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Above: Schlieffen's Twilight Bat (*Nycticeinops schlieffenii*) (ECJS-93-2009), caught in Botswana.

Inside this issue:

RECENT LITERATURE

PUBLISHED PAPERS

BRITO, J. C., ÁLVARES, F., MARTÍNEZ-FREIRÁ, F., SIERRA, P., SILLERO, N., and TARROSO, P., 2010. Data on the distribution of mammals from Mauritania, West Africa. *Mammalia* 74(4): 449-455. DOI: 10.1515/MAMM.2010.055.

DANIEL, S., KORINE, C., and PINSHOW, B., 2010. Foraging behavior of a desert dwelling arthropod-gleaning bat (*Otonycteris hemprichii*) during pregnancy and nursing. *Acta Chiropterologica* 12(2): 293-299. DOI: 10.3161/150811010X537873.

Abstract: We studied the role of behavioral activities used by desert-dwelling, arthropod gleaning Hemprich's long-eared bat (*Otonycteris hemprichii*), hypothesizing that there is a trade off between their own and their offspring's food needs. Specifically, we tested the following predictions: 1) females will bring forward their emergence time from their roosts and increase foraging bout length progressively from the first through the second trimesters of pregnancy, and during nursing as their pups grow; but, that 2) during the last trimester of pregnancy, namely, in the final stages of foetus development, females will emerge later and there will be a reduction in foraging effort (time); and that 3) females will spend more time foraging during nursing than during pregnancy. We found that the bats emerged from their roosts to forage earlier during the first trimester, but not during the last two trimesters of pregnancy, and that they did not change their emergence time as nursing progressed. Bats that emerged later at night during pregnancy spent more time foraging, and, except for the third trimester, the length of the first daily foraging bout increased as both pregnancy and nursing progressed. Total daily foraging time increased as pregnancy and nursing progressed. Generally, these results support our hypothesis; through adjustment of their foraging behavior as embryos and pups develop, breeding female Hemprich's long-eared bats contend with the potentially conflicting food requirements of their offspring and their own needs.

DIEULEVEUT, T., LIERON, V., and HINGRAT, Y., 2010. Nouvelles données sur la répartition des Chiroptères dans le Maroc oriental (années 2007 à 2009). *Bulletin de l'Institut Scientifique, Rabat, Sciences de la Vie* 32(1): 33-40.

New records of 19 bat species from eastern Morocco are presented, including *Rhinopoma microphyllum*, *Rhinopoma cystops*, *Rhinolophus ferrumequinum*, *Rhinolophus hipposideros*, *Rhinolophus mehelyi*, *Rhinolophus blasii*, *Asellia tridens*, *Myotis punicus*, *Myotis nattereri*, *Myotis emarginatus*, *Eptesicus isabellinus*, *Hypsugo savii*, *Pipistrellus pipistrellus*, *Pipistrellus kuhlii*, *Pipistrellus rueppellii*, *Otonycteris hemprichii*, *Plecotus gaisleri*, *Miniopterus schreibersii*, *Tadarida teniotis*. All data have been collected between 2007 and 2009. Some of them relate to species until now rarely detected in Morocco previously, *Rhinopoma microphyllum*, *Rhinolophus blasii*, *Myotis nattereri*, *Myotis emarginatus*, *Pipistrellus rueppellii*, *Otonycteris hemprichii* and *Tadarida teniotis*, and new data are provided on their status and distribution.

GOODMAN, S. M., BUCCAS, W., NAIDOO, T., RATRIMOMANARIVO, F., TAYLOR, P. J., and LAMB, J., 2010. Patterns of morphological and genetic variation in western Indian Ocean members of the *Chaerephon* '*pumilus*' complex (Chiroptera: Molossidae), with the description of a new species from Madagascar. *Zootaxa* 2551: 1-36.

