syndrome*-CoV was linked to a zoonotic origin from rhinolophid bats in 2005. Since then, numerous studies have described novel bat CoVs, including close relatives of the newly emerging *Middle East respiratory syndrome*

(MERS)-CoV. In this paper we discuss CoV genomic properties and compare different taxonomic approaches in light of the technical difficulties of obtaining full genomic sequences directly from bat specimens. We first present an overview of the available studies on bat CoVs, with details on their chiropteran hosts, then comparatively analyze the increase in bat CoV studies and novel genomic sequences obtained since the SARS pandemic. We then conduct a comprehensive phylogenetic analysis of the genera *Alpha*- and *Betacoronavirus*, to show that bats harbour more CoV diversity than other mammalian hosts and are widely represented in most, but not all parts of the tree of mammalian CoVs. We next discuss preliminary evidence for phylogenetic co-segregation of CoVs and bat hosts encompassing the *Betacoronavirus* clades b and d, with an emphasis on the sampling bias that exists among bat species and other mammals, then present examples of CoVs infecting different hosts on the one hand and viruses apparently confined to host genera on the other. We also demonstrate a geographic bias within available studies on bat CoVs, and identify a critical lack of information from biodiversity hotspots in Africa, Asia and Latin America. We then present evidence for a zoonotic origin of four of the six known human CoVs (HCoV), three of which likely involved bats, namely SARS-CoV, MERS-CoV and HCoV-229E; compare the available data on CoV pathogenesis in bats to that in other mammalian hosts; and discuss hypotheses on the putative insect origins of CoV ancestors. Finally, we suggest caution with conclusions on the zoonotic potential of bat viruses, based only on genomic sequence data, and emphasize the need to preserve these ecologically highly relevant animals. This paper forms part of a symposium in *Antiviral Research* on "from SARS to MERS: 10 years of research on highly pathogenic human coronaviruses".

Drexler, J.F., A. Geipel, A. König, V.M. Corman, D. van Riel, L.M. Leijten, C.M. Bremer, A. Rasche, V.M. Cottontail, G.D. Maganga, M. Schlegel, M.A. Müller, A. Adam, S.M. Klose, A.J. Borges Carneiro, A. Stöcker, C.R. Franke, F. Gloza-Rausch, J. Geyer, A. Annan, Y. Adu-Sarkodie, S. Oppong, T. Binger, P. Vallo, M. Tschapka, R.G. Ulrich, W.H. Gerlich, E. Leroy, T. Kuiken, D. Glebe and C. Drosten. 2013. Bats carry pathogenic hepadnaviruses antigenically related to hepatitis B virus and capable of infecting human hepatocytes. *Proceedings of the National Academy of Sciences of the United States of America* 110(40): 16151–16156. doi: 10.1073/pnas.1308049110.

The hepatitis B virus (HBV), family *Hepadnaviridae*, is one of most relevant human pathogens. HBV origins are enigmatic, and no zoonotic reservoirs are known. Here, we screened 3,080 specimens from 54 bat species representing 11 bat families for hepadnaviral DNA. Ten specimens (0.3%) from Panama and Gabon yielded unique hepadnaviruses in coancestral relation to HBV. Full genome sequencing allowed classification as three putative orthohepadnavirus species based on genome lengths (3,149-3,377 nt), presence of middle HBV surface and X-protein genes, and sequence distance criteria. Hepatic tropism in bats was shown by quantitative PCR and in situ hybridization. Infected livers showed histopathologic changes compatible with hepatitis. Human hepatocytes transfected with all three bat viruses cross-reacted with sera against the HBV core protein, concordant with the phylogenetic relatedness of these hepadnaviruses and HBV. One virus from *Uroderma bilobatum*, the tent-making bat, cross-reacted with monoclonal antibodies against the HBV antigenicity determining S domain. Up to 18.4% of bat sera contained antibodies against bat hepadnaviruses. Infectious clones were generated to study all three viruses in detail. Hepatitis D virus particles pseudotyped with surface proteins of *U. bilobatum* HBV, but neither of the other two viruses could infect primary human and *Tupaia belangeri* hepatocytes. Hepatocyte infection occurred through the human HBV receptor sodium taurocholate cotransporting polypeptide but could not be neutralized by sera from vaccinated humans. Antihepadnaviral treatment using an approved reverse transcriptase inhibitor blocked replication of all bat hepadnaviruses. Our data suggest that bats may have been ancestral sources of primate hepadnaviruses. The observed zoonotic potential might affect concepts aimed at eradicating HBV.

Eckerle, I., L. Ehlen, R. Kallies, R. Wollny, V.M. Corman, V.M., Cottontail, M. Tschapka, S. Oppong, C. Drosten and M.A. Müller. 2014. Bat airway epithelial cells: a novel tool for the study of zoonotic viruses. *PloS one* 9(1): e84679. doi: <u>10.1371/journal.pone.0084679</u>.

Bats have been increasingly recognized as reservoir of important zoonotic viruses. However, until now many attempts to isolate batborne viruses in cell culture have been unsuccessful. Further, experimental studies on reservoir host species have been limited by the difficulty of rearing these species. The epithelium of the respiratory tract plays a central role during airborne transmission, as it is the first tissue encountered by viral particles. Although several cell lines from bats were established recently, no well-characterized, selectively cultured airway epithelial cells were available so far. Here, primary cells and immortalized cell lines from bats of the two important suborders Yangochiroptera and Yinpterochiroptera, *Carollia perspicillata* (Seba's short-tailed bat) and *Eidolon helvum* (Straw-colored fruit bat), were successfully cultured under standardized conditions from both fresh and frozen organ specimens by cell outgrowth of organ explants and by the use of serum-free primary cell culture medium. Cells were immortalized to generate permanent cell lines. Cells were characterized for their epithelial properties such as expression of cytokeratin and tight junctions proteins and permissiveness for viral infection with Rift-Valley fever virus and vesicular stomatitis virus Indiana. These cells can serve as suitable models for the study of bat-borne viruses and complement cell culture models for virus infection in human airway epithelial cells.

Giribet, G., B.L. de Bivort, A. Hitchcock and P. Swart. 2013. On Speleosiro argasiformis - a troglobitic Cyphophthalmi (Arachnida: Opiliones: Pettalidae) from Table Mountain, South Africa. The Journal of Arachnology 41(3): 416–419. doi: <u>10.1636/Ha12-78.1</u>.

We report the recent collection and observation of large numbers of specimens of the troglobitic harvestman *Speleosiro argasiformis* Lawrence 1931 in the Wynberg Cave system, Table Mountain, South Africa. Specimens were collected and/or photographed in different caves of the system. Live observation showed specimens fleeing bat carcasses when disturbed.

Gortazar, C. and J. Segalés. 2013. Middle East Respiratory Syndrome (MERS) Coronavirus: A new challenge for veterinarians? *Veterinary Pathology* 50(6): 954–955. doi: <u>10.1177/0300985813506391</u>.

Gunnell, G.F., N.B. Simmons and E.R. Seiffert. 2014. New Myzopodidae (Chiroptera) from the Late Paleogene of Egypt: Emended Family Diagnosis and Biogeographic Origins of Noctilionoidea. PLoS ONE, 9 (2): e86712. doi: <u>10.1371/journal.pone.0086712</u>.

Myzopodidae is a family of bats today represented by two extant species of the genus Myzopoda that are restricted to the island of

Madagascar. These bats possess uniquely derived adhesive pads on their thumbs and ankles that they use for clinging to smooth roosting surfaces. Only one fossil myzopodid has been reported previously, a humerus from Pleistocene deposits at Olduvai Gorge in Tanzania that was tentatively referred to the genus *Myzopoda*. Here we describe a new genus and two new species of myzopodids based on dental remains from Paleogene deposits in the Fayum Depression in Egypt, and provide an emended diagnosis for the family Myzopodidae. *Phasmatonycteris phiomensis* n. sp. is represented by four specimens from the early Oligocene Jebel Qatrani Formation and *P. butleri* n. sp. is known from a single specimen from the late Eocene Birket Qarun Formation. Together these specimens extend the temporal range of Myzopodidae by 36+ million years, and the geographic range by nearly 4000 kilometers. The new myzopodids, along with previously described bats from the Fayum and Australia, suggest that eastern Gondwana played a critical role in the origin and diversification of several bats clades notably including the superfamily Noctilionoidea, the majority of which live in the Neotropics today.

Helbig-Bonitz, M., G. Rutten, and E.K.V. Kalko. 2013. Fruit bats can disperse figs over different land-use types on Mount Kilimandjaro, Tanzania. *African Journal of Ecology* 52(1): 122–125. doi: <u>10.1111/aje.12090</u>.

Horáček, I., L.C. Maul, K.T. Smith, R. Barkai and A. Gopher. 2013. Bat remains (Mammalia, Chiroptera) from the Middle Pleistocene site of Qesem Cave, Israel, with the first Pleistocene record of fruit bats in the Mediterranean region. *Palaeontologica Electronica* 16(3 23A): 19 pp. <u>www.palaeo-electronica.org/</u> <u>content/2013/513-gesem-bats</u>.

Very few data are available on fossil bats of the Near East, a region of great biogeographic significance for that group in the Western Palaearctic. Here, we report on a collection of fossil bats from the Middle Pleistocene site Qesem Cave, Israel, famous for lithic artifacts, hominin remains and rich vertebrate faunas. We identified five micro-chiropteran species, viz. *Rhinolophus ferrumequinum*, *R. euryale*, *R. mehelyi*, *Miniopterus* cf. *schreibersii*, and *Myotis blythii*, all typical cave-dwellers common also in extant communities in the region. Their appearance suggests mild conditions with variegated vegetation at the time of deposition. In addition, two tooth fragments, tentatively identified as cf. *Rousettus* sp., provide the first Pleistocene record of fruit bats beyond the tropics. If these remains pass muster, the Quaternary history of fruit bats in this region could be traced back to the Pleistocene, earlier than previously thought, and then the extant extralimital population of *Rousettus aegyptiacus* could be seen as a palaeochoric element of the Mediterranean biota. In general, the Pleistocene record of bats in the Levant (including Qesem) is characterized by the absence of the Ethiopian elements that dominate the extant Levantine fauna, while the vast majority of the fossil bat forms are elements of the Palaearctic clades.

Husemann, M., T. Schmitt, F.E. Zachos, W. Ulrich and J.C. Habel. 2014. Palaearctic biogeography revisited: evidence for the existence of a North African refugium for Western Palaearctic biota. *Journal of Biogeography* 41(1): 81–94. doi: <u>10.1111/jbi.12180</u>.

Aim In contrast to the attention given to southern Europe both as a centre of speciation and differentiation and as a Pleistocene refugium of Western Palaearctic taxa, North Africa has been relatively neglected. In this paper, we set out to address this shortfall. **Location** North-West Africa and the Mediterranean. **Methods** We reviewed the existing literature on the biogeography of North Africa, and carried out analyses of species distribution data using parsimony, nestedness and co-occurrence methods. **Results** In many cases, distribution patterns of non-flying mammals, bats, amphibians, reptiles, butterflies, zygaenid moths and odonates demonstrated important biogeographical affinities between Europe and North Africa at the species level. On the other hand, species co-occurrence, nestedness and parsimony analysis also revealed some deep splits between the Maghreb and Europe; yet even in these cases the closest affinities were found between the Iberian Peninsula and the Maghreb. Furthermore, North Africa harbours the highest proportion of endemic taxa (13.7%) across all groups analysed. Many molecular studies demonstrated a strong genetic cohesiveness between North Africa and Europe despite the potential barrier effect of the Mediterranean Sea. In other taxa, however, remarkable splits were detected. In addition, southern European genetic lineages were often nested within North African clades, and many taxa showed exceptionally high genetic variability and differentiation in this region. **Main conclusions** The Maghreb was an important differentiation and speciation centre for thermophilic organisms during the Pliocene and Pleistocene with high relevance as a colonization source for Europe. The regions around the sea straits of Gibraltar and Sicily have acted as important biogeographical links between North Africa and Europe at different times.

Ithete, N.L., S. Stoffberg, V.M. Corman, V.M. Cottontail, L.R. Richards, M.C. Schoeman, C. Drosten, J.F. Drexler and W. Preiser. 2013. Close relative of human Middle East Respiratory Syndrome coronavirus in bat, South Africa. *Emerging Infectious Diseases* 19(10): 1697–1699. doi: <u>10.3201/eid1910.130946</u>.

Jacobs, D.S., H. Babiker, A. Bastian, T. Kearney, R. van Eeden and J.M. Bishop. 2013. Phenotypic convergence in genetically distinct lineages of a *Rhinolophus* species complex (Mammalia, Chiroptera). *PloS one* 8(12): e82614. doi: <u>10.1371/journal.pone.0082614</u>.

