
**Inside this issue:**

**Scientific contributions**
The first record of the African Sheath-tailed Bat *Coleura afrabilateralis* (Peters, 1852) (Mammalia, Chiroptera) in Cameroon with information on its ecology

**Recent Literature**
Papers

**Notice Board**
Conferences

Call for contributions

Download and subscribe to African Bat Conservation News published by AfricanBats at: [www.africanbats.org](http://www.africanbats.org)

The views and opinions expressed in articles are no necessarily those of the editor or publisher. Articles and news items appearing in African Bat Conservation News may be reprinted, provided the author’s and newsletter reference are given.
THE FIRST RECORD OF THE AFRICAN SHEATH-TAILED BAT *Coleura afra* (PETERS, 1852) (MAMMALIA, CHIOPTERA) IN CAMEROON WITH INFORMATION ON ITS ECOLOGY

MATTHEW LEBRETON1,2, ERIC MOISE BAKWO FILS3, JEAN MICHEL TAKUO3 and JOSEPH LE DOUX DIFFO JOSEPH DIFFO LEDOUX1

1 Mosaic, BP 35322, Yaoundé, CAMEROON. 2 Global Viral Cameroon, BP 7039, Yaoundé, CAMEROON. 3 Department of Biological Sciences; Faculty of Sciences; University of Maroua; CAMEROON

*Corresponding author. E-mail address: filbkw27@gmail.com

*KEY WORDS: first record, bat, Coleura afra, Cameroon.*

**Introduction**

With some 1300 species, bats are the second most diverse group of mammals (SIMMONS, 2005). However, knowledge of the central African bat fauna remains sparse and the species occurring in Cameroon are poorly known (BAKWO FILS et al., 2012, 2014). During the last 10 years, Cameroon has received increased attention by bat biologists and recent studies have detected species which were previously not known to be present (SEDLAČEK et al., 2006; BAKWO FILS, 2010; BAKWO FILS et al., 2012, 2014; HASSANIN, 2014). These new records emphasize the need for additional studies in Cameroon, and demonstrate that the local bat fauna is still insufficiently sampled. Here we present another example of a taxon previously unknown from the country.

**Materials and methods**

During an ongoing surveillance visit on 7 December 2012 to a *Rousettus aegyptiacus* roost in Leplikoung (Latitude: 3.6524° N; Longitude: 10.2272° E) in the Littoral Region of Cameroon, we found a colony of about 5,000 *Coleura afra*. The colony was found in a cave in a rocky, forest-covered hill and about 3 km east of the village. The site actually includes two different caves, the larger occupied by the *C. afra* being about 5-6 m deep and 15 m large at the opening and narrowing to around 2 m. The cave was formed through fracturing of iron rich rock. The area is covered by lowland rainforest with an annual rainfall of 1600-2500 mm. While rainfall occurs throughout the year, maximum precipitation is recorded in September and minimum in December-January.

Two females were collected with mist nets to confirm identification using the keys of ROSEVEAR (1965), HAYMAN and HILL (1971) and MONADJEM et al. (2010). External characteristics of the voucher specimens were measured with a vernier caliper. The specimens are in the collection of Global Viral Cameroon (GV), specimen numbers: GV-CM-ECO06308 (Figure 1) and GV-CM-ECO06309 (Figure 2).

**Discussion**

We identified the animals collected in the Leplikoung cave as *C. afra* based on morphometric characters. In our specimens, the dorsal fur is deep sepia-brown and paler below. The forearm (FA) measurements of the voucher specimens are as follows: GV-CM-ECO06308 = 49.3 mm; GV-CM-ECO06309 = 51.6 mm.

The Emballonuridae are distinguished from all other small insect-eating bats by their characteristic tail which emerges from the interfemoral membrane before reaching the fringe (TAYLOR, 2000, MONADJEM et al., 2010). *Coleura afra* is the smallest species of the family in Africa and is distinguished from all other Emballonuridae by the absence of a gular sack and radiocarpal pouches, a body weight of 10-12 g, its deep brown fur which is paler at the base than at the tip, its smaller size (FA < 55 mm) and the three pairs of lower incisors (MONADJEM et al., 2010).

*Coleura afra* is the only *Coleura* known from mainland Africa and one of three members of the genus, which also includes *C. kibomalandy* Goodman et al., 2012 from Madagascar and *C. seychellensis* Peters, 1868 from the Seychelles. The measurements of the Cameroon specimens do not exceed the variation range reported for *C. afra* by ROSEVEAR (1965): HAYMAN and HILL (1971); DUNLOP (1997), PATTERSON and WEBALA (2012).

*Coleura afra* is ranked as Least Concern (LC) in the IUCN Redlist (MICKLEBURGH et al., 2008). Before its discovery in Cameroon, this species was known from scattered localities across sub-Saharan Africa: in the west from Ghana, Guinea Bissau, Togo, Benin, and Nigeria; in the east from western Central African Republic, Democratic Republic of Congo, Sudan, South Sudan, Somalia, Tanzania, Uganda and Kenya; in the south from Angola and Mozambique (ROSEVEAR, 1965; DUNLOP, 1997; GOODMAN et al., 2008; SIMMONS, 2005; SINSIN and KAMPMMANN, 2010; HAPPOLD, 2013; ACR, 2013). Along with a recently reported record of this species from Gabon (MAGANGA et al., 2011) this record fills an important distribution gap between the west and east African records (see Figure 3).
The few records of this species in mainland Africa have been from rocky habitats in woodland savannas, drier bushlands, thicket-scrub and grassy steppes (HAPPOLD, 2013). ROSEVEAR (1965) suggests that this species probably occurs in more varied vegetation types which have suitable day roost sites. The present record comes from a lowland rainforest area and confirms this view.

We could not determine how long C. afra had occupied the site, but they were not observed during a previous visit to the cave on 29 March 2009, when many hundreds of R. aegyptiacus were found and no other bat species was observed. We returned to the cave on 7 December 2012 and found only a few individuals of R. aegyptiacus and many C. afra. During our last visit on 8 June 2013 no C. afra were found, but thousands of R. aegyptiacus. While C. afra have been reported as a non-migratory species (McWILLIAM, 1987), our observations suggest that this species may have seasonal movements, a suggestion also supported by other authors (HAPPOLD 1987; SKINNER and SMITHERS, 1990).

Conclusion
Despite considerable work on Cameroonian bats, the recent addition of several taxa previously unknown from the country underlines that additional work is needed to have a good understanding of the diversity of species present in the country. Further, additional research is urgently needed to understand the role of bats in disease emergence and pest management ecology.

Acknowledgements
The Ministry of Forestry and Wildlife and the Ministry of Scientific Research and Innovation in Cameroon provided permits for this research. The work was conducted by Global Viral under the coordination of Ubald Tamoufe, in partnership with the Military Health Research Center (CRESAR) and with funding from Metabiota Inc. This research was made possible by the generous support of the American people through the United States Agency for International Development (USAID) Emerging Pandemic Threats PREDICT program. The contents are the responsibility of the authors and do not necessarily reflect the views of USAID or the United States Government.