Abstract: The species delimitations of African, Arabian Peninsula, and western Indian Ocean island members of the Molossidae bat species complex *Chaerephon pumilus* remain largely unresolved. Based on genetic analyses this group is paraphyletic, with *C. leucogaster* nested within *C. pumilus* sensu lato, and the latter is composed of several distinct clades. DNA was isolated from a specimen of *C. p. pumilus* obtained at the type locality (Massawa, Eritrea). Although incomplete, this sequence allowed us to clearly define which clade is referable to nominate *pumilus*, a critical step in resolving the systematics of this species complex. Using morphological and molecular genetic (cytochrome *b* and Dloop sequences) characters, we establish that *C. leucogaster* and *C.* '*pumilus*' on Madagascar represent two different lineages and that the Malagasy population referred to *C.* '*pumilus*' is specifically distinct from those on Africa, the Arabian Peninsula, the Comoros Archipelago, and the western Seychelles (Aldabra). The Madagascar population is here described as a new species, *Chaerephon atsinanana* sp. nov. This taxon is common in the eastern portion of Madagascar, particularly in synanthropic settings, across an elevational range from near sea level to 1100 m, and there are no immediate conservation concerns. Members of the *C. pumilus* species complex from the western Seychelles are referable to *C. pusillus*, to which populations from the Comoros (Mayotte, Anjouan, Mohéli, and Grande Comore) are also assigned.

HAUGE, K. B., 2010. Bat (Chiroptera) activity and community composition in contrasting agricultural landscapes and the adjacent Budongo forest reserve, Uganda. Masters Thesis. University of Bergen : 1-42; i - iii. URL: https://bora.uib.no/bitstream/1956/4326/1/71960966.pdf

Abstract: Human activities are causing a biodiversity crisis in all biomes of the Earth. As the world's population continues to grow, more land will be converted to agricultural land to meet the growing food demands, especially in the tropics where we find the most species rich habitats in the world. Many of these species and ecosystems provide valuable services to the humans living here. To best protect species richness and the people dependent on rural livelihoods in the tropics, two types of managed agricultural landscapes have been suggested: land sparing and land sharing. Land sparing promotes high yield agriculture in order to have as large an area as possible protected, while land sharing is farming a more extensive area of the landscape, but is able to retain more species and ecosystem services by using agricultural methods such as agroforestry. The potential for conservation and retaining ecosystem services in a land sharing or a land sparing type landscape in Uganda is addressed using data about insectivorous bats recorded with Anabat detectors in habitats from sugarcane, home garden and forest in and around Budongo forest, Uganda. Species richness, diversity, activity and species composition were determined for all habitats and used to give a picture of the conservation value of the different habitat types. As found in other studies both agricultural landscape types have a higher species richness and diversity than the forest habitat. But the higher activity and number of species related to the forest gives the home garden landscape better potential for conservation of microbats. Scattered trees and distance to the forest in the sugarcane landscape type does not add any conservation value compared to the sugarcane habitat. This study helps to demonstrate the value of land sharing type agriculture for conserving species richness and retaining ecosystem services.

HUTTERER, R., and PETERS, G., 2010. Type specimens of mammals (Mammalia) in the collections of the Zoologisches Forschungsmuseum Alexander Koenig, Bonn. *Bonn zoological Bulletin* 59: 3-27. URL: http://zfmk.de/BZB/Band_59/01_hutterer_BZB_59_20101205.pdf

Abstract: An annotated catalogue of type specimens of Mammalia in the collections of the Zoologisches Forschungsmuseum Alexander Koenig in Bonn is given. By the end of 2010, the Bonn collections housed name-bearing types (five syn-, 77 holo-, two lecto- and one neotype) for 85 taxa and para- and paralectotypes for 105 taxa. Casts of rare type specimens of 3 extinct taxa are also listed. The collections also include vouchers for karyotypes and GenBank entries. A lectotype is selected for *Microtus savii niethammericus* Contoli, 2003, and replacement names are proposed for homonyms of two preoccupied taxa, *Apodemus maximus* Thaler, 1972 (Muridae) and *Sciurus vulgaris hoffmanni* Valverde, 1967 (Sciuridae).

JOHNSON, S. A., PERRYMAN, R. J. Y., STEER, M. D., and BELLE, E. M. S., 2010. Observations of a *Pteropus rufus* colony in a dry deciduous forest fragment of Northern Madagascar. *African Bat Conservation News* 23: 3-6. URL: http://www.africanbats.org/wwwroot/Docs/ABCN/Johnson_et_al_2010.pdf

KEARNEY, T. C., SEAMARK, E. C. J., MATEKE, C., and HOOD, D., 2010. Chiroptera of Lufupa Camp, Kafue National Park, Zambia; with taxonomic notes on *Epomophorus*, *Nycticeinops*, *Scotophilus* and *Scotoecus*. *African Bat Conservation News* 23: 7-31. URL: http://www.africanbats.org/wwwroot/Docs/ABCN/Kearney_et_al_2010.pdf

KOUBÍNOVÁ, D., SREEPADA, K. S., KOUBEK, P., and ZIMA, J., 2010. Karyotypic variation in rhinolophid and hipposiderid bats (Chiroptera: Rhinolophidae, Hipposideridae). *Acta Chiropterologica* 12(2): 393-400. DOI: 10.3161/150811010X537972.

Abstract: According to current phylogenetic hypotheses, the bats of the families Rhinolophidae and Hipposideridae are sister groups nested within the clade of Pteropodiformes. A conservative nature of karyotypic evolution was previously reported within the two families. Karyotypes with diploid number (2n) varying between 58 and 62 chromosomes were assumed to prevail among the rhinolophid species, whereas, karyotypes with 32 chromosomes were found in most of the hipposiderid bats. However, divergent lower or higher 2n numbers have been recorded in some species in both families. Variation is documented in the present paper by examination of non-differentially stained karyotypes in 10 species belonging to genera *Rhinolophus* and *Hipposideros* from western Africa and southern India. Among the species studied, the karyotypes with a 2n of 32, 36, 52, 56, 58, and 62, and with relatively stable number of autosomal arms (Fna = 60, 62, 64) were recorded.

LACK, J. B., ROEHRS, Z. P., STANLEY JR, C. E., RUEDI, M., and VAN DEN BUSSCHE, R. A., 2010. Molecular phylogenetics of *Myotis* indicate familial-level divergence for the genus *Cistugo* (Chiroptera). *Journal of Mammalogy* 91(4): 976-992. DOI: 10.1644/09-MAMM-A-192.1.

Abstract: The genus *Myotis* has undergone significant taxonomic revision since the advent of DNA sequencing techniques. Prior morphological examination of *Myotis* has indicated as many as 4 subgenera correlated with foraging strategies. Recent studies using mitochondrial DNA (mtDNA) sequence data have questioned the validity of these subgenera and have indicated that several taxa may require reevaluation as to their position within Vespertilionidae. Nevertheless, no study has used large-scale nuclear DNA sequencing to examine relationships within *Myotis*. We generated 4,656 base pairs (bp) of nuclear intron (PRKC1, STAT5A, and THY) and exon (APOB, DMP1, and RAG2) sequence data in addition to 2,866 bp of mtDNA sequence data to test previously hypothesized subgeneric groupings of *Myotis*. We included 21 species of *Myotis* from all morphological subgenera previously suggested, representatives of all subfamilies and tribes currently recognized in Vespertilionidae, and multiple representatives of all other families currently included in the superfamily Vespertilionoidea. We also included a representative of the rare African genus *Cistugo*, because significant doubt exists about its familial position. Our phylogenetic analyses did not support the morphologically defined *Myotis* subgenera and confirm that morphological similarities among *Myotis* are the result of convergent evolution. Divergence estimates derived from the total data set were concordant with previous studies, suggesting a middle Miocene trans-Beringian dispersal from Asia colonized North America, with subsequent South American colonization and diversification prior to the formation of the Isthmus of Panama 3-4 million years ago. *Myotis latirostris* fell outside of *Myotis*, and the high genetic distance separating it from other *Myotis* suggested that *M. latirostris* represented a distinct genus. The genus *Cistugo*, previously a subgenus within *Myotis*, fell basal to all vespertilionids, with a high genetic distance separating it from Vespertilionidae. We conclude that *Cistugo* should constitute a distinct family within Vespertilionoidea.

MARAIS, W., 2011. Specialist bat (Chiroptera) sensitivity assessment. For the proposed Deep River Wind Energy Facility on Portion 4 & 16 of the farm Diepriviermond 358 and the remaining extent of Farm 891, near Humansdorp, Eastern Cape. Animalia - Zoological & Ecological Consultation - Weltevredenpark, Gauteng: 32 pp. URL: http://www.savannahsa.com/documents/1441/Deep%20River%20DEIR%20Appendix%20H%20-%20Bats.pdf

MONADJEM, A., ELLSTROM, M., MALDONALDO , C., and FASEL, N., 2010. The activity of an insectivorous bat *Neoromicia nana* on tracks in logged and unlogged forest in tropical Africa. *African Journal of Ecology* 48(4): 1083-1091. DOI: 10.1111/j.1365-2028.2010.01219.x.

Abstract: Logging activities and the associated creation of roads and tracks can disturb and fragment forests, which may lead to a loss of forest-dependent species and possibly favour nonforest generalists and edge species. The effects of such disturbance are poorly known for African insectivorous bats. We studied the activity patterns of insectivorous bats in a tropical African forest at Kibale National Park, Uganda, using an Anabat bat detector. The echolocation calls of the vespertilionid bat *Neoromicia nana* were the most frequently detected. This species was most active in the first 5 h after sunset with activity declining rapidly after midnight until sampling finished at 01:00 h. There was no difference in activity of *N. nana* levels between logged or undisturbed forest; however, this species exhibited higher levels of activity along the wide tracks running through the two forests than either 30 m off these tracks or along the narrow forest trails. The wing morphology and echolocation call of *N. nana* may be constraining it to flying in uncluttered space on the edge of the forest, penetrating mostly along wider tracks and roads. Further research (in particular radio-telemetry) is required to test and validate these data.

MONADJEM, A., SCHOEMAN, M.C., RESIDE, A., PIO, D. V., STOFFBERG, S., BAYLISS, J., COTTERILL, F. P. D., CURRAN, M., KOPP, M., and TAYLOR, P. J., 2010. A recent inventory of the bats of Mozambique with documentation of seven new species for the country. *Acta Chiropterologica* 12(2): 371-391. DOI: 10.3161/150811010X537963.

Abstract: The bat fauna of Mozambique is poorly documented. We conducted a series of inventories across the country between 2005 and 2009, resulting in the identification of 50 species from 41 sites. Of these, seven species represent new national records that increase the country total to 67 species. These data include results from the first detailed surveys across northern Mozambique, over an area representing almost 50% of the country. We detail information on new distribution records and measurements of these specimens. Special attention is paid to the Rhinolophidae, because these include several taxa that are currently in a state of taxonomic confusion. Furthermore, we also present some notes on taxonomy, ecology and echolocation calls. Finally, we combine modelled distributions to present predicted species richness across the country. Species richness was lowest across the coastal plain, to the east and far north, and is predicted to increase in association with rising altitude and higher topographic unevenness of the landscape.

QUAN, P.-L., FIRTH, C., STREET, C., HENRIQUEZ, J. A., PETROSOV, A., TASHMUKHAMEDOVA, A., HUTCHISON, S. K., EGHOLM, M., OSINUBI, M. O. V., NIEZGODA, M., OGUNKOYA, A. B., BRIESE, T., RUPPRECHT, C. E., and LIPKIN, W. I., 2010. Identification of a severe acute respiratory syndrome coronavirus-like virus in a leaf-nosed bat in Nigeria. *mBio* 1(4): -e00208-10: 1 - 9. DOI: 10.1128/mBio.00208-10.