Phenotypes of distantly related species may converge through adaptation to similar habitats and/or because they share biological constraints that limit the phenotypic variants produced. A common theme in bats is the sympatric occurrence of cryptic species that are convergent in morphology but divergent in echolocation frequency, suggesting that echolocation may facilitate niche partitioning, reducing competition. If so, allopatric populations freed from competition, could converge in both morphology and echolocation provided they occupy similar niches or share biological constraints. We investigated the evolutionary history of a widely distributed African horseshoe bat, *Rhinolophus darlingi*, in the context of phenotypic convergence. We used phylogenetic inference to identify and date lineage divergence together with phenotypic comparisons and ecological niche modelling to identify morphological and geographical correlates of those lineages. Our results indicate that *R. darlingi* is paraphyletic, the eastern and western parts of its distribution forming two distinct non-sister lineages that diverged ~9.7 Mya. We retain *R. darlingi* for the eastern lineage and argue that the western lineage, currently the sub-species *R. d. damarensis*, should be elevated to full species status. *R. damarensis* comprises two lineages that diverged ~5 Mya. Our findings concur with patterns of divergence of other co-distributed taxa which are associated with increased regional aridification between 7-5 Mya suggesting possible vicariant evolution. The morphology and echolocation calls of *R. darlingi* and *R. damarensis* are convergent despite occupying different biomes. This suggests that adaptation to similar habitats is not responsible for the convergence. Furthermore, *R. darlingi* forms part of a clade comprising species that are

bigger and echolocate at lower frequencies than *R. darlingi*, suggesting that biological constraints are unlikely to have influenced the convergence. Instead, the striking similarity in morphology and sensory biology are probably the result of neutral evolutionary processes, resulting in the independent evolution of similar phenotypes.

Kerbis Peterhans, J.C., J. Fahr, M.H. Huhndorf, P. Kaleme, A.J. Plumptre, B.D. Marks and R. Kizungu. 2013. Bats (Chiroptera) from the Albertine Rift, eastern Democratic Republic of Congo, with the description of two new species of the *Rhinolophus maclaudi* group. *Bonner Zoological Bulletin* 62(2): 186–202. <u>www.</u> zoologicalbulletin.de/BzB Volumes/Volume 62 2/186 202 BzB62 2 Kerbis JC et al.pdf

Horseshoe bats of the *Rhinolophus maclaudi* species group were recently revised by Fahr *et al.* (2002). Known members of the group are located in the mountainous region of West Africa and the Albertine Rift, east of the Congo River basin with a major gap (4300 km) between the two recognized sub-groups. Here we describe two additional species within this species group from the Albertine Rift center of endemism in the eastern Democratic Republic of Congo. One derives from the Misotschi-Kabogo highlands, a heretofore poorly documented region half-way down the western shore of Lake Tanganyika. Additional bat records from this locality are also documented. The second new taxon was collected in Kahuzi-Biega National Park, a World Heritage Site adjacent to the shore of Lake Kivu.

Korine, C., S. Daniel and B. Pinshow. 2013. Roost selection by female Hemprich's long-eared bats. *Behavioural Processes* 100: 131–138. doi: <u>10.1016/j.beproc.2013.08.013</u>.

Selection of suitable roosts by bats can have fitness benefits by providing shelter and a place to rear young. Assuming that lactating bats behave differently from, and have greater food requirements than pregnant bats, we predicted that near the end of pregnancy, desert-dwelling bats would move to roosts appropriate to their changing needs. We followed radio-tagged pregnant and lactating female Hemprich's long-eared bats, *Otonycteris hemprichii*, to their roosts and characterized the shape of 38 roosts by measuring their linear dimensions, compass direction of the outer rock face, roost temperature (T_r) and the distance from the roost to the bats' main foraging site. We also compared roosts used by bats to randomly chosen "potential" roosts. During reproduction, female *O. hemprichii* roosts used by pregnant bats or distances to their main foraging site were not different from those used by lactating individuals. However, pregnant females used horizontal cracks while lactating females used vertical cracks. Comparing roosts used by bats to "potential" roosts, we found that the former had smaller daily amplitudes of T_r than the "potential" ones. Female *O. hemprichii* used only a small number of the available roosts in the area, and re-used some of them year after year. We suggest that, in contrast to bats that live in temperate habitats, *O. hemprichii* do not need to seek roosts with temperature conditions specific to the periods of pregnancy or lactation because natural changes in T_r suffice, and other factors are involved in the decision to choose a roost or to abandon it.

Krüger, N., M. Hoffmann, M. Weis, J.F. Drexler, M.A. Müller, C. Winter, V.M. Corman, T. Gützkow, C. Drosten, A. Maisner and G. Herrler. 2013. Surface glycoproteins of an African Henipavirus induce syncytium formation in a cell line derived from an African Fruit Bat, *Hypsignathus monstrosus*. *Journal of Virology* 87(24): 13889–13891. doi: <u>10.1128/JVI.02458-13</u>

Serological screening and detection of genomic RNA indicates that members of the genus Henipavirus are present not only in Southeast Asia but also in African fruit bats. We demonstrate that the surface glycoproteins F and G of an African henipavirus (M74) induce syncytium formation in a kidney cell line derived from an African fruit bat, *Hypsignathus monstrosus*. Despite a less broad cell tropism, the M74 glycoproteins show functional similarities to glycoproteins of Nipah virus.

Madej, J.P., L. Mikulová, A. Gorošová, Š. Mikula, Z. Řehák, F. Tichý and M. Buchtová. 2012 (for 2013). Skin structure and hair morphology of different body parts in the Common Pipistrelle (*Pipistrellus pipistrellus*). Acta Zoologica, 94 (4): 478-489. doi: <u>10.1111/j.1463-6395.2012.00578.x</u>

The bat skin shows an unusual morphology that corresponds to flying adaptations but also performs multiple functions including a protective barrier against microbes and parasites. Here, we compare the microscopic structure of the skin and hairs collected from the membranes with other body parts in the Common Pipistrelle (*Pipistrellus pipistrellus*) in relation to parasite availability. Statistical analysis of whole-skin thickness revealed two main groups according to body regions; the first with thin skin (wing and tail membrane) and the second with thick skin (head and dorsum, abdomen, footpad). The density of hair was evaluated by a novel method, and it revealed that the density was significantly higher in the head region than in dorsal and ventral body parts. These differences possibly play a role for bat ectoparasites when choosing the preferred region of their host. Along the axis of each hair, the scale morphology was found to be variable. Hair morphology, however, did not vary among body regions. Mast cells were numerous in the hairy areas around vessels and hair follicles of the dorsum and abdomen, which are easily accessible to ectoparasites. Increased numbers of mast cells in hair-bearing skin are part of the host adaptation system in parasite-preferred locations.

Markotter, W., A. Monadjem and L.H. Nel. 2013. Antibodies against Duvenhage virus in insectivorous bats in Swaziland. *Journal of Wildlife Diseases* 49(4): 1000–1003. doi: <u>10.7589/2012-10-257</u>.

Several rabies-related lyssaviruses have been associated with bat species in southern Africa, the rarest of these being Duvenhage virus (DUVV), for which only five isolations have been made over five decades. Three of these were from human fatalities, and it is not known which bat species acts as reservoir. In studying a population of *Nycteris thebaica* in the kingdom of Swaziland, a landlocked country bordering Mozambique and South Africa, we found evidence of the circulation of a lyssavirus. Virus-neutralization assays indicated DUVV-neutralizing antibodies in 30% of the sera collected from this population of *N. thebaica*, providing the first indication of a Duvenhage virus circulating in this particular species and the first evidence of a bat lyssavirus circulating in Swaziland bats.

Matos, M., N.L. Pinto, M.J.R. Pereira and C. Fonseca. 2013. Triggering bat detectors: automatic vs. manual mode. *Mammalia* 77(4): 461–466. doi: <u>10.1515/mammalia-2013-0029</u>.

Ultrasound detectors have revolutionized the study of bats, as they allow for cost-effective gathering of large amounts of data on bat activity. The identification of bat species through the analysis of echolocation calls is possible, as long as the researcher is well aware of the features and limitations of the detector and methods used. In bat studies, field logistics frequently leads to the need of

leaving the ultrasound detector in the study area for a given number of nights, set to an automatic triggering mode. Nonetheless, the reliability of this option, in comparison with the manual mode, is still uncertain, even for commonly used bat detector models. In this study, we assessed the efficacy of a popular time-expansion bat detector model set to the automatic trigger mode, when compared with the manual mode. We sampled bat activity in five different habitats for 23 nights with two bat detectors operating simultaneously, side by side, one set to manual mode and the other set to automatic mode. Our results showed significant differences in detected species richness, species diversity, and bat activity between the manual and the automatic modes. We present practical information and clarify the adequacy of using the analyzed bat detector in automatic conditions.

Monadjem, A., S.M. Goodman, W.T. Stanley and B. Appleton. 2013. A cryptic new species of *Miniopterus* from south-eastern Africa based on molecular and morphological characters. *Zootaxa* 3746(1): 123–142. doi: 10.11646/zootaxa.3746.1.5.

Resolving species limits within the genus *Miniopterus* has traditionally been complicated by the presence of cryptic species with overlapping morphological features. We use molecular techniques, cranio-dental characters and tragus shape to describe a new species of *Miniopterus* from Mozambique, *M. mossambicus*. *Miniopterus mossambicus* shows > 12% divergence in cytochrome-b sequence from its nearest congeners (the Malagasy *M. gleni* and *M. griveaudi*) and > 15% divergence from the morphologically similar *M. natalensis*, *M. fraterculus* and *M. minor* (all of which occur in southern and eastern Africa). There is considerable overlap in cranio-dental characters of the southern African species, particularly *M. natalensis* and *M. mossambicus*. However, tragus shape and multivariate comparisons of skull measurements can be used to separate these species. Based on morphological comparisons of museum specimens, this species may also be present in neighbouring Malawi and Zimbabwe, suggesting that it is probably distributed widely in south-central Africa.

Monadjem, A., L. Richards, P.J. Taylor, C. Denys, A. Dower and S. Stoffberg. 2013. Diversity of Hipposideridae in the Mount Nimba massif, West Africa, and the taxonomic status of *Hipposideros lamottei*. Acta *Chiropterologica* 15(2): 341–352. doi: <u>10.3161/150811013X678964</u>.

Several species complexes exist within the African representatives of the genus *Hipposideros* and the relationships between these taxa are not yet well understood. We present evidence showing that at least seven species of *Hipposideros* co-occur at Mount Nimba at the northern boundary of the Upper Guinean forest zone. The species *H. lamottei* has been misdiagnosed previously, partly as a result of errors in published measurements. This taxon is currently known only from high-altitude grasslands in northern (Guinean) Mount Nimba. Cytochrome *b* sequences and echolocation calls of this species, as well as for *H. marisae*, are presented for the first time. Also, at least two different species groups, previously lumped in *H. ruber*, co-exist syntopically here. Mount Nimba apparently represents a diversity hotspot for species of Hipposideros in West Africa, and as a result may be an important site for their conservation.

Orr, T.J. and M. Zuk. 2013. Does delayed fertilization facilitate sperm competition in bats? *Behavioral Ecology* and Sociobiology 67(12): 1903–1913. doi: <u>10.1007/s00265-013-1598-2</u>.

Reproductive delays between mating and birth may provide a previously unconsidered avenue for postcopulatory sexual selection in mammals. In particular, delayed fertilization could provide an enhanced opportunity for sperm competition by extending the time for ejaculates to interact in the female reproductive tract. We tested the prediction that species with delayed fertilization exhibit greater degrees of sperm competition than those without delays by examining testis volume (a proxy for sperm competition) in 38 species of bats. Examination of fluid-preserved museum specimens of bat species with and without delays revealed that species with delaye (in particular those with delayed fertilization) had significantly larger testes than species without them. Although it predicts the presence of delayed fertilization, hibernation did not predict relative testis size. We conclude that, once they evolve, reproductive delays may facilitate sperm competition.

Oubaziz, B. 2012. Recherches Écologiques Sur Les Chiroptères de L'extrême Ouest Algérien: Habitat, Répartition et Statut. Master's thesis, Abou Bekr Belkaid, 1-188 pp + 6 Appendicies.

The study of the settlement of bat carried to the extreme western Algeria between October 2010 and June 2011 has highlighted the existence of nine species belonging to three families and four genera *Rhinolophus blasii, Rhinolophus euryale, Rhinolophus ferrumequinum, Rhinolophus hipposideros, Rhinolophus mehelyi, Myotis capaccinii, Myotis punicus, Pipistrellus pipistrellus, Miniopterus schreibersi.* The surveys were carried out in 20 stations of Tlemcen, from the rocky cliffs of the coast, up mountains of Tlemcen. The inventory method used is direct observation in lodging. The study of the distribution of sites shows that the region has characteristics very favorable to the presence of bats. The numerous caves, abandoned mines, multiple hunting grounds are all factors favorable to the installation of bats.

Parker, J., G. Tsagkogeorga, J.A. Cotton, Y. Liu, P. Provero, E. Stupka and S.J. Rossiter. 2013. Genome-wide signatures of convergent evolution in echolocating mammals. *Nature* 502(7470): 228–231. doi: <u>10.1038/</u><u>nature12511</u>.

Evolution is typically thought to proceed through divergence of genes, proteins and ultimately phenotypes. However, similar traits might also evolve convergently in unrelated taxa owing to similar selection pressures. Adaptive phenotypic convergence is widespread in nature, and recent results from several genes have suggested that this phenomenon is powerful enough to also drive recurrent evolution at the sequence level. Where homoplasious substitutions do occur these have long been considered the result of neutral processes. However, recent studies have demonstrated that adaptive convergent sequence evolution can be detected in vertebrates using statistical methods that model parallel evolution, although the extent to which sequence convergence between genera occurs across genomes is unknown. Here we analyse genomic sequence data in mammals that have independently evolved echolocation and show that convergence is not a rare process restricted to several loci but is instead widespread, continuously distributed and commonly driven by natural selection acting on a small number of sites per locus. Systematic analyses of convergent sequence evolution in 805,053 amino acids within 2,326 orthologous coding gene sequences compared across 22 mammals (including four newly sequenced bat genomes) revealed signatures consistent with convergence in nearly 200 loci. Strong and significant support for convergence among bats and the bottlenose dolphin was seen in numerous genes linked to vision: the convergent with an involvement in echolocation. Unexpectedly, we also found convergence in many genes linked to vision: the convergent

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signal of many sensory genes was robustly correlated with the strength of natural selection. This first attempt to detect genomewide convergent sequence evolution across divergent taxa reveals the phenomenon to be much more pervasive than previously recognized.

Peel, A.J., T.J. McKinley, K.S. Baker, J.A. Barr, G. Crameri, D.T.S. Hayman, Y.-R. Feng, C.C. Broder, L.-F. Wang, A.A. Cunningham and J.L.N. Wood. 2013. Use of cross-reactive serological assays for detecting novel pathogens in wildlife: Assessing an appropriate cutoff for henipavirus assays in African bats. *Journal of Virological Methods* 193(2): 295–303. doi: <u>10.1016/j.jviromet.2013.06.030</u>.

Reservoir hosts of novel pathogens are often identified or suspected as such on the basis of serological assay results, prior to the isolation of the pathogen itself. Serological assays might therefore be used outside of their original, validated scope in order to infer seroprevalences in reservoir host populations, until such time that specific diagnostic assays can be developed. This is particularly the case in wildlife disease research. The absence of positive and negative control samples and gold standard diagnostic assays presents challenges in determining an appropriate threshold, or 'cutoff', for the assay that enables differentiation between seronegative and seropositive individuals. Here, multiple methods were explored to determine an appropriate cutoff for a multiplexed microsphere assay that is used to detect henipavirus antibody binding in fruit bat plasma. These methods included calculating multiples of 'negative' control assay values, receiver operating characteristic curve analyses, and Bayesian mixture models to assess the distribution of assay outputs for classifying seropositive and seronegative individuals within different age classes. As for any diagnostic assay, the most appropriate cutoff determination method and value selected must be made according to the aims of the study. This study is presented as an example for others where reference samples, and assays that have been characterised previously, are absent.

Peel, A.J., D.R. Sargan, K.S. Baker, D.T.S. Hayman, J.A. Barr, G. Crameri, R. Suu-Ire, C.C. Broder, T. Lembo, L.-F. Wang, A.R. Fooks, S.J. Rossiter, J.L.N. Wood and A.A. Cunningham. 2013. Continent-wide panmixia of an African fruit bat facilitates transmission of potentially zoonotic viruses. *Nature Communications* 4(2770): 1–14. doi: <u>10.1038/ncomms3770</u>.

The straw-coloured fruit bat, *Eidolon helvum*, is Africa's most widely distributed and commonly hunted fruit bat, often living in close proximity to human populations. This species has been identified as a reservoir of potentially zoonotic viruses, but uncertainties remain regarding viral transmission dynamics and mechanisms of persistence. Here we combine genetic and serological analyses of populations across Africa, to determine the extent of epidemiological connectivity among *E. helvum* populations. Multiple markers reveal panmixia across the continental range, at a greater geographical scale than previously recorded for any other mammal, whereas populations on remote islands were genetically distinct. Multiple serological assays reveal antibodies to henipaviruses and Lagos bat virus in all locations, including small isolated island populations, indicating that factors other than population size and connectivity may be responsible for viral persistence. Our findings have potentially important public health implications, and highlight a need to avoid disturbances that may precipitate viral spillover.

Presetnik, P. and S. Aulagnier. 2013. The diet of Schreiber's bent-winged bat, *Miniopterus schreibersii* (Chiroptera: Miniopteridae), in northeastern Slovenia (Central Europe). *Mammalia* 77(3): 297–305. doi: <u>10.1515/mammalia-2012-0033</u>.

The diet of *Miniopterus schreibersii* was investigated by morphological analysis of prey remains in droppings from the spring to the autumn of 2000 from a bat roost in northeastern Slovenia (Central Europe). Lepidoptera dominated, having an average percent volume (APV) of 79 % and constituting the bulk of the diet throughout the year. By decreasing importance in the diet, the insects identified were Neuroptera – mostly Chrysopidae (APV 9.2 %), Diptera (APV 7.4 %), Trichoptera (APV 2.2 %) and Coleoptera (APV 1.4 %). The diet was most diverse in late October. It seems that *M. schreibersii* is an aerial hawker that specialises in eating moths, but can opportunistically switch to other seasonably abundant prey. It hunts small- to medium-sized winged prey (wing length: 2 - 18 mm), of which most are tympanate insects.

Ramasindrazana, B., S.M. Goodman, C.F. Rakotondramanana and M.C. Schoeman. 2013. Morphological and echolocation call variation in Malagasy Trident Bats, *Triaenops* Dobson, 1871 (Chiroptera: Hipposideridae). *Acta Chiropterologica* 15(2): 431–439. doi: <u>10.3161/150811013X679053</u>.

Patterns of interspecific and intraspecific variation in the three endemic species of Malagasy *Triaenops* bats were investigated using morphology and bioacoustics. Adult bats were captured at different localities across the island, measured, and their echolocation calls recorded. On average, male *T. auritus* and *T. furculus* have shorter forearms (47.0 and 44.0 mm, respectively) and emit higher frequency calls (107.8 and 113.1 kHz, respectively) than females (47.5 and 45.7 mm and 95.6 and 98.2 kHz, respectively), representing a form of reversed sexual dimorphism (females larger than males). However, *T. menamena* shows typical patterns of sexual size dimorphism with males having a longer forearm (51.7 mm) and lower frequency echolocation calls (82.3 kHz) than females (49.0 mm and 93.5 kHz, respectively). When segregated by sex, there was a strong allometric relationship between forearm length, used as a measure of body size, and the resting frequency in these three species, as well as two African hipposiderids (*T. afer* and *Cloeotis percivali*). *Triaenops auritus* males and both sexes of *T. furculus* deviated from the relationship between these two variables. Hypotheses are explored to explain the drivers of these sexual dimorphism patterns. On the basis of the allometric relationship, the strong correlation is in parallel to other groups of bats and is probably associated with ecological constraints. Recent phylogenetic analyses showed a separation of Afro-Malagasy *Triaenops* into two sister clades: *T. auritus/T. furculus* (suggested to be placed in a new genus, *Paratriaenops*) and *T. menamena/T. afer*. The patterns of sexual dimorphism in these taxa are congruent with clade membership. Further studies are needed to understand strategies used by these taxa when in sympatry to share habitat and ecological niches.

Rollinson, D.P., J.C. Coleman and C.T. Downs. 2013. Seasonal differences in foraging dynamics, habitat use and home range size of Wahlberg's epauletted fruit bat in an urban environment. *African Zoology* 48(2): 340–350. doi: <u>10.3377/004.048.0218</u>

Urbanization through the process of habitat loss and fragmentation affects ecosystems. Many species are no longer able to survive in these urban areas; however, there are some that have been able to persist and even thrive in these habitats. One such species

is Wahlberg's epauletted fruit bat (*Epomophorus wahlbergi*). Little is known about its existence in urban areas. Consequently we studied their seasonal variation in home range size, movements and foraging dynamics in the urban environment of Pietermaritzburg, South Africa. In a pilot study in summer, adult fruit bats (n = 8) were caught, fitted with radio-transmitters, and their movements followed for 12 nights and days. Although their movements varied considerably, no bats left the urban environment. Some of the larger distances covered in a single night were 2 and 5 km. In winter, an additional ten adult fruit bats were caught and fitted with radio-transmitters. Movements were followed for three weeks during winter and spring respectively. Winter home range size was greater than spring home range size. During winter the bats fed mostly on syringa fruits (*Melia azedarach*), an alien invasive, while their diet in spring was more varied and included species of indigenous and exotic fruits. The reduced variety of fruit eaten in winter may be explained by a reduction in fruiting plant species, and thus a reliance on a few species to meet their dietary requirements. The bats would have a role in seed dispersal but therein lies the problem of them also dispersing invasive plants. Further research is needed to assess the role played by exotic and alien plant species in the continued success of urban wildlife, in particular fruit bats. The seasonal variation in home range size gives insight into the urban movements of Wahlberg's epauletted fruit bats. The use of exotic and invasive plants by these bats is also significant.

Santana, S.E. and S.E. Lofgren. 2013. Does nasal echolocation influence the modularity of the mammal skull? *Journal of Evolutionary Biology* 26(11): 2520–2526. doi: <u>10.1111/jeb.12235</u>.

In vertebrates, changes in cranial modularity can evolve rapidly in response to selection. However, mammals have apparently maintained their pattern of cranial integration throughout their evolutionary history and across tremendous morphological and ecological diversity. Here, we use phylogenetic, geometric morphometric and comparative analyses to test the hypothesis that the modularity of the mammalian skull has been remodelled in rhinolophid bats due to the novel and critical function of the nasal cavity in echolocation. We predicted that nasal echolocation has resulted in the evolution of a third cranial module, the 'nasal dome', in addition to the braincase and rostrum modules, which are conserved across mammals. We also test for similarities in the evolution of skull shape in relation to habitat across rhinolophids. We find that, despite broad variation in the shape of the nasal dome, the integration of the rhinolophid skull is highly consistent with conserved patterns of modularity found in other mammals. Across their broad geographical distribution, cranial shape in rhinolophids follows two major divisions that could reflect adaptations to dietary and environmental differences in African versus South Asian distributions. Our results highlight the potential of a relatively simple modular template to generate broad morphological and functional variation in mammals.

Schaer, J., S.L. Perkins, J. Decher, F.H. Leendertz, J. Fahr, N. Weber and K. Matuschewski. 2013. High diversity of West African bat malaria parasites and a tight link with rodent *Plasmodium* taxa. *Proceedings of the National Academy of Sciences* 110(43): 17415–17419. doi: <u>10.1073/pnas.1311016110</u>.

As the only volant mammals, bats are captivating for their high taxonomic diversity, for their vital roles in ecosystems—particularly as pollinators and insectivores—and, more recently, for their important roles in the maintenance and transmission of zoonotic viral diseases. Genome sequences have identified evidence for a striking expansion of and positive selection in gene families associated with immunity. Bats have also been known to be hosts of malaria parasites for over a century, and as hosts, they possess perhaps the most phylogenetically diverse set of hemosporidian genera and species. To provide a molecular framework for the study of these parasites, we surveyed bats in three remote areas of the Upper Guinean forest ecosystem. We detected four distinct genera of hemosporidian parasites: *Plasmodium, Polychromophilus, Nycteria*, and *Hepatocystis*. Intriguingly, the two species of *Plasmodium* in bats fall within the clade of rodent malaria parasites, indicative of multiple host switches across mammalian orders. We show that *Nycteria* species form a very distinct phylogenetic group and that *Hepatocystis* parasites display an unusually high diversity and prevalence in epauletted fruit bats. The diversity and high prevalence of novel lineages of chiropteran hemosporidians underscore the exceptional position of bats among all other mammalian hosts of hemosporidian parasites and support hypotheses of pathogen tolerance consistent with the exceptional immunology of bats.

Seamark, E.C.J. 2013. The use of incidence data to estimate bat (Mammalia: Chiroptera) species richness and taxonomic diversity and distinctness within and between the biomes of South Africa, Lesotho and Swaziland. University of the Witwatersrand; School of Animal, Plant and Environmental Sciences: 31 pp. url: <u>http://wiredspace.wits.ac.za/handle/10539/13420</u>.

Species richness and estimates of species richness were calculated based on assemblages of bats, within the biomes of South Africa, Lesotho and Swaziland following the vegetation classification of Mucina and Rutherford (2006). Similarity indices were used to explore the various relationships between the assemblages between the various biomes. Taxonomic diversity and distinctness examined the various assemblages within each of the biomes to investigate which biomes contained assemblages that were taxonomically diverse and/or taxonomically distinct compared to all species known to occur within South Africa, Lesotho and Swaziland.

The Desert biome had the lowest recorded species richness (5 species), and there was insufficient data to calculate estimates of species richness for this biome. While the Albany had 11 species recorded with species estimates (Est.) ranging between 11-12, then in increasing order - Nama-Karoo (12 species, Est. 13-25 species), Succulent-Karoo (13 species, Est. 15-30 species), Fynbos (17 species, Est. 18-25 species), Indian Ocean Coastal Belt (31 species, Est. 32-36 species), Forest (32 species, Est. 37-46 species), Grassland (39 species, Est. 42-54 species), Azonal (45 species, Est. 49-63 species) and Savanna (57 species, Est. 59-67 species). The mean recorded estimates (based on the averages of all models) and rounding up to a full species indicates that the Albany biome contains the lowest expected species richness of 12 species, then Fynbos and Nama-Karoo (21 species), Succulent-Karoo (22 species), Indian Ocean Coastal Belt (34 species), Forest (43 species), Grassland (49 species), Azonal (54 species) and Savanna (64 species).

Sample completeness was calculated for each of the biomes which indicates in ascending order that the Albany biome is 93.2% complete followed by the Indian Ocean Coastal Belt biome (91.1%), Savanna biome (89.9%), Azonal biome (84.1%), Fynbos biome (81.5%), Grassland biome (80.7%), Forest biome (75.8%), Succulent-Karoo biome (61.3%), and Nama-Karoo biome (59.9%). This showed that the Albany biome was found to be the only biome that has been sufficiently sampled.

The Jaccard and Sørensen pair wise indices resulted in the clustering of the biomes with similar species richness, due to the large range in species richness (5-57 species) between the biomes. The Lennon {\i et al.} (2001) index which is not affected by large species richness between the samples indicated that the Desert and Nama-Karoo assemblages were most dissimilar to one

Recent Literature

another, while the Indian Ocean Coastal Belt assemblage was the most similar to the remaining biome assemblages. The Albany biome assemblage and Azonal biome assemblage were shown to the most dissimilar to one another.

The Grassland, Nama-Karoo and Savanna biomes contribute to higher taxonomic diversity, while the Albany, Azonal, Fynbos, Nama-Karoo and Succulent-Karoo biomes contain lower species richness generally but represent a higher taxonomic distinctness from the chiroptera assemblages in the Grassland and Savanna biomes. The Desert, Forest and Indian Ocean Coastal Belt biomes do not contain bat assemblages that are neither taxonomically distinct nor diverse when compared to the taxa of South Africa, Lesotho and Swaziland.

The bat assemblage within the Nama-Karoo are both taxonomically diverse and distinct from chiroptera assemblages found within the other nine biomes, requiring a greater focus on conservation actions for the bat species assemblage located within this biome.

Skibiel, A.L., L.M. Downing, T.J. Orr and W.R. Hood. 2013. The evolution of the nutrient composition of mammalian milks. The Journal of Animal Ecology 82(6): 1254–1264. doi: <u>10.1111/1365-2656.12095</u>.

1. In mammals, nutrient allocation during lactation is a critical component of maternal care as milk intake promotes juvenile growth and survival, and hence maternal and offspring fitness. 2. Milk composition varies widely across mammals and is hypothesized to have arisen via selection pressures associated with environment, diet and life history. These hypotheses have been proposed based on observations and/or cross-species comparisons that did not standardize for stage of lactation and did not consider evolutionary history of the species in analyses. 3. We conducted the largest comparative analysis of milk composition to date accounting for phylogenetic relationships among species in order to understand the selective advantage of producing milk with specific nutritional profiles. We examined four milk constituents in association with species ecology while incorporating phylogeny in analyses. 4. Phylogenetic signal was apparent for all milk constituents examined. After controlling for phylogeny, diet and relative lactation length explained the greatest amount of variation in milk composition. Several aspects of species' ecologies, including adaptation to arid environments, reproductive output and maternal body mass were not associated with milk composition after accounting for phylogeny. 5. Our results suggest that milk composition is largely a function of evolutionary history, maternal nutrient intake and duration of milk production. Arriving at these conclusions was made possible by including the evolutionary relationships among species.

Smith, J.D.L., J.W. Bickham and T.R. Gregory. 2013. Patterns of genome size diversity in bats (order Chiroptera). Genome / National Research Council Canada = Génome / Conseil national de recherches Canada 56(8): 457–472. doi: <u>10.1139/gen-2013-0046</u>.

Despite being a group of particular interest in considering relationships between genome size and metabolic parameters, bats have not been well studied from this perspective. This study presents new estimates for 121 "microbat" species from 12 families and complements a previous study on members of the family Pteropodidae ("megabats"). The results confirm that diversity in genome size in bats is very limited even compared with other mammals, varying approximately 2-fold from 1.63 pg in *Lophostoma carrikeri* to 3.17 pg in *Rhinopoma hardwickii* and averaging only 2.35 pg \pm 0.02 SE (versus 3.5 pg overall for mammals). However, contrary to some other vertebrate groups, and perhaps owing to the narrow range observed, genome size correlations were not apparent with any chromosomal, physiological, flight-related, developmental, or ecological characteristics within the order Chiroptera. Genome size is positively correlated with measures of body size in bats, though the strength of the relationships differs between pteropodids ("megabats") and nonpteropodids ("microbats").

Stoetzel, E. 2013. Late Cenozoic micromammal biochronology of northwestern Africa. *Palaeogeography, Palaeoclimatology, Palaeoecology* 392: 359–381. doi: <u>10.1016/j.palaeo.2013.09.026</u>.

This synthesis aims to integrate former, recent and unpublished data on fossil micromammals (Rodentia, Erinaceomorpha, Soricomorpha, Chiroptera) from Moroccan, Algerian and Tunisian archeological and paleontological sites. An updated biochronology of these taxa is established from the middle Miocene to the Holocene. Ten main biozones are defined: they are characterized by specific faunal assemblages, whose evolution and migrations were influenced by geologic and climatic events throughout the studied period. During the Miocene, Myocricetodontinae were dominant. This period was followed by a progressive diversification among Murinae, Gerbillinae, and Crocidurinae from the Plio-Pleistocene onwards, along with sporadic occurrences of European, Asian and sub-Saharan taxa, before a decrease in small mammal diversity at the beginning of the late Pleistocene, while modern faunas stabilized. Overall, the new biochronology matches well with the former ones. However, some slight discrepancies emerge, notably because the former biochronologies were based on more sporadic data and often did not consider the whole small mammal faunas. The present work represents the first complete biochronological synthesis of North African small faunas for the whole late Cenozoic, which should be useful for paleontologists and archeologists in providing an up-to-date framework into which future discoveries will easily find their place.

