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## **Description of a new species belonging to the *Murina* ‘suilla-group’ (Chiroptera: Vespertilionidae: Murinae) from north Vietnam**

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Based on a series of 11 specimens collected in north Vietnam between 2006 and 2007, a new species of tube-nosed bat belonging to the genus *Murina* is described. Externally similar to *Murina aurata* Milne-Edwards, 1872, from which it differs primarily in dental characteristics, the new species is distinguished from all other existing species of *Murina* by a combination of its small size, pelage and craniodental features. It is currently known from three localities in north Vietnam, all of which include significant areas of forest over limestone karst.

*Key words:* karst, *Murina* sp. nov., tube-nosed bats, taxonomy, Vietnam

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## **Taxonomy of *Rhinolophus yunanensis* Dobson, 1872 (Chiroptera: Rhinolophidae) with a description of a new species from Thailand**

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The taxonomy of *Rhinolophus yunanensis* Dobson, 1872 (Chiroptera: Rhinolophidae) is revised by reference to specimens collected from the provinces of Sichuan and Yunnan, China, and from Thailand. The Thai specimens are found to differ from the Chinese ones in external and cranial morphology and karyotype, and it is thus concluded that what has hitherto been *R. yunanