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Above: An adult Trident Leaf-nosed Bat (*Cloeotis percivali*) caught at Gatkop Cave, Limpopo Province, South Africa, January 2013.

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Observations, Discussions and Updates



AfriBats – a citizen-science project documenting bat distributions in Africa and surrounding islands

Aims: The bat fauna of Africa and surrounding islands boasts nearly 300 species, but the distributions of many species are poorly known. Despite the crucial role of bats as pollinators and seed dispersers of plants as well as predators of insects, one-fifth of the bat species in Africa are threatened, and populations are declining due to habitat loss, disturbance and destruction of roost sites, hunting for bushmeat, land use, and pesticides. AfriBats seeks to mobilize both amateur and professional knowledge through the iNaturalist platform at <www.inaturalist.org/projects/afribats>. These data will be used for scientific projects and informed conservation actions, which require

robust data on the distributions of bat species.

Features

- Checklist: a list of all species known from the area of interest, with links to individual taxon pages.
- Taxon pages: individual pages summarizing information from various sources such as IUCN Red List status, distribution range (with observations superimposed), Wikipedia articles.
- Journal: occasional updates, highlighting observations of particular significance (for instance substantial range extensions, first records for countries), and news on the general development of the project.

Functionality

- Get identifications support and feed-back from the AfriBats community. For instance, your observation initially identified to genus or family level can be refined by the community to species level.
- Identotron – a tool suggesting potential identifications, e.g. all species of a genus occurring in the region around the observation, which is based on IUCN range maps.
- Locate your observation with a mapping tool. You can also enter geographic coordinates if these are known, e.g. from a GPS.
- Add natural history data such as observation, measurements, sex, breeding information.
- Access your own pictures on Flickr, Picasa, and Facebook by linking your accounts, and chose pictures on these sites for your observations on AfriBats.
- Use apps for iPhone and Android smart phones.

Users can specify the copyright licence for their pictures, and if they decide to choose a [Creative Commons-license](http://creativecommons.org/licenses/by/4.0/), the pictures will be further shared with the [Encyclopedia of Life](http://eol.org/) (EoL). Eventually data will be also shared with the [Global Biodiversity Information Facility](http://gbif.org/) (GBIF). If users are concerned about copyright infringement, they might want to add a copyright note on the picture before sharing it through iNaturalist.

Join the network now! You can sign up as a new user, or sign in with your Google-, Facebook-, Flickr-, Yahoo- or Twitter-accounts. Then chose "Add observation" under <www.inaturalist.org/projects/afribats>, upload one or several pictures for this observation from your hard drive, or select them from your Flickr-, Facebook- or Picasa-folders, locate the observation on the map (or enter coordinates), provide date of observation, and save the new contribution with your identification. You can provide additional data such as a general description of the observation or more structured data (habitat, count, sex, age, forearm length, body mass).

You can also support the project by telling your friends and colleagues about AfriBats, and by spreading the word on social media and networks.

The project is endorsed by the [IUCN Bat Specialist Group](http://www.iucn.org/) and [Bat Conservation International](http://www.batcon.org/).



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RECENT LITERATURE

NEWSLETTER

Congo Biodiversity Initiative Newsflash

The Congo Biodiversity Initiative Newsflash is published whenever the need arises to inform the biodiversity research community on new developments in biodiversity related matters in the Congo Basin. The Congo Biodiversity Initiative is an initiative of the Consortium Congo 2010 and is supported by the Belgian Development Cooperation and the Belgian Science Policy.

Please consult www.congobiodiv.org for more information.

PUBLISHED PAPERS

AMMAN, B.R., CARROLL, S.A., REED, Z.D., SEALY, T.K., BALINANDI, S., SWANEPOEL, R., KEMP, A., ERICKSON, B.R., COMER, J.A., CAMPBELL, S., CANNON, D.L., KHRISTOVA, M.L., ATIMNEDI, P., PADDOCK, C.D., KENT CROCKETT, R.J., FLIETSTRA, T.D., WARFIELD, K.L., UNFER, R., KATONGOLE-MBIDDE, E., DOWNING, R., TAPPERO, J.W., ZAKI, S.R., ROLLIN, P.E., KSIAZEK, T.G., NICHOL, S.T. and TOWNER, J.S., 2012. Seasonal pulses of Marburg virus circulation in juvenile *Rousettus aegyptiacus* bats coincide with periods of increased risk of human infection. *PLoS Pathogens* 8(10): e1002877. DOI: [10.1371/journal.ppat.1002877](https://doi.org/10.1371/journal.ppat.1002877)