Taylor, P.J., A. Monadjem and J.N. Steyn. 2013. Seasonal patterns of habitat use by insectivorous bats in a subtropical African agro-ecosystem dominated by macadamia orchards. *African Journal of Ecology* 51(4): 552–561. doi: <u>10.1111/aje.12066</u>.

We report on acoustic surveys of insectivorous bats conducted during seven months of the year using ANABAT recordings in two habitats (macadamia orchards and adjacent riparian bush) in a subtropical agro- ecosystem in northern South Africa. We defined two functional foraging groups of bats based on their echolocation calls: (i) open-air foragers (family Molossidae) having narrowband, low-frequency, low duty cycle calls; and (ii) clutter-edge foragers (families Miniopteridae and Vespertilionidae), having broadband, higher frequency, low duty cycle calls. Bat activity (number of bat passes) was not significantly influenced by habitat. Total bat activity and activity of both functional groups varied significantly between seasons, being highest in summer and autumn (coinciding with annual peaks in numbers of Twin spotted (*Bathycoelia natalicola*) and Green (*Nezara* spp) Stinkbugs, order Heteroptera, family Pentatomidae, and Macadamia Nut Borer moths, *Cryptophlebia ombrodelta*) and lower in winter and spring. No significant effect of moon phase was detected, either on total activity of bats in macadamia orchards (which is more marked in open-air foragers) may be driven by the seasonal abundance of pest insects such as stinkbugs and Macadamia Nut Borer moths.

Tortosa, P., N. Dsouli, Y. Gomard, B. Ramasindrazana, C.W. Dick and S.M. Goodman. 2013. Evolutionary history of Indian ocean nycteribiid bat flies mirroring the ecology of their hosts. *PloS one* 8(9): e75215. doi: 10.1371/journal.pone.0075215.

Bats and their parasites are increasingly investigated for their role in maintenance and transmission of potentially emerging pathogens. The islands of the western Indian Ocean hold nearly 50 bat species, mostly endemic and taxonomically well studied. However, investigation of associated viral, bacterial, and external parasites has lagged behind. In the case of their ectoparasites, more detailed information should provide insights into the evolutionary history of their hosts, as well as pathogen cycles in these wild animals. Here we investigate species of Nycteribiidae, a family of obligate hematophagous wingless flies parasitizing bats. Using morphological and molecular approaches, we describe fly species diversity sampled on Madagascar and the Comoros for two cave-roosting bat genera with contrasting ecologies: *Miniopterus* and *Rousettus*. Within the sampling area, 11 endemic species of insect-feeding *Miniopterus* occur, two of which are common to Madagascar and Comoros, while fruit-consuming *Rousettus* are represented by one species endemic to each of these zones. Morphological and molecular characterization of flies reveals that nycteribiids associated with *Miniopterus* bats comprise three species largely shared by most host species. Flies of *M. griveaudi*, one of the two bats found on Madagascar and certain islands in the Comoros, belong to the same taxon, which accords with continued over-water population exchange of this bat species and the lack of inter-island genetic structuring. Flies parasitizing *Rousettus* belong to two distinct species, each associated with a single host species, again in accordance with the distribution of each endemic bat species.

Tsagkogeorga, G., J. Parker, E. Stupka, J.A. Cotton and S.J. Rossiter. 2013. Phylogenomic analyses elucidate the evolutionary relationships of bats. *Current Biology* 23(22): 2262–2267. doi: <u>10.1016/j.cub.2013.09.014</u>.

Molecular phylogenetics has rapidly established the evolutionary positions of most major mammal groups, yet analyses have repeatedly failed to agree on that of bats (order Chiroptera). Moreover, the relationship among the major bat lineages has proven equally contentious, with ongoing disagreements about whether echolocating bats are paraphyletic or a true group having profound implications for whether echolocation evolved once or possibly multiple times. By generating new bat genome data and applying model-based phylogenomic analyses designed to accommodate heterogeneous evolutionary processes, we show that-contrary to recent suggestions-bats are not closely related to odd-toed ungulates but instead have a more ancient origin as sister group to a large clade of carnivores, ungulates, and cetaceans. Additionally, we provide the first genome-scale support showing that laryngeal echolocating bats are not a true group and that this paraphyly is robust to their position within mammals. We suggest that earlier disagreements in the literature may reflect model misspecification, long-branch artifacts, poor taxonomic coverage, and differences in the phylogenetic markers used. These findings are a timely reminder of the relevance of experimental design and careful statistical analysis as we move into the phylogenomic era.

Notice Board

Conferences



1st International Conference on the Biodiversity of the Congo Basin

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

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

Further information: <u>www.congobiodiv.org/en</u>

AFRICAN SMALL MAMMAL SYMPOSIUM

To be held in: Antananarivo, Madagascar, 12-18 April 2015 Further information: <u>sgoodman@fieldmuseum.org</u>

17TH INTERNATIONAL BAT RESEARCH CONFERENCE

To be held in: Durban, South Africa, 2016

Opportunities

AMERICAN SOCIETY OF MAMMALOGISTS – AFRICAN GRADUATE RESEARCH FUND

The American Society of Mammalogists has recently established a program to fund African nationals in studying mammals in their countries of origin. The intent is to help promote the science of mammalogy in Africa, a continent with exceptional mammalian diversity but lacking in adequate resources for training and educating young professionals. This program, the African Graduate Research Fund, supports African graduate students who show promise of becoming leaders of the next generation of mammalogists.

Further information can be found at: <u>http://mammalogy.org/committees/african-graduate-student-fund#tab1</u>.

Recent Literature / Notice Board

AMERICAN SOCIETY OF MAMMALOGISTS – SPONSORED MEMBERSHIP

The American Society of Mammalogists (ASM) has developed a program to provide the opportunity for young individuals who show promise in the field of mammalogy, in this case African nationals but they can be from any developing country, and may be eligible for a sponsored membership in the American Society of Mammalogists.

If you know of a young promising individual who you believe would benefit from membership in the ASM, send the name and contact information to Dr. Ricardo Ojeda (*rojeda@mendoza-conicet.gob.ar*) or Duane A. Schlitter (*happygd@suddenlink.net*). They will contact the person and ascertain if sponsored membership is suitable.

Call for contributions

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

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

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

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

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

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

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

African Bat Conservation News Project Cycle

Issues will be published Quarterly (January, April, July, October). Deadlines for scientific contributions (1 November, 1 February, 1 May, 1 August). Deadlines for non-scientific contributions (1 December, 1 March, 1 June, 1 September).

Non scientific contributions should be sent to the *Editor* while scientific contributions should be sent to the *Scientific Editor*. Notes to authors are available at *www.africanbats.org* or download PDF.

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