Bibliography
The continued detection of zoonotic viral infections in bats has led to the microbial fauna of these mammals being studied at a greater depth. This has shed light on the role of bats as potential reservoirs of emerging viruses, especially lyssaviruses. Bats have been shown to be hosts for viruses that can cause serious diseases in humans, such as Marburgvirus and Lyssavirus (rabies virus).

Recent literature


Formerly thought to be a strictly insectivorous trawling bat, recent studies have shown that Myotis capaccinii also preys on fish. To determine if differences exist in bat flight behaviour, prey handling, and echolocation characteristics when catching fish and insects of different sizes, we conducted a field experiment focused on the last stage of prey capture. We used synchronized video and scientific contribution to determine if differences exist in bat flight behaviour, prey handling, and echolocation characteristics when catching fish and insects of different sizes. Insectivorous trawling bats are known to change their echolocation strategies depending on the size and type of prey they are catching. These studies provide insights into how bats use their echolocation abilities to effectively capture a diverse range of prey items.


This study highlights the importance of considering the role of bats as potential reservoirs of zoonotic viruses, particularly in the context of mining operations where bat populations may be disturbed or exterminated.


The continued detection of zoonotic viral infections in bats has led to the microbial fauna of these mammals being studied at a greater depth. This has shed light on the role of bats as potential reservoirs of emerging viruses, especially lyssaviruses. Bats have been shown to be hosts for viruses that can cause serious diseases in humans, such as Marburgvirus and Lyssavirus (rabies virus).


This study provides an overview of the current knowledge regarding the role of bats as potential reservoirs of zoonotic viruses, particularly lyssaviruses, and highlights the need for further research to understand the ecological and epidemiological implications of these infections.
level than ever before. Whilst numerous pathogens have been discovered in bat species, infection with lyssaviruses is of particular significance from a zoonotic perspective as, where human infection has been reported, it is invariably fatal. Here we review the detection of lyssaviruses within different bat species and overview what is understood regarding their maintenance and transmission following both experimental and natural infection. We discuss the relevance of these pathogens as zoonotic agents and the threat of newly discovered viruses to human populations.


Rodents have long been recognized as the principal reservoirs of hantaviruses. However, with the discovery of genetically distinct and phylogenetically divergent lineages of hantaviruses in multiple species of shrews, moles, and insectivorous bats from widely separated geographic regions, a far more complex landscape of hantavirus host distribution, evolution, and phylogeography is emerging. Detailed phylogenetic analyses, based on partial and full-length genomes of previously described rodent-borne hantaviruses and newly detected non-rodent-borne hantaviruses, indicate an Asian origin and support the emerging concept that ancestral non-rodent mammals may have served as the hosts of primordial hantaviruses.


We examined the distribution of *Ficus sycomorus* in relation to the movements and feeding, behavior of two species of epauletted fruit bats in Kruger National Park in order to learn about the scale and tempo of the seed dispersal of this riparian tree. Radio-tagged *Epomophorus crypturus* and *Epomophorus wahlbergi* restricted > 90% of activity within riparian forests having *F. sycomorus* present; whereas, < 10% of activity occurred in thorn thickets where folivory on *Balanites maughami* and frugivory on *Sclerocarya birrea* appeared to offer secondary sources of forage. Bats usually carried figs to foliage perches within 200 m of the fruiting tree before feeding. Within a night, maximum one-way movement was 13.9 km as bats visited 5-4 foraging patches. No significant difference occurred between foraging ranges of *E. wahlbergi* at Skukuza (16.0 ± 3.0 ha) and *E. crypturus* at Shingwedzi (19.9 ± 5.1 ha). However, *E. crypturus* at Babalala had significantly larger mean foraging range (52.4 ± 4.5 ha) than either species elsewhere. Mean foraging range, core use area, and long axis across foraging range of *E. wahlbergi* changed significantly with season, year, and fig abundance. Our study suggests interdependence between *F. sycomorus* and the two species of fruit bats in Kruger National Park with bat movements largely following the distribution of available ripe figs.


The hepatitis B virus (HBV) is a cosmopolitan infectious agent currently affecting over 350 million people worldwide, presently accounting for more than two billion infections. In addition to man, other hepatitis virus strains infect species of several mammalian families of the Primates, Rodentia and Chiroptera orders, in addition to birds. The mounting evidence of HBV infection in African, Asian and neotropical primates draws attention to the potential cross-species, zoonotic transmission of these viruses to man. Moreover, recent evidence also suggests the humans may also function as a source of viral infection to other mammals, particularly to domestic animals like poultry and swine. In this review, we list all evidence of HBV and HBV-like infection of nonhuman mammals and discuss their potential roles as donors or recipients of these viruses to humans and to other closely-related species.


A previous phylogenetic study of bats of the genus *Scotophilus* (house bats) showed deep subdivisions and paraphyletic relationships among populations of *S. dinganii* (four distinct clades) and *S. viridis* (two distinct clades). According to the genetic species concept, these clades may represent distinct species. Herein, we assess morphological differences of specimens of four clades representing hypothesized unrecognized species compared to specimens of nominate *S. dinganii* and *S. viridis*. Statistically significant morphological differences provided characters for accurate diagnosis of each clade. Therefore we recognize and formally describe four new species of sub-Saharan African *Scotophilus* (*Scotophilus andrewreborii* sp. nov., *Scotophilus livingstonii* sp. nov., *Scotophilus ejetai* sp. nov., and *Scotophilus trujilloi* sp. nov.).


Filoviral hemorrhagic fever (FHF) is caused by ebolaviruses and marburgviruses, which both belong to the family Filoviridae. Egyptian fruit bats (*Rousettus aegyptiacus*) are the most likely natural reservoir for marburgviruses and entry into caves and mines that they stay in has often been associated with outbreaks of MVD. On the other hand, the natural reservoir for ebola viruses remains elusive; however, handling of wild animal carcasses has been associated with some outbreaks of EVD. In the last two decades, there has been an increase in the incidence of FHF outbreaks in Africa, some being caused by a newly found virus and some occurring in previously unaffected areas such as Guinea, Liberia and Sierra Leone, in which the most recent EVD outbreak occurred in 2014. Indeed, the predicted geographic distribution of filoviruses and their potential reservoirs in Africa includes many countries in which FHF has not been reported. To minimize the risk of virus dissemination in previously unaffected areas, there is a need for increased investment in health infrastructure in African countries, policies to facilitate collaboration between health authorities from different countries, implementation of outbreak control measures by relevant multi-disciplinary teams and education of the populations at risk.


A previous study investigating potential adult hippocampal neurogenesis in microchiropteran bats failed to reveal a strong presence of this neural trait. As microchiropterans have a high field metabolic rate and a small body mass, it is possible that capture/handling stress may lead to a decrease in the detectable presence of adult hippocampal neurogenesis. Here we looked for evidence of adult hippocampal neurogenesis using immunohistochemical techniques for the endogenous marker doublecortin (DCX) in 10 species of microchiropterans euthanized and perfused at specific time points following capture. Our results reveal that when euthanized and perfused within 15 min of capture, abundant putative adult hippocampal neurogenesis could be detected using DCX immunohistochemistry. Between 15 and 30 min post-capture, the detectable levels of DCX dropped dramatically and after 30 min post-capture, immunohistochemistry for DCX could not reveal any significant evidence of putative adult hippocampal neurogenesis. Thus, as with all other mammals studied to date apart from cetaceans, bats, including both microchiropterans and megachiropterans, appear to exhibit substantial levels of adult hippocampal neurogenesis. The present study underscores the concept that, with laboratory experiments, studies conducted on wild-caught animals need to be cognizant of the fact that acute stress (capture/handling) may induce major changes in the appearance of specific neural traits.


Emerging infectious diseases remain a significant threat to public health. Most emerging infectious disease agents in humans are of zoonotic origin. Bats are important reservoir hosts of many highly lethal zoonotic viruses and have been implicated in numerous emerging infectious disease events in recent years. It is essential to enhance our knowledge and understanding of the genetic diversity of the bat-associated viruses to prevent future outbreaks. To facilitate further research, we constructed the database of bat-associated viruses (DBatVir). Known viral sequences detected in bat samples were manually collected and curated, along with the related metadata, such as the sampling time, location, bat species and specimen type. Additional information concerning the bats, including common names, diet type, geographic distribution and phylogeny were integrated into the database to bridge the gap between virologists and zoologists. The database currently covers >4100 bat-associated animal viruses of 23 viral families detected from 196 bat species in 69 countries worldwide. It provides an overview and snapshot of the current research regarding bat-associated viruses, which is essential now that the field is rapidly expanding. With a user-friendly interface and integrated online bioinformatics tools, DBatVir provides a convenient and powerful platform for virologists and zoologists to analyze the virome diversity of bats, as well as for epidemiologists and public health researchers to monitor and track current and future bat-related infectious diseases. Database URL: [http://www.mgc.ac.cn/DBatVir/](http://www.mgc.ac.cn/DBatVir/).


We screened 217 bats of at least 20 species from 17 locations in Kenya during July and August of 2006 for the presence of adenovirus, rhabdovirus, and paramyxovirus nucleic acids using generic reverse transcription polymerase chain reaction (RT-PCR) and PCR assays. Of 217 bat fecal swabs examined, 4 bats were adenovirus DNA-positive, 11 bats were paramyxovirus RNA-positive, and 2 bats were rhabdovirus RNA-positive. Three bats were coinfected by two different viruses. By sequence comparison and phylogenetic analysis, the Kenya bat paramyxoviruses and rhabdoviruses from this study may represent novel viral lineages within their respective families; the Kenya bat adenoviruses could not be confirmed as novel, because the same region sequences from other known bat adenovirus genomes for comparison were lacking. Our study adds to previous evidence that bats carry diverse, potentially zoonotic viruses and may be coinfected with more than one virus.

The emerging Middle East respiratory syndrome-coronavirus (MERS-CoV) causes lethal respiratory infections mainly on the Arabian Peninsula. The evolutionary origins of MERS-CoV are unknown. We determined the full genome sequence of a CoV directly from fecal material obtained from a South African *Neoromicia capensis* bat (NeoCoV). NeoCoV shared essential details of genome architecture with MERS-CoV. 85% of the NeoCoV genome was identical to MERS-CoV on nucleotide level. Based on taxonomic criteria, NeoCoV and MERS-CoV belonged to one viral species. Presence of a genetically divergent S1 subunit within the NeoCoV Spike gene indicated that intra-Spike recombination events may have been involved in the emergence of MERS-CoV. NeoCoV constitutes a sister taxon to MERS-CoV, placing the MERS-CoV root between a recently-described virus from African camels and all other viruses. This suggests a higher viral diversity in camels than in humans. Together with serologic evidence for widespread MERS-CoV infection in camels sampled up to 20 years back in Africa and the Arabian Peninsula, the genetic data indicates that camels act as sources of virus for humans rather than vice versa. The majority of camels on the Arabian Peninsula is imported from the greater Horn of Africa, where several *Neoromicia* species occur. The acquisition of MERS-CoV by camels from bats might have taken place in Sub-Saharan Africa. Camelds may represent mixing vessels for MERS-CoV and other mammalian CoVs.


*Chrysopteron* Jentink, 1910 is 1 of the 7 subgenera of *Myotis* Kaup, 1829 recognized by Tate that traditionally comprises Asian and African species characterized by conspicuously parti-colored wing membranes. Definition of *Myotis* subgenera has long challenged taxonomists and prior to the present study the systematic status of numerous forms within *Chrysopteron* remained unclear. Following examination of material (including available type specimens) in 21 European, North American, and Asian collections, and using morphological (external, cranial, and dental characters) and genetic data, we evaluate the validity of the *Chrysopteron* subgenus, revise the taxonomy of the named Asian forms, and review their distinguishing characters, distribution, and taxonomic history. We argue that *Chrysopteron* is an available name for a monophyletic “Ethiopian clade” recovered with high support in our analyses, which comprises species characterized by striking reddish or yellowish dorsal fur that strongly differentiates them from congeners. We also determine that *M. formosus sensu lato* contains several morphologically distinct forms, some of which occur in sympatry and some in widely separated localities. A morphological key is provided for all Asian species of *Chrysopteron* revealed by our study: *M. bartelsi* Jentink, 1910 (Java and Bali), *M. formosus* (Hodgson, 1835) (Afghanistan, India, Nepal, China, Taiwan, and Vietnam), *M. hermani* Thomas, 1923 (Sumatra, Thailand, and Malaysia), *M. rufoniger* (Tomes, 1858) (Korea, Japan, China, Taiwan, Laos, and Vietnam), *M. rufopictus* (Waterhouse, 1845) (Philippines), and *M. weberi* (Jentink, 1890) (Sulawesi).


An adult female, intact Egyptian fruit bat (*Rousettus aegyptiacus*) was presented for lethargy, anorexia, and markedly reduced flying activity. Physical and ultrasound examinations were suggestive of an abdominal mass with free fluid within the abdomen. Based on the poor and deteriorating clinical condition of the animal, euthanasia was elected. Gross necropsy revealed an irregular thickening at the root of the mesentery and a diffusely, dark-red liver with rounded hepatic margins. Histologic examination revealed extensive neoplastic effacement of the pancreas with invasion into the surrounding mesentery and mesenteric lymph nodes and metastatic spread to the liver. Based on the morphology of the neoplastic cells, the involvement of the pancreas, and immunohistochemistry, a diagnosis of metastatic pancreatic carcinoma was made. Additionally, two small neoplasms were identified in the lungs. These masses were distinct from the carcinoma, and their morphology was consistent with bronchioalveolar adenomas. This is the first known report of either benign pulmonary lesions or pancreatic carcinomas in the order Chiroptera.


We surveyed the bat fauna of the National Park of Jebel Mghilla (Central Tunisia) in the five main habitats from the lowland to the summit: cultivated area, open juniper (*Juniperus* spp.) forest, Stipa tenacessima steppe, open and dense forest of *Pinus halepensis*, with a special emphasis on water bodies. We mist-netted three bat species: *Eptesicus isabellinus*, *Myotis emarginatus* and *Myotis punicus*. We also identified echolocation calls of Rhinolophus blasii, *Rhinolophus ferrumequinum*, *Rhinolophus hipposideros*, *Tadarida teniotis*, *Miniopterus schreibersii*, *Pipistrellus kuhlii*, Plecotus gaisleri and Hypsugo savii. *Pipistrellus kuhlii* and *E. isabellinus* were the most active and widely distributed species. The bat fauna was richer in the dense and open pine forest than in cultivated area and open juniper forest, but water bodies are also very attractive for bats.


Bats are important components in tropical mammal assemblages. Unravelling the mechanisms allowing multiple syntopic bat species to coexist can provide insights into community ecology. However, dietary information on component species of these assemblages.
is often difficult to obtain. Here we measured stable carbon and nitrogen isotopes in hair samples clipped from the backs of 94 specimens to indirectly examine whether trophic niche differentiation and microhabitat segregation explain the coexistence of 16 bat species at Ankara, northern Madagascar. The assemblage ranged over 4.4‰ in δ¹³C and was structured into two trophic levels with phytophagous Pteropodidae as primary consumers (c.3‰ enriched over plants) and different insectivorous bats as secondary consumers (c.4‰ enriched over primary consumers). Bat species utilizing different microhabitats formed distinct isotopic clusters (metric analyses of δ¹³C–δ¹⁵N bi-plots), but taxa foraging in the same microhabitat did not show more pronounced trophic differentiation than those occupying different microhabitats. As revealed by multivariate analyses, no discernible feeding competition was found in the local assemblage amongst congeneric species as compared with non-congeners. In contrast to ecological niche theory, but in accordance with studies on New and Old World bat assemblages, competitive interactions appear to be relaxed at Ankara and not a prevailing structuring force.


Since the recognition of hantavirus as the agent responsible for haemorrhagic fever in Eurasia in the 1970s and, 20 years later, the discovery of hantavirus pulmonary syndrome in the Americas, the genus Hantavirus has been continually described throughout the World in a variety of wild animals. The diversity of wild animals infected with hantaviruses has only recently come into focus as a result of expanded wildlife studies. The known reservoirs are more than 80, belonging to 51 species of rodents, 7 bats (order Chiroptera) and 20 shrews and moles (order Soricomorpha). More than 80 genetically related viruses have been classified within Hantavirus genus; 25 recognized as human pathogens responsible for a large spectrum of diseases in the Old and New World. In Brazil, where the diversity of mammals and especially rodents is considered one of the largest in the world, 9 hantavirus genotypes have been identified in 12 rodent species belonging to the genus Akodon, Calomys, Holochilus, Oligoryzomys, Oxymycterus, Necromys and Rattus. Considering the increasing number of animals that have been implicated as reservoirs of different hantaviruses, the understanding of this diversity is important for evaluating the risk of distinct hantavirus species as human pathogens.


New bats were recorded from various habitats on the Guinean side of Mount Nimba during two surveys in 2008 and coupled with a cytogenetic survey. A total of 152 specimens comprising 15 species in 12 genera from five families were collected, of which 13 individuals were karyotyped. The most numerous species was Rhinolophus guineensis followed by four fruit bats (Epomops buettikoferi, Lissonycteris angolensis, Roussettus aegyptiacus, Nanonycteris veldkampi). We confirm the presence of Hipposideros lamottei in the mine adits at 1500mas as well as the exceptional diversity of this habitat. First standard karyotypes are provided for Epomops buettikoferi and Nanonycteris intermedia. We also document for the first time karyotypes for West African populations of Mops thyrsoidea, Lissonycteris angolensis and Roussettus aegyptiacus, and cytogenetical comparisons with the existing literature are provided. We add five new species to the list of Guinean Nimba and two to the whole Nimba list (including Liberian side), which now stands at 42 species. This confirms the importance of Mount Nimba as a hotspot of diversity and the necessity to protect it.


Biodiversity hotspots and associated endemism are ideal systems for the study of parasite diversity within host communities. Here, we investigated the ecological and evolutionary forces acting on the diversification of an emerging bacterial pathogen, Leptospira spp., in communities of endemic Malagasy small mammals. We determined the infection rate with pathogenic Leptospira in 20 species of sympatric rodents (subfamily Nesomyinae) and tenrecids (family Tenrecidae) at two eastern humid forest localities. A multilocus genotyping analysis allowed the characterization of bacterial diversity within small mammals and gave insights into their genetic relationships with Leptospira infecting endemic Malagasy bats (family Miniopteridae and Vespertilionidae). We report for the first time the presence of pathogenic Leptospira in Malagasy endemic small mammals, with an overall prevalence of 13%. In addition, these hosts harbour species of Leptospira (L. kirschneri, L. borgpetersenii and L. borgpeterseni group B) which are different from those reported in introduced rats (L. interrogans) on Madagascar. The diversification of Leptospira on Madagascar can be traced millions of years into evolutionary history, resulting in the divergence of endemic lineages and strong host specificity. These observations are discussed in relation to the relative roles of endemic vs. introduced mammal species in the evolution and epidemiology of Leptospira on Madagascar, specifically how biodiversity and biogeographical processes can shape community ecology of an emerging pathogen and lead to its diversification within native animal communities.


The evolutionary fate of chimeric fusion genes may be strongly influenced by their recombinational mode of origin and the nature of functional divergence between the parental genes. In the β-globin gene family of placental mammals, the two postnatally expressed α- and β-globin genes (HBD and HBB, respectively) have a propensity for recombinational exchange via gene conversion and unequal crossing-over. In the latter case, there are good reasons to expect differences in retention rates for the reciprocal HBB/HBD and HBD/HBB fusion genes due to thetasemia pathologies associated with the HBD/HBB “Lepore” deletion mutant in humans. Here, we report a comparative genonomic analysis of the mammalian β-globin gene cluster, which revealed that chimeric HBB/HBD fusion genes originated independently in four separate lineages of laurasiatherian mammals: Eulipotyphlans (shrews, moles, and hedgehogs), carnivores, microchiropteran bats, and cetaceans. In cases where an independently derived “anti-Lepore” duplication mutant has become fixed, the parental HBD and/or HBB genes have typically been inactivated or deleted, so that the newly created HBB/HBD fusion gene is primarily responsible for synthesizing the β-prop subunits of adult and fetal hemoglobin (Hb). Contrary to conventional wisdom that the HBD gene is a vestigial relic that is typically inactivated or expressed at negligible levels, we show that HBD-like genes often encode a substantial fraction (20-100%) of β-chain Hbs in laurasiatherian taxa. Our results indicate that the ascendency or resuscitation of genes with HBD-like coding sequence requires the secondary acquisition of HBD-like promoter sequence via unequal crossing-over or interparalog gene conversion.


With the recent and continuing discovery of further cryptic bat species, it is essential to find morphological species discriminating characteristics. Pipistrellus pipistrellus (common pipistrelle) and Pipistrellus pygmaeus (soprano pipistrelle) have been recognized as separate species since 1997, but no reliable morphological species discriminating trait has yet been found. The most commonly used morphological species discrimination traits are ‘wing vein’ pattern and shape and color of the penis, but these have not been validated on sets of genetically identified specimens. The baculum (os penis) has long been used successfully in species discrimination in bats and other mammals. In this study, we tested the reliability of the established traits and demonstrated how to reliably separate the common pipistrelle and the soprano pipistrelle by simple baculum measurements. The bacula of museum specimens of these two species and of Pipistrellus hanaki were imaged with high-resolution microCT. Several measurements were taken on the size-calibrated volume images, and their value for species discrimination was tested by discriminant analysis with leave-one-out cross validation. We showed that P. pipistrellus and P. pygmaeus specimens can be discriminated by measuring the projected length, height, and width of the baculum (n = 48; all but one classified correctly). Geometric morphometrics was used to analyze and locate variations in baculum shape. Principal component analysis of baculum variation was not sufficient to separate these species. Most of the interspecific variation in baculum shape can be found in the proximal third (the base) of the baculum, and most individual variation can be observed in lateral view, especially in the dorsoventral curve. Quantitative details of morphology are becoming more important to distinguish cryptic species and understand their phylogeographic distributions. The simple baculum measurements can be used to classify single specimens and could be taken without microCT, on a resected baculum.


In 2009, a novel lyssavirus (subsequently named Ikoma lyssavirus, IKOV) was detected in the brain of an African civet (Civettictis civetta) with clinical rabies in the Serengeti National Park of Tanzania. The degree of nucleotide divergence between the genome of IKOV and those of other lyssaviruses predicted antigenic distinction from, and lack of protection provided by, available rabies vaccines. In addition, the index case was considered likely to be an incidental spillover event, and therefore the true reservoir of IKOV remained to be identified. The advent of sensitive molecular techniques has led to a rapid increase in the discovery of novel viruses. Detecting viral sequence alone, however, only allows for prediction of phenotypic characteristics and not their measurement. In the present study we describe the in vitro and in vivo characterization of IKOV, demonstrating that it is (1) pathogenic by peripheral inoculation in an animal model, (2) antigenically distinct from current rabies vaccine strains and (3) poorly neutralized by sera from humans and animals immunized against rabies. In a laboratory mouse model, no protection was elicited by a licensed rabies
vaccine. We also investigated the role of bats as reservoirs of IKOV. We found no evidence for infection among 483 individuals of at least 13 bat species sampled across sites in the Serengeti and Southern Kenya.


The recent discovery of hantaviruses in shrews and bats in West Africa suggests that other genetically distinct hantaviruses exist in East Africa. Genetic and phylogenetic analyses of newfound hantaviruses, detected in archival tissues from the Geata mouse shrew (*Myosorex geata*) and Kilimanjaro mouse shrew (*Myosorex zinki*) captured in Tanzania, expands the host diversity and geographic distribution of hantaviruses and suggests that ancestral shrews and/or bats may have served as the original mammalian hosts of primordial hantaviruses.


Bats are being increasingly recognized as reservoir hosts of highly pathogenic and zoonotic emerging viruses (Marburg virus, Nipah virus, Hendra virus, Rabies virus, and coronaviruses). While numerous studies have focused on the mentioned highly human-pathogenic bat viruses in tropical regions, little is known on similar human-pathogenic viruses that may be present in European bats. Although novel viruses are being detected, their zoonotic potential remains unclear unless further studies are conducted. At present, it is assumed that the risk posed by bats to the general public is rather low. In this review, selected viruses detected and isolated in Europe are discussed from our point of view in regard to their human-pathogenic potential. All European bat species and their roosts are legally protected and some European species are even endangered. Nevertheless, the increasing public fear of bats and their viruses is an obstacle to their protection. Educating the public regarding bat lyssaviruses might result in reduced threats to both the public and the bats.


BACKGROUND: Emerging bacterial zoonoses in bats and rodents remain relatively understudied. We conduct the first comparative host-pathogen coevolutionary analyses of bacterial pathogens in these hosts, using *Bartonella* spp. and *Leptospira* spp. as a model.

METHODOLOGY/PRINCIPAL FINDINGS: We used published genetic data for 51 *Bartonella* genotypes from 24 bat species, 129 *Bartonella* from 38 rodents, and 26 *Leptospira* from 20 bats. We generated maximum likelihood and Bayesian phylogenies for hosts and bacteria, and tested for coevolutionary congruence using programs ParaFit, PACO, and Jane. *Bartonella* spp. and their bat hosts had a significant coevolutionary fit (ParaFitGlobal = 1.9703, P≤0.001; m² global value = 7.3320, P≤0.0001). *Bartonella* spp. and rodent hosts also indicated strong overall patterns of cospeciation (ParaFitGlobal = 102.4409, P≤0.001; m² global value = 86.532, P≤0.0001). In contrast, we were unable to reject independence of speciation events in *Leptospira* and bats (ParaFitGlobal = 0.0042, P = 0.84; m² global value = 4.6310, P = 0.5629). Separate analyses of New World and Old World data subsets yielded results congruent with analysis from entire datasets. We also conducted event-based cophylogeny analyses to reconstruct likely evolutionary histories for each group of pathogens and hosts. *Leptospira* and bats had the greatest number of host switches per parasite (0.731), while *Bartonella* and rodents had the fewest (0.264).

CONCLUSIONS/SIGNIFICANCE: In both bat and rodent hosts, *Bartonella* exhibits significant coevolution with minimal host switching, while *Leptospira* in bats lacks evolutionary congruence with its host and has high number of host switches. Reasons underlying these variable coevolutionary patterns in host range are likely due to differences in disease-specific transmission and host ecology. Understanding the coevolutionary patterns and frequency of host-switching events between bacterial pathogens and their hosts will allow better prediction of spillover between mammal reservoirs, and ultimately to humans.


Bats are important indicator species which can help in identifying areas where conservation efforts should be concentrated and whether these areas are affected by ongoing climate change. To elucidate factors limiting and influencing the elevational distribution of bats in a recognised biodiversity hotspot, the Soutpansberg mountain range (in Vhembe Biosphere Reserve) of northern South Africa, we collected data in and around the Luvhondo Private Nature Reserve, by catching and acoustically monitoring bats over an altitudinal gradient from 900 to 1,748 m. A total of 18 different species could be recorded. Two species, namely *Pipistrellus hesperidus* and *Chaerephon cf. ansorgei* appeared to be present and dominant at all altitudes. Activity, species richness and diversity significantly decreased with increasing altitude, whereas community composition was not related to altitude and no endemics to either low or high altitude were detected. It is likely that the change of species richness and diversity over altitude is caused by other factors correlated with altitude such as vegetation type, area size, energy availability and climatic differences. Our
research demonstrated that lower altitudes are richer and more diverse in bat species and since no highland endemics have been discovered, conservation efforts in the area, regarding bats, should not ignore these lower altitudes which are most susceptible to human impacts leading to habitat degradation due to over-grazing, bush encroachment, cultivation and denudation of large trees for firewood collection.


In dry Mediterranean forests, ponds constitute essential water resources for animals, especially during summer months. In south-eastern Spain, land use changes and the human abandonment of mountainous zones have led to the loss of many ponds. These ponds are scarce landscape elements and, despite their usually small size (< 1,000 m²), they support a considerable amount of biodiversity. We studied the patterns of use of these ponds by bats during the activity season in dry forest landscapes of a Mediterranean region using acoustic monitoring. Our hypothesis was that these ponds are valuable landscape elements for bats, and bat activity and richness species will be high over them. Bat activity and species richness were compared between ponds and adjacent sampling points in the forest matrix. We recorded 14 bat species and our results show that both general bat activity (all species grouped together) and species richness were higher in the ponds than in the forest areas. Bat activity was higher in June, however it decreased during drier months (July–August), while activity in the forest increased. The number of species was constant in the areas surrounding the ponds through the study period, but in the forest we observed an increase in July and a gradual decrease in August–September. Similar results were obtained for most individual species, although in some species activity was also influenced by temporal variables. Our study shows that the maintenance of small ponds may have important consequences for bat conservation, as they support high bat diversity, including some species of conservation concern like horseshoe bats (Rhinolophus spp.) or Myotis spp.


Habitat preference of the meridional serotine bat Eptesicus isabellinus (Temminck, 1840) in semiarid Mediterranean landscapes.—Several molecular studies have recently reported the presence of a second species of the genus Eptesicus in the Iberian peninsula, the meridional serotine bat, E. isabellinus. This species is present in the south of Iberia and it seems to have an allopatric distribution with its twin species, E. serotinus. Ecological studies are now needed to understand the biology of E. isabellinus in southeast Spain. In this study, we used presence–only data for E. isabellinus to perform an ecological niche factor analysis (ENFA) and to create a habitat suitability map (HSM). Our results show that the species has a low marginality index, suggesting it is well adapted to the semiarid conditions of the study area. The main habitats used by E. isabellinus are water courses, scrublands, and zones with high primary productivity. The species avoids non–irrigated cropland and shows no preference for human settlements or irrigated cropland. This study provides information about the ecology of E. isabellinus in southeast Spain and allows us to discuss relevant aspects for its conservation.


The rising incidence of emerging infectious diseases (EID) is mostly linked to biodiversity loss, changes in habitat use and increasing habitat fragmentation. Bats are linked to a growing number of EID but few studies have explored the factors of viral richness in bats. These may have implications for role of bats as potential reservoirs. We investigated the determinants of viral richness in 15 species of African bats (8 Pteropodidae and 7 Microchiroptera) in Central and West Africa for which we provide new information on virus infection and bat phylogeny. We performed the first comparative analysis testing the correlation of the fragmented geographical distribution (defined as the perimeter to area ratio) with viral richness in bats. Because of their potential effect, sampling effort, host body weight, ecological and behavioural traits such as roosting behaviour, migration and geographical range, were included into the analysis as variables. The results showed that the geographical distribution size, shape and host body weight have significant effects on viral richness in bats. Viral richness was higher in large-bodied bats which had larger and more fragmented distribution areas. Accumulation of viruses may be related to the historical expansion and contraction of bat species distribution range, with potentially strong effects of distribution edges on virus transmission. Two potential explanations may explain these results. A positive distribution edge effect on the abundance or distribution of some bat species could have facilitated host switches. Alternatively, parasitism could play a direct role in shaping the distribution range of hosts through host local extinction by virulent parasites. This study highlights the importance of considering the fragmentation of bat species geographical distribution in order to understand their role in the circulation of viruses in Africa.


Ebola virus disease (EVD) is a complex zoonosis that is highly virulent in humans. The largest recorded outbreak of EVD is ongoing in West Africa, outside of its previously reported and predicted niche. We assembled location data on all recorded zoonotic transmission to humans and Ebola virus infection in bats and primates (1976–2014). Using species distribution models, these...
occurrence data were paired with environmental covariates to predict a zoonotic transmission niche covering 22 countries across Central and West Africa. Vegetation, elevation, temperature, evapotranspiration, and suspected reservoir bat distributions define this relationship. At-risk areas are inhabited by 22 million people; however, the rarity of human outbreaks emphasises the very low probability of transmission to humans. Increasing population sizes and international connectivity by air since the first detection of EVD in 1976 suggest that the dynamics of human-to-human secondary transmission in contemporary outbreaks will be very different to those of the past.


Animals employ an array of signals (i.e. visual, acoustic, olfactory) for communication. Natural selection favours signals, receptors, and signalling behaviour that optimise the received signal relative to background noise. When the signal is used for more than one function, antagonisms amongst the different signalling functions may constrain the optimisation of the signal for any one function. Sexual selection through mate choice can strongly modify the effects of natural selection on signalling systems ultimately causing maladaptive signals to evolve. Echolocating bats represent a fascinating group in which to study the evolution of signalling systems as unlike bird songs or frog calls, echolocation has a dual role in foraging and communication. The function of bat echolocation is to generate echoes that the calling bat uses for orientation and food detection with call characteristics being directly related to the exploitation of particular ecological niches. Therefore, it is commonly assumed that echolocation has been shaped by ecology via natural selection. Here we demonstrate for the first time using a novel combined behavioural, ecological and genetic approach that in a bat species, Rhinolophus mehelyi: (1) echolocation peak frequency is an honest signal of body size; (2) females preferentially select males with high frequency calls during the mating season; (3) high frequency males sire more off-spring, providing evidence that echolocation calls may play a role in female mate choice. Our data refute the sole role of ecology in the evolution of echolocation and highlight the antagonistic interplay between natural and sexual selection in shaping acoustic signals.


The taxonomic uncertainty surrounding several prominent genera of Australian microbat has been a long-standing impediment to research and conservation efforts on these groups. The free-tailed bat genus Mormopterus is perhaps the most significant example, with a long history of acknowledged species-level confusion. This study uses a combined molecular and morphological approach to conduct a comprehensive assessment of species and subgeneric boundaries, between-species phylogenetic affinities and within-species phylogeographic structure in Australian members of Mormopterus. Phylogenetic analyses based on 759 base pairs of the NADH Dehydrogenase subunit 2 mitochondrial gene were concordant with species boundaries delineated using an expanded allozyme data set and by phallicmorphology, and also revealed strong phylogeographic structure within two species. The levels of divergence evident in the molecular and morphological analyses led us to recognise three subgenera within Australia: Micronomus, Setirostris subgen. nov. and Ozimops subgen. nov. Within Ozimops we recognise seven Australian species, three of which are new, and none are conspecific with Indo-Papuan species. The family Molossidae now comprises eleven species across three subgenera in Australia, making it the continent's second most speciose family of bats.


In most mammals, reproductive cost differs between males and females in timing and duration because of the different sex-specific energy allocation strategies to maximize fitness. The differences in reproductive strategy adopted by sexes may result in differences in seasonal variation of body mass. Here seasonal variations in body mass are discussed for two species of vespertilionid bats: Daubentons’s bat (Myotis daubentoni) and Savi’s pipistrelle (Hypsugo savi). Both species were observed to have a seasonal variability in body conditions, which was sex dependent. In late spring and for a given forearm length, females were heavier than males, but differences were small in late summer. Furthermore, female’s body mass decreased during late spring and summer likely to support the energy requirement for lactation, while male’s mass did not change (H. savi) or slightly increase (M. daubentoni) over the same period. On the contrary male M. daubentoni depleted body fat reserves during early autumn, likely because of the energy expenditure to increase mating opportunities. Our results suggest that seasonal changes in body condition in hibernating bats may reflect the differences in reproductive strategies between sexes.


Remains of various fossil mammals were found within a large quarry close to Baixas village (E-Pyrénées Dept., France). Among
them are tooth remains of a bat poorly known as a fossil: a rhinopomatid one. The presumed age of the associated fauna, especially obtained from the rodents, is recognized to be the MN 4 biozone (Early Miocene, about 16 My). The *Rhinopoma* Geoffroy Saint-Hilaire, 1818 genus is mostly known from the recent fauna, with rare species (two more common ones), extending across warm to arid areas of the Western Old World. Rare fossil rhinopomatids are reported, from Fayum (Egypt), Israel, and north-mediterrean egean Greece. The Baixas ones are 65 specimens. They display the typical tooth morphology of these bats, nevertheless preserving some structures which vanished from recent ones, or less evolved (as regards lower and upper canines, or P4). The originality of this rhinopomatid species supports its recognition as a new genus and species, *Corbatinha handae* n. gen., n. sp. Recent molecular considerations supported the rhinopomatids origin from rhinolophoid ancestry. The position here promoted from tooth morphology retains the rhinopomatid origin from emballonurid ancestors.


Bat-borne viruses can pose a serious threat to human health, with examples including Nipah virus (NiV) in Bangladesh and Malaysia, and Marburg virus (MARV) in Africa. To date, significant human outbreaks of such viruses have not been reported in the European Union (EU). However, EU countries have strong historical links with many of the countries where NiV and MARV are present and a corresponding high volume of commercial trade and human travel, which poses a potential risk of introduction of these viruses into the EU. In assessing the risks of introduction of these bat-borne zoonotic viruses to the EU, it is important to consider the location and range of bat species known to be susceptible to infection, together with the virus prevalence, seasonality of viral pulses, duration of infection and titre of virus in different bat tissues. In this paper, we review the current scientific knowledge of all these factors, in relation to the introduction of NiV and MARV into the EU.


Many regions in Africa are currently being converted from subsistence to cash crop farming such as cotton. Agricultural intensification is usually accompanied by increased use of pesticides, which can have an impact on non-target organisms. Bats are particularly sensitive to insecticide loads while providing substantial ecosystem services as predators of herbivorous insects. In this study, pesticide residues in bats in a landscape in northern Benin were investigated, which spanned a land use gradient from an agricultural zone dominated by cotton farms, through a buffer zone, and into a national park. Insecticides used in cotton cultivation, such as endosulfan, chlorpyrifos, flubeniamide, and spirotetramat, as well as persistent insecticides such as bis(4-chlorophenyl)-1,1,1-trichloroethane (DDT), lindane, and aldrine, were analysed. Insecticide residues detected in bats comprised DDT, endosulfan, and their corresponding transformation products. Maximum concentrations in the sampled bats were 11.2 mg/kg lipid of p,p’-DDE (median: 0.0136 mg/kg lipid) and 0.797 mg/kg lipid of β-endosulfan (median: below detection limit [DL]). While insecticide concentrations were below lethal concentrations our data suggest that DDT had probably been recently used in the study region, and larger scale use would pose an increased risk for bat populations due to the high biomagnification of DDT.


Population fluctuations, roost site selection and diet of straw-coloured fruit bats, *Eidolon helvum* (Kerr, 1792) were studied for > one year in western Kenya. Total counts of bats at three identified roosts varied from 7,000 to 48,000 individuals. The bats moved between roosts within the same general area, probably reflecting seasonal variation in the availability of preferred foods and/or harassment and direct persecution at some roost sites by the rural community. Our study suggests that tree density and number of branches on trees were important factors in roost site selection for *E. helvum*, and the removal of roost trees has serious ramifications for their conservation in the region. Germination experiments and observations at roost sites indicated that *E. helvum* consumed fruits from 31 plant species of 16 families, potentially assisting in the dispersal of their seeds. Further monitoring is needed to provide a complete picture of the status and migration patterns of *E. helvum* in Kenya. Additionally, because the bats were viewed negatively and persecuted by roost tree clearance and direct eradication attempts, an education and community outreach programme in local schools and communities is proposed for the long-term conservation of viable populations of *E. helvum* in western Kenya.


The Paramyxoviridae form an increasingly diverse viral family, infecting a wide variety of different hosts. In recent years, they have been linked to disease emergence in many different animal populations and in humans. Bats and rodents have been identified as major animal populations capable of harboring paramyxoviruses, and host shifting between these animals is likely to be an important driving factor in the underlying evolutionary processes that eventually lead to disease emergence. Here, we have studied paramyxovirus circulation within populations of endemic and introduced wild small mammals of the southwestern Indian Ocean region and belonging to four taxonomic orders: Rodentia, Afrotheria, Soricomorpha, and Chiroptera. We report elevated infection levels as well as widespread paramyxovirus dispersal and frequent host exchange of a newly emerging genus of the Paramyxoviridae, currently referred to as the unclassified morbillivirus-related viruses (UMRVs). In contrast to other genera of the Paramyxoviridae, where bats have been shown to be a key host species, we show that rodents (and, in particular, *Rattus rattus*) are significant spreaders of UMRVs. We predict that the ecological particularities of the southwestern Indian Ocean, where small mammal species often live in densely packed, multispecies communities, in combination with the increasing invasion of *R. rattus* and perturbations of endemic animal communities by active anthropological development, will have a major influence on the dynamics of UMRV infection.

**IMPORTANT:** Identification of the infectious agents that circulate within wild animal reservoirs is essential for several reasons: (i) infectious disease outbreaks often originate from wild fauna; (ii) anthropological expansion increases the risk of contact between human and animal populations and, as a result, the risk of disease emergence; (iii) evaluation of pathogen reservoirs helps in elaborating preventive measures to limit the risk of disease emergence. Many paramyxoviruses for which bats and rodents serve as major reservoirs have demonstrated their potential to cause disease in humans and animals. In the context of the biodiversity hot spot of southwestern Indian Ocean Islands and their rich endemic fauna, we show that highly diverse UMRVs exchange between various endemic animal species, and their dissemination likely is facilitated by the introduced *Rattus rattus*. Hence, many members of the Paramyxoviridae appear well adapted for the study of the viral phylodynamics that may be associated with disease emergence.


This paper summarizes the progress in the search for hantaviruses and hantavirus infections in Africa. After having collected molecular evidence of an indigenous African hantavirus in 2006, an intensive investigation for new hantaviruses has been started in small mammals. Various novel hantaviruses have been molecularly identified not only in rodents but also in shrews and bats. In addition, the first African hantavirus, Sangassou virus, has been isolated and functionally characterized in cell culture. Less is known about the ability of these hantaviruses to infect humans and to cause diseases. To date, no hantavirus genetic material could be amplified from patients’ specimens collected in Africa. Serological studies in West Africa, based on a battery of screening and confirmatory assays, led to the detection of hantavirus antibodies in the human population and in patients with putative hantavirus disease. In addition to this overview, we present original data from seroepidemiological and field studies conducted in the Southern part of Africa. A human seroprevalence rate of 1.0% (*n*=1442) was detected in the South African Cape Region whereas no molecular evidence for the presence of hantavirus was found in 2500 small animals trapped in South Africa and Namibia.


Virus and host gene phylogenies, indicating that antigenically distinct hantaviruses (family Bunyaviridae, genus Hantavirus) segregate into clades, which parallel the molecular evolution of rodents belonging to the Murinae, Arvicolinae, Neotominae and Sigmodontinae subfamilies, suggested co-divergence of hantaviruses and their rodent reservoirs. Lately, this concept has been vigorously contested in favor of preferential host switching and local host-specific adaptation. To gain insights into the host range, spatial and temporal distribution, genetic diversity and evolutionary origins of hantaviruses, we employed reverse transcription-polymerase chain reaction to analyze frozen, RNAlater®-preserved and ethanol-fixed tissues from 1546 shrews (9 genera and 47 species), 281 moles (8 genera and 10 species) and 520 bats (26 genera and 53 species), collected in Europe, Asia, Africa and North America during 1980-2012. Thus far, we have identified 24 novel hantaviruses in shrews, moles and bats. That these newfound hantaviruses are geographically widespread and genetically more diverse than those harbored by rodents suggests that the evolutionary history of hantaviruses is far more complex than previously conjectured. Phylogenetic analyses indicate four distinct clades, with the most divergent comprising hantaviruses harbored by the European mole and insectivorous bats, with evidence for both co-divergence and host switching. Future studies will provide new knowledge about the transmission dynamics and pathogenic potential of these newly discovered, still-orphan, non-rodent-borne hantaviruses.


Hantaviruses are among the most important zoonotic pathogens of humans, causing either hemorrhagic fever with renal syndrome (HFRS) or hantavirus pulmonary syndrome (HPS). From the period 1964-2006 almost all hantaviruses had been identified in rodents, with the exception of Thottapalayam virus (TPMV) isolated from shrews sampled in India. As a consequence, rodents were considered as the natural reservoir hosts. However, over the past seven years, most of the newly found hantavirus genotypes have been from either shrews or moles. Remarkably, in recent years divergent hantaviruses have also been identified in bats sampled from both Africa and Asia. All these data indicate that hantaviruses have a broad range of natural reservoir hosts. Phylogenetic
analyses of the available sequences of hantaviruses suggest that hantaviruses might have first appeared in Chiroptera (bats) or Soricomorpha (moles and shrews), before emerging in rodent species. Although rodent hantaviruses cluster according to whether their hosts are members of the Murinae and Cricetidae, the phylogenetic histories of the viruses are not always congruent with those of their hosts, indicating that cross-species transmission events have occurred at all taxonomic levels. In sum, both cross-species transmission and co-divergence have produced the high genetic diversity of hantaviruses described to date.

**Notice Board**

**Conferences**

**AFRICAN SMALL MAMMAL SYMPOSIUM**
To be held in: Antananarivo, Madagascar, 12-18 April 2015  
Further information: sgoodman@fieldmuseum.org

**ZOOLOGICAL SOCIETY OF SOUTHERN AFRICA 37TH ZSSA CONGRESS**
To be held at: Rhodes University, Grahamstown, South Africa, 12 to 17 July 2015.  
Further information: http://zssa.co.za/

**17TH INTERNATIONAL BAT RESEARCH CONFERENCE**
To be held in: Durban, South Africa, 2016

**Call for contributions**

African Bat Conservation News is divided into two main parts: peer reviewed and non peer reviewed articles.  
The non peer reviewed part is further subdivided into a two sections:  
- Research and Conservation - which aims to promote projects, organizations and individuals working on bat related research, conservation and/or education within Africa and its surrounding islands. Updates on projects and activities are also encouraged.  
- Observations, Discussions and Updates - This section is used to inform and allow readers to comment on various issues of a thematic nature. It is also used to capture information (e.g. Observations) which may not have enough information to make the scientific contribution section (these observations will be moderated by the editorial board).  
The scientific contribution part of African Bat Conservation News is peer reviewed and publishes brief notes concerning the biology of bats, new geographical distributions (preferably at least 100 km from the nearest previously published record), sparsely annotated species lists resulting from local surveys, roost counts, and echolocation of bat species occurring on the African continent and adjacent regions, including the Arabian peninsula, Madagascar, and other surrounding islands in the Indian and Atlantic oceans and those islands just off Africa within the Mediterranean and Red Seas.  
Two additional sections are also included in the newsletter - Recent literature - this includes abstracts from recent conferences and recently published works. If you are involved in a conference or have published a paper and wish to have it included in this section please send a copy of the PDF of the paper to the Editor or Scientific Editor.  
Notice Board - includes information on future planned conferences, workshops or training opportunities. If you are an organizer of such an event and wish it to be promoted in ABCN then please send the information to the Editor.

**African Bat Conservation News Project Cycle**
Issues will be published Quarterly (January, April, July, October).  
Deadlines for scientific contributions (1 November, 1 February, 1 May, 1 August).  
Deadlines for non-scientific contributions (1 December, 1 March, 1 June, 1 September).  
Non scientific contributions should be sent to the Editor while scientific contributions should be sent to the Scientific Editor.  
Notes to authors are available at www.africanbats.org or download PDF.

**Editorial Team**

Editor: Ernest C.J. Seamark (ABCN_Editor@africanbats.org)  
Scientific Editor: Victor Van Cakenberghe (ABCN_ScientificEditor@africanbats.org)  
Editorial Board: Eric Bakwo Fils (University of Maroua, Cameroon); Jakob Fahr (Max Planck Institute for Ornithology, Radolfzell & Zoological Institute, Germany); Steve Goodman (Chicago Field Museum of Natural History, United States of America); Kim Howell (University of Dar es Salaam, Tanzania); Teresa Kearney (Ditsong National Museum of Natural History, formerly Transvaal Museum, South Africa); Robert Kityo (Makerere University, Uganda); Ara Monadjem (University of Swaziland, Swaziland); Peter Taylor (University of Venda, South Africa); Victor Van Cakenberghe (University of Antwerp, Belgium); Paul Webala (Karatina University College, Kenya).