Abstract: Bats are reservoirs for emerging zoonotic viruses that can have a profound impact on human and animal health, including lyssaviruses, filoviruses, paramyxoviruses, and severe acute respiratory syndrome coronaviruses (SARS-CoVs). In the course of a project focused on pathogen discovery in contexts where human-bat contact might facilitate more efficient interspecies transmission of viruses, we surveyes gastrointestinal tissue obtained from bats collected in caves in Nigeria that are frequented by humans. Coronavirus consensus PCR and unbiased high-throughput pyrosequencing revealed the presence of coronavirus sequences related to those of SARS-CoV in a Commerson's leaf-nosed bat (*Hipposideros commersoni*). Additional genomic sequencing indicated that this virus, unlike subgroup 2b CoVs, which includes SARS-CoV, is unique, comprising three overlapping open reading frames between the M and N genes and two conserved stem-loop II motifs. Phylogenetic analysis in conjunction with these features suggest that this virus represents a new subgroup within group 2 CoVs.

RAINHO, A., MEYER, C. F. J., THORSTEINSDÓTTIR, S., JUSTINO, J., SAMBA, S., and PALMEIRIM, J. M., 2010. *Distribuição, estatuto e conservação dos morcegos de São Tomé*. Centro de Biologia Ambiental - Falculdade de Ciências - Universidade de Lisboa: 1 - 48.

ROEHRS, Z. P., LACK, J. B., and VAN DEN BUSSCHE, R. A., 2010. Tribal phylogenetic relationships within Vespertilioninae (Chiroptera: Vespertilionidae) based on mitochondrial and nuclear sequence data. *Journal of Mammalogy* 91(5): 1073-1092. DOI: 10.1644/09-MAMM-A-325.1.

Abstract: A paucity of useful characters, morphological convergence, and potential rapid radiation has hindered systematists in elucidating evolutionary relationships within Vespertilioninae. In this study .8,500 base pairs of digenomic DNA for 111 taxa were sequenced and analyzed using maximum-parsimony and Bayesian phylogenetic methods to construct trees and reexamine hypotheses of supergeneric evolutionary relationships in Vespertilioninae. Results of these analyses validate monophyly of Vespertilioninae with the exclusion of *Myotis* and support recognition of 6 tribes: Antrozoini, Lasiurini, Scotophilini, Vespertilionini, and 2 new unnamed tribal clades, the perimyotine group and the hypsugine group. Tree topologies indicate a Nycticeiini-Eptesicini group, but this clade is not supported. The heuristically pleasing tribe Plecotini also is unresolved in these analyses. These results provided further support and greater resolution for previously proposed hypotheses of Vespertilioninae evolution based on mitochondrial DNA, and although deep branching patterns are not fully resolved, these data increase our understanding of the evolution of this ecologically important and diverse group of bats.

SCHOEMAN, M.C., and JACOBS, D. S., 2010. The relative influence of competition and prey defences on the tropic structure of animalivorous bat ensembles. *Oecologia*: e14. DOI: 10.1007/s00442-010-1854-3.

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

NOTICE BOARD

Conferences

11th African Small Mammal Symposium

To be held in: Swaziland, Kwaluseni, 3-8 July 2011.
Further information: http://www.asms.uniswa.sz or email: asms@uniswacc.uniswa.sz

16th International Bat Research Conference

To be held in: Costa Rica, 2014.
Further information: *watch this space*

Call for contributions

African Bat Conservation News 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 including roost counts and echolocation and sonograms 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.

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).

Contributions should be sent to the editor: ABCNEditor@gmail.com

Scientific contributions should be sent to the Scientific Editor: ScientificEditorABCN@gmail.com or
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Notes to authors are available at www.africanbats.org/ABCN.htm or download notes here