Marburg virus (family Filoviridae) causes sporadic outbreaks of severe hemorrhagic disease in sub-Saharan Africa. Bats have been implicated as likely natural reservoir hosts based most recently on an investigation of cases among miners infected in 2007 at the Kitaka mine, Uganda, which contained a large population of Marburg virus-infected *Rousettus aegyptiacus* fruit bats. Described here is an ecologic investigation of Python Cave, Uganda, where an American and a Dutch tourist acquired Marburg virus infection in December 2007 and July 2008. More than 40,000 *R. aegyptiacus* were found in the cave and were the sole bat species present. Between August 2008 and November 2009, 1,622 bats were captured and tested for Marburg virus. Q-RT-PCR analysis of bat liver/spleen tissues indicated ~2.5% of the bats were actively infected, seven of which yielded Marburg virus isolates. Moreover, Q-RT-PCR-positive lung, kidney, colon and reproductive tissues were found, consistent with potential for oral, urine, fecal or sexual transmission. The combined data for *R. aegyptiacus* tested from Python Cave and Kitaka mine indicate low level horizontal transmission throughout the year. However, Q-RT-PCR data show distinct pulses of virus infection in older juvenile bats (~six months of age) that temporarily coincide with the peak twice-yearly birthing seasons. Retrospective analysis of historical human infections suspected to have been the result of discrete spillover events directly from nature found 83% (54/65) events occurred during these seasonal pulses in virus circulation, perhaps demonstrating periods of increased risk of human infection. The discovery of two tags at Python Cave from bats marked at Kitaka mine, together with the close genetic linkages evident between viruses detected in geographically distant locations, are consistent with *R. aegyptiacus* bats existing as a large meta-population with associated virus circulation over broad geographic ranges. These findings provide a basis for developing Marburg hemorrhagic fever risk reduction strategies.

ANDRIANAIVOARIVELO, R.A., JENKINS, R.K.B., PETIT, E.J., RAMILIJAONA, O., RAZAFINDRAKOTO, N. and RACEY, P.A., 2012. *Rousettus madagascariensis* (Chiroptera: Pteropodidae) shows a preference for native and commercially unimportant fruits. *Endangered Species Research* 19(1): 19–27. DOI: [10.3354/esr00441](https://doi.org/10.3354/esr00441)

Flight cage choice experiments carried out over 4 mo demonstrated that a Malagasy fruit bat, *Rousettus madagascariensis* G. Grandidier, 1928, prefers native or introduced fruit of no commercial value (*Ficus polita*, *Syzygium jambos* and *S. malaccense*) to commercially important fruits (*Litchi chinensis* and *Diospyros kaki*). We presented 10 fruit species to the bats: one native (*F. polita*) and the remainder introduced, 3 of which are commercially important. Most bats responded to fruit presented in a flight cage. Bats swallowed fruit juice and pulp and spat out the fibre of all fruit species provided except *L. chinensis* and *Eugenia jambolana*, the flesh of which was swallowed. Chemical composition was the most important determinant of selection by bats. Feeding preference was evidenced by large amounts of chewed pulp, repeated visits to the same fruits and more intensive feeding on lipid- and calcium-rich fruit species. Although commercially important fruit such as *L. chinensis* and *D. kaki* tended to have higher fructose content than other species, our results indicate that lipid and calcium content were more important in fruit selection. We suggest that maintaining natural food availability in humid forests and providing alternative sources of fruit (e.g. *Syzygium* spp.) may contribute to limiting the damage caused by *R. madagascariensis* to commercially important crops.

BENDA, P., VALLO, P., HULVA, P. and HORÁČEK, I., 2012. The Egyptian fruit bat *Rousettus aegyptiacus* (Chiroptera: Pteropodidae) in the Palaearctic: Geographical variation and taxonomic status. *Biologia* 67(6): 1230–1244. DOI: [10.2478/s11756-012-0105-y](https://doi.org/10.2478/s11756-012-0105-y)

Two metrically defined subspecies have traditionally been recognised within the Palaearctic distribution range of the Egyptian fruit bat *Rousettus aegyptiacus*; the larger *R. a. aegyptiacus* in Egypt and the northern part of the Middle East and the smaller *R. a. arabicus* in the southern Middle East. An extensive material of *R. aegyptiacus* from all parts of this area, i.e. the Levant (incl. Turkey and Cyprus), Egypt (incl. Sinai), northern Sudan, Yemen, Oman, Iran, and Pakistan, as well as comparative samples from its sub-Saharan range, were tested using both morphological and genetic approaches in order to revise the species' taxonomic status. The results indicated

two possible processes, depending on the method used. Genetic analysis of the mitochondrial genome (nd1 and cyt b) indicated low variation (< 2.0% of genetic distance) and lack of geographical structure while morphometric analysis indicated significant metric differences. Two basic size morphotypes were found within the Palaearctic range, with a rather mosaic-like geographical distribution and a lack of clear size distinction between the two categories, though intermediate types were detected. Thus, we suggest that all Palaearctic populations of *R. aegyptiacus* represent one form, the nominotypical subspecies, which is uniform in genetic traits but plastic in metric traits.

CLAUSS, M. and PAGLIA, D.E., 2012. Iron storage disorders in captive wild mammals: The comparative evidence. *Journal of Zoo and Wildlife Medicine* 43(3S): S6–S18. DOI: [10.1638/2011-0152.1](https://doi.org/10.1638/2011-0152.1)

Excessive burden of iron, or iron storage disease (ISD), has been reported in a large variety of captive mammal species, including browsing rhinoceroses; tapirs; fruit bats; lemurs; marmosets and some other primates; sugar gliders; hyraxes; some rodents and lagomorphs; dolphins; and some carnivores; including procyonids and pinnipeds. This report collates the comparative evidence for species' susceptibility, recognizing that the data for mammal species are limited. Differences reported in the occurrence of ISD between facilities, or within facilities over periods that span management changes, have been reported in individual cases but are underused in ISD research. Given the species composition, the hypothesis that evolutionary adaptations to the iron content and availability in the natural diet determine a species' susceptibility to ISD (in the face of deviating iron content and availability in diets offered in captivity) seems plausible in many cases. But exceptions, and additional species putatively susceptible based on this rationale, should be investigated. Whereas screening for ISD should be routine in zoo animal necropsy, screening of live individuals may be implemented for valuable species, to decide on therapeutic measures such as chelator application or phlebotomy. Whatever the reasons for ISD susceptibility, reducing dietary iron levels to maintenance requirements of the species in question seems to be a logical, preventive measure.

CORY TOUSSAINT, D. and MCKECHNIE, A.E., 2012. Interspecific variation in thermoregulation among three sympatric bats inhabiting a hot, semi-arid environment. *Journal of Comparative Physiology. B* 182(8): 1129–1140. DOI: [10.1007/s00360-012-0683-6](https://doi.org/10.1007/s00360-012-0683-6)

Bats in hot roosts experience some of the most thermally challenging environments of any endotherms, but little is known about how heat tolerance and evaporative cooling capacity vary among species. We investigated thermoregulation in three sympatric species (*Nycteris thebaica*, *Taphozous mauritanus* and *Sauromys petrophilus*) in a hot, semi-arid environment by measuring body temperature (T_b), metabolic rate and evaporative water loss (EWL) at air temperatures (T_a) of 10–42 °C. *S. petrophilus* was highly heterothermic with no clear thermoneutral zone, and exhibited rapid increases in EWL at high T_a to a maximum of $23.7 \pm 7.4 \text{ mg g}^{-1} \text{ h}^{-1}$ at $T_a \approx 42 \text{ °C}$, with a concomitant maximum T_b of $43.7 \pm 1.0 \text{ °C}$. *T. mauritanus* remained largely normothermic at T_a s below thermoneutrality and increased EWL to $14.7 \pm 1.3 \text{ mg g}^{-1} \text{ h}^{-1}$ at $T_a \approx 42 \text{ °C}$, with a maximum T_b of $42.9 \pm 1.6 \text{ °C}$. In *N. thebaica*, EWL began increasing at lower T_a than in either of the other species and reached a maximum of $18.6 \pm 2.1 \text{ mg g}^{-1} \text{ h}^{-1}$ at $T_a = 39.4 \text{ °C}$, with comparatively high maximum T_b values of $45.0 \pm 0.9 \text{ °C}$. Under the conditions of our study, *N. thebaica* was considerably less heat tolerant than the other two species. Among seven species of bats for which data on T_b as well as roost temperatures in comparison to outside T_a are available, we found limited evidence for a correlation between overall heat tolerance and the extent to which roosts are buffered from high T_a .

CRAVEN, S.A., 2012. Henry Paul William Lyster Jameson , MA, DSc, PhD (1875–1922) – a polymath: zoologist, Transvaal educationist, entrepreneur, civil servant and Marxist. *Transactions of the Royal Society of South Africa* 67(3): 127–134. DOI: [10.1080/0035919X.2012.720300](https://doi.org/10.1080/0035919X.2012.720300)

An account is given of the little known and energetic life of Henry Lyster Jameson, including his substantial contributions to the zoology of Ireland, to his pioneering biospeleology of Derbyshire and Ireland, to the pearl industry, to academic life in Natal and the Transvaal, and to Marxist ideology. He was an intelligent man who successfully overcame chronic ill-health and the academic limitations of Irish birth. He made an important contribution to tertiary education in the Transvaal shortly after the Boer War, and is still known for his researches into the mechanism of formation of natural pearls.

DUVAL, L., MEJEAN, C., MAGANGA, G.D., MAKANGA, B.K., MANGAMA KOUNBA, L.B., PEIRCE, M. A, ARIEY, F. and BOURGAREL, M., 2012. The chiropteran haemosporidian *Polychromophilus melanipherus*: a worldwide species complex restricted to the family Miniopteridae. *Infection, Genetics and Evolution* 12 (7): 1558–1566. DOI: [10.1016/j.meegid.2012.06.006](https://doi.org/10.1016/j.meegid.2012.06.006)

This paper attempts to expand on the current knowledge regarding the evolutionary history of bat haemosporidian parasites. Using modern molecular tools as adjuncts to existing morphological descriptions, our understanding of the diversity of these parasites is discussed. The biogeography and host range distribution together with possible host-parasite interactions remain to be evaluated in more detail. Using a nested-PCR cytochrome *b* mitochondrial gene approach, we established a screening programme and survey of several months duration for haemosporidian parasites in four central African bat species living in an ecological community. The aim of the study was to describe parasites morphologically and molecularly, together with parasite prevalence variations over time, and evaluate parasite host-specificity in these sympatric cave bats. Over the survey period, *Polychromophilus melanipherus* was the only haemosporidian parasite identified in *Miniopterus inflatus*, with a continuous molecular prevalence of at least 60%. Molecular phylogenetic analyses show that *P. melanipherus* is a monophyletic group infecting *Miniopterus* bats which is, a sister group to *P. murinus* and *Polychromophilus* spp. This monophyletic group is composed of different *cyt b* haplotypes molecularly distantly related (but morphologically similar), circulating without geographic or host species distinction. This suggests that *P. melanipherus* is a species complex restricted to the family Miniopteridae. The phylogenetic analysis confirms that *Polychromophilus* parasites are distributed worldwide and supports the view that they are more closely related to avian haemosporidian parasites.

GOODMAN, S.M., PUECHMAILLE, S.J., FRIEDLI-WEYENETH, N., GERLACH, J., RUEDI, M., SCHOEMAN, M.C., STANLEY, W.T. and TEELING, E.C., 2012. Phylogeny of the Emballonurini (Emballonuridae) with descriptions of a new genus and species from Madagascar. *Journal of Mammalogy* 93(6): 1440–1455. DOI: [10.1644/11-MAMM-A-271.1](https://doi.org/10.1644/11-MAMM-A-271.1)

Molecular phylogenetic studies suggest that the genus *Emballonura*, a member of the Old World tribe Emballonurini (Family Emballonuridae), is paraphyletic. This genus has a broad distribution across islands in the Indo-Pacific, southern Asia, and Madagascar. The paraphyly is the result of the genus *Coleura*, known from sub-Saharan Africa, portions of the Arabian Peninsula, Madagascar, and the Seychelles, being embedded between the Malagasy and Asian/Indo-Pacific clades of *Emballonura*, and the latter clade has priority for the use of the name. To resolve this situation, we propose a new genus for the Malagasy *Emballonura* clade. Furthermore, with greater molecular sampling of *Coleura* across portions of its range in association with morphological and bioacoustical characters, we are able to resolve aspects of the phylogenetic history and species limits of this genus. *Coleura* contains two well supported clades, including *C. afra* from mainland Tanzania and the offshore island of Pemba and a sister clade composed of *C. cf. afra* from Madagascar and *C. seychellensis* from the Seychelles. The average genetic distance between animals from Madagascar and the Seychelles is 6%, whereas Pemba/Tanzania and Madagascar is 10%. Because of the paraphyletic relationship of populations of *C. afra* with respect to *C. seychellensis*, we describe a new species of *Coleura* from Madagascar.

HAYMAN, D.T.S., FOOKS, A.R., ROWCLIFFE, J.M., MCCREA, R., RESTIF, O., BAKER, K.S., HORTON, D.L., SUU-IRE, R., CUNNINGHAM, A.A. and WOOD, J.L.N., 2012. Endemic Lagos bat virus infection in *Eidolon helvum*. *Epidemiology and Infection* 140: 2163–2171. DOI: [10.1017/S0950268812000167](https://doi.org/10.1017/S0950268812000167)

Phylogenetic analyses suggest lyssaviruses, including Rabies virus, originated from bats. However, the role of bats in the maintenance, transmission and evolution of lyssaviruses is poorly understood. A number of genetically diverse lyssaviruses are present in Africa, including Lagos bat virus (LBV). A high seroprevalence of antibodies against LBV was detected in *Eidolon helvum* bats. Longitudinal seroprevalence and age-specific seroprevalence data were analysed and capture-mark-recapture (CMR) analysis used to follow 98 bats over 18 months. These data demonstrate endemic infection, with evidence of horizontal transmission, and force of infection was estimated for differing age categories. The CMR analysis found survival probabilities of seronegative and seropositive bats were not significantly different. The lack of increased mortality in seropositive animals suggests infection is not causing disease after extended incubation. These key findings point towards acute transmission of bat lyssaviruses in adapted bat hosts that occurs at a far higher rate than the occurrence of disease.

HULVA, P., MAREŠOVÁ, T., DUNDAROVA, H., BILGIN, R., BENDA, P., BARTONIČKA, T. and HORÁČEK, I., 2012. Environmental margin and island evolution in Middle Eastern populations of the Egyptian fruit bat. *Molecular Ecology* 21(24): 6104–6116. DOI: [10.1111/mec.12078](https://doi.org/10.1111/mec.12078)

Here, we present a study of the population genetic architecture and microevolution of the Egyptian fruit bat (*Rousettus aegyptiacus*) at the environmental margins in the Middle East using mitochondrial sequences and nuclear microsatellites. In contrast to the rather homogenous population structure typical of cave-dwelling bats in climax tropical ecosystems, a relatively pronounced isolation by distance and population diversification was observed. The evolution of this pattern could be ascribed to the complicated demographic history at higher latitudes related to the range margin fragmentation and complex geomorphology of the studied area. Lineages from East Africa and Arabia show divergent positions. Within the northwestern unit, the most marked pattern of the microsatellite data set is connected with insularity, as demonstrated by the separate status of populations from Saharan oases and Cyprus. These demes also exhibit a reduction in genetic variability, which is presumably connected with founder effects, drift and other potential factors related to island evolution as site-specific selection. Genetic clustering indicates a semipermeability of the desert barriers in the Sahara and Arabian Peninsula and a corridor role of the Nile Valley. The results emphasize the role of the island environment in restricting the gene flow in megabats, which is also corroborated by biogeographic patterns within the family, and suggests the possibility of nascent island speciation on Cyprus. Demographic analyses suggest that the colonization of the region was connected to the spread of agricultural plants; therefore, the peripatric processes described above might be because of or strengthened by anthropogenic changes in the environment.

KEARNEY, T.C. and SEAMARK, E.C.J., 2012. Report for Shangoni Management Services Pty Ltd. Assessment of the bats of Gatkop cave, and possible mitigation measures. *Africanbats.org Technical Report* 1/2012: i–v + 1–47 pp. Available at: http://www.shangoni.co.za/Cms_Data/Contents/shangoniDB/Media/documents/addendum/Addendum%20A-%20Assessment%20of%20the%20bats%20at%20Gatkop%20Cave.pdf

KOBAYASI, K.I., HIRYU, S., SHIMOZAWA, R. and RIQUIMAROUX, H., 2012. Vocalization of echolocation-like pulses for interindividual interaction in horseshoe bats (*Rhinolophus ferrumequinum*). *The Journal of the Acoustical Society of America* 132(5): EL417–422. DOI: [10.1121/1.4757695](https://doi.org/10.1121/1.4757695)

Although much is known about the echolocation of horseshoe bats (*Rhinolophus* spp.), little is known about the characteristics and function of their communication calls. This study focused on a stereotyped behavior of a bat approaching a companion animal in the colony, and examined their interaction and vocalization during this behavior. The bats emit echolocation-like vocalizations when approaching each other and these vocalizations contain a “buildup” pulse sequence, in which the frequency of the pulse increases gradually to normal echolocation pulse frequencies. The results suggest that the echolocation-like pulses serve an important role in communication within the colony.

LIMA, L., SILVA, F.M. DA, NEVES, L., ATTIAS, M., TAKATA, C.S. A, CAMPANER, M., DE SOUZA, W., HAMILTON, P.B. AND TEIXEIRA, M.M.G., 2012. Evolutionary insights from bat Trypanosomes: morphological, developmental and phylogenetic evidence of a new species, *Trypanosoma (Schizotrypanum) erneyi* sp. nov., in African bats closely related to *Trypanosoma (Schizotrypanum) cruzi* and allied species. *Protist* 163(6): 856–72. DOI: [10.1016/j.protis.2011.12.003](https://doi.org/10.1016/j.protis.2011.12.003)

Parasites of the genus *Trypanosoma* are common in bats and those of the subgenus *Schizotrypanum* are restricted to bats throughout the world, with the exception of *Trypanosoma (Schizotrypanum) cruzi* that also infects other mammals and is restricted to the American Continent. We have characterized trypanosome isolates from Molossidae bats captured in Mozambique, Africa. Morphology and behaviour in culture, supported by phylogenetic inferences using SSU (small subunit) rRNA, gGAPDH (glycosomal glyceraldehyde 3-phosphate dehydrogenase) and *Cyt b* (cytochrome *b*) genes, allowed to classify the isolates as a new *Schizotrypanum* species named *Trypanosoma (Schizotrypanum) erneyi* sp. nov. This is the first report of a *Schizotrypanum* species from African bats cultured, characterized morphologically and biologically, and positioned in phylogenetic trees. The unprecedented finding of a new species of the subgenus *Schizotrypanum* from Africa that is closest related to the America-restricted *Trypanosoma (Schizotrypanum) cruzi marinkellei* and *T. cruzi* provides new insights into the origin and evolutionary history of *T. cruzi* and closely related bat trypanosomes. Altogether, data from our study support the hypothesis of an ancestor trypanosome parasite of bats evolving to infect other mammals, even humans, and adapted to transmission by triatomine bugs in the evolutionary history of *T. cruzi* in the New World.

OLUDURO, A.O., 2012. Antibiotic-resistant commensal *Escherichia coli* in faecal droplets from bats and poultry in Nigeria. *Veterinaria Italiana* 48(3): 297–308. Available at: <http://www.ncbi.nlm.nih.gov/pubmed/23038076>

The prevalence of antibiotic resistance and plasmid carriage among commensal faecal *Escherichia coli* isolates of bats, broilers and free-range chickens in Ile-Ife, Osun State, Nigeria was studied. A total of 125 *E. coli* isolates were recovered from the fresh faecal samples of bats, broilers and free-range chickens on eosin methylene blue agar plates and characterised using standard biochemical tests. The susceptibility of the isolates to antibiotics was performed using the disk diffusion method. All isolates developed resistance to antibiotics to varying degrees; resistance to augumentin, amoxicillin and tetracycline was significantly higher ($p < 0.05$), compared to the other antibiotics. The lowest resistance was recorded with ofloxacin, ciprofloxacin and pefloxacin in bats and free-range isolates. In general, resistance was higher ($p < 0.05$) in broilers than in free-range isolates, but was comparable in bat isolates ($p > 0.05$) with the exception of ciprofloxacin, pefloxacin gentamicin and ofloxacin. A total of 90% of the bat isolates developed multiple antibiotic resistance with 28 multiple antibiotic resistance patterns. The free-range chicken and broiler isolates displayed 10 and 38 multiple antibiotic resistance patterns, respectively. Resistance was mostly plasmid-mediated with molecular weights ranging between 0.91 kb and 40.42 kb. Antibiotic resistance and plasmid carriage among the commensal *E. coli* isolates studied was relatively high and may be implicated in zoonotic infections.

PATTERSON, B.D. and WEBALA, P.W., 2012. Keys to the Bats (Mammalia: Chiroptera) of East Africa. *Fieldiana Life and Earth Sciences* 6: 1–60. DOI: [10.3158/2158-5520-12.6.1](https://doi.org/10.3158/2158-5520-12.6.1)

Keys and ancillary information are provided to summarize understanding of the diversity of bats (Mammalia: Chiroptera) in East Africa. We reviewed literature and online databases to aid identification of 145 species of bats known to inhabit Kenya, Tanzania, Burundi, Rwanda, and Uganda. National tallies of species were as follows: Kenya, 108; Tanzania, 105; Uganda, 98; Rwanda, 49; and Burundi, 33. Kenya, Tanzania, and Uganda harbor three of Africa's four richest known bat faunas, but all are incompletely known. Ordination analysis via multidimensional scaling suggests that the East African bat fauna shares elements with those in North Africa, West Africa, and South Africa. We constructed keys to species, drawing from the literature and modifying or expanding them to suit the East African bat fauna. Insofar as possible, we used characters that are visible externally or through cursory cranial or dental inspection. The keys are organized taxonomically: an initial key to the 10 families of bats in East Africa directs the user to separate keys for each family and, in the case of Molossidae and Vespertilionidae, to separate keys for the more diverse genera. Each key is flanked by a brief introduction, a measurement table containing the ranges of various external and cranial measurements (in some cases augmented by salient diagnostic characters), and individual species accounts. The latter contain scientific and common names, type locality and description, geographic range, and current conservation status as determined by IUCN in 2011. Species of certain vespertilionids are too subtly distinguished and/or incompletely documented to be identified with our keys; additional studies of tragus size and shape, bacular morphology, and call notes will be needed to resolve these species. We conclude with accounts for species that we excluded from the East African fauna (with our rationales) and a list of species that may eventually be added to the East African fauna.

PAWESKA, J.T., JANSEN VAN VUREN, P., MASUMU, J., LEMAN, P.A., GROBBELAAR, A.A., BIRKHEAD, M., CLIFT, S., SWANEPOEL, R. and KEMP, A., 2012. Virological and serological findings in *Rousettus aegyptiacus* experimentally inoculated with vero cells-adapted Hogan strain of Marburg virus. *PloS one* 7(9): e45479. DOI: [10.1371/journal.pone.0045479](https://doi.org/10.1371/journal.pone.0045479)

The Egyptian fruit bat, *Rousettus aegyptiacus*, is currently regarded as a potential reservoir host for Marburg virus (MARV). However, the modes of transmission, the level of viral replication, tissue tropism and viral shedding pattern remains to be described. Captive-bred *R. aegyptiacus*, including adult males, females and pups were exposed to MARV by different inoculation routes. Blood, tissues, feces and urine from 9 bats inoculated by combination of nasal and oral routes were all negative for the virus and ELISA IgG antibody could not be demonstrated for up to 21 days post inoculation (p.i.). In 21 bats inoculated by a combination of intraperitoneal/subcutaneous route, viremia and the presence of MARV in different tissues was detected on days 2-9 p.i., and IgG antibody on days 9-21 p.i. In 3 bats inoculated subcutaneously, viremia was detected on days 5 and 8 (termination of experiment), with virus isolation from different organs. MARV could not be detected in urine, feces or oral swabs in any of the 3 experimental groups. However, it was detected in tissues which might contribute to horizontal or vertical transmission, e.g. lung, intestines, kidney, bladder, salivary glands, and female reproductive tract. Viremia lasting at least 5 days could also facilitate MARV mechanical transmission by blood sucking arthropods and infections of susceptible vertebrate hosts by direct contact with infected blood. All bats were clinically normal and no gross pathology was identified on post mortem examination. This work confirms the susceptibility of *R. aegyptiacus* to infection with

MARV irrespective of sex and age and contributes to establishing a bat-filovirus experimental model. Further studies are required to uncover the mode of MARV transmission, and to investigate the putative role of *R. aegyptiacus* as a reservoir host.

PODTURKIN, A.A., 2011. Effect of group size on the intensity of exploratory behaviour in Egyptian rousettes (*Rousettus aegyptiacus*). *Plecotus et al.* 14: 60–74. <http://zmmu.msu.ru/bats/biblio/rousett.pdf> (In Russian with English summary)

For the first time, exploratory behaviour of fruit bats (*Rousettus aegyptiacus*) is described in detail. A direct relationship between the intensity of exploratory activity and the group size is shown. To study this dependence, we created in the Moscow Zoo two related groups of rousettes with the opposite changes in the group size (Table 1) and provided them with novel objects. It is proposed to use an assessment of the intensity of exploratory behaviour to determine the sensitivity of fruit bats to stress and the level of their welfare.

ŠEVČÍK, M., BENDA, P. and LUČAN, R.K., 2013. Diptera Pupipara from bats of two large eastern Mediterranean islands, Crete and Cyprus. *Turkish Journal of Zoology* 37(1): 31–37. DOI: [10.3906/zoo-1112-20](https://doi.org/10.3906/zoo-1112-20)

This paper presents a review of records of bat flies (families Nycteribiidae and Streblidae) from Crete and Cyprus, based on new findings and published data. Seven species representing 4 genera belonging to the family Nycteribiidae and 1 species from the family Streblidae from 5 bat species in Crete are reported, and 7 Nycteribiidae species (4 genera) and 1 Streblidae species from 9 bat species in Cyprus are reported. The bat flies *Nycteribia latreillii* (Leach, 1817), *Basilia mongolensis nudior* Hürka 1972, *Penicillidia conspicua* Speiser, 1900, *P. dufourii* Westwood, 1835, and *Brachytarsina flavipennis* Macquart, 1851 are reported from Crete for the first time, and *Phthiridium integrum* (Theodor and Moscona, 1954), *P. dufourii*, and *B. flavipennis* are reported from Cyprus for the first time.

SMAERS, J.B., DECHMANN, D.K.N., GOSWAMI, A., SOLIGO, C. and SAFI, K., 2012. Comparative analyses of evolutionary rates reveal different pathways to encephalization in bats, carnivorans, and primates. *PNAS* 109(44): 18006 – 18011. DOI: [10.1073/pnas.1212181109](https://doi.org/10.1073/pnas.1212181109)

Variation in relative brain size is commonly interpreted as the result of selection on neuronal capacity. However, this approach ignores that relative brain size is also linked to another highly adaptive variable: body size. Considering that one-way tradeoff mechanisms are unlikely to provide satisfactory evolutionary explanations, we introduce an analytical framework that describes and quantifies all possible evolutionary scenarios between two traits. To investigate the effects of body mass changes on the interpretation of relative brain size evolution, we analyze three mammalian orders that are expected to be subject to different selective pressures on body size due to differences in locomotor adaptation: bats (powered flight), primates (primarily arboreal), and carnivorans (primarily terrestrial). We quantify rates of brain and body mass changes along individual branches of phylogenetic trees using an adaptive peak model of evolution. We find that the magnitude and variance of the level of integration of brain and body mass rates, and the subsequent relative influence of either brain or body size evolution on the brain-body relationship, differ significantly between orders and subgroups within orders. Importantly, we find that variation in brain-body relationships was driven primarily by variability in body mass. Our approach allows a more detailed interpretation of correlated trait evolution and variation in the underlying evolutionary pathways. Results demonstrate that a principal focus on interpreting relative brain size evolution as selection on neuronal capacity confounds the effects of body mass changes, thereby hiding important aspects that may contribute to explaining animal diversity.

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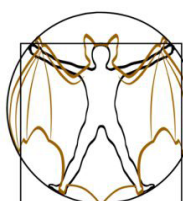
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Further information: www.savetcon.co.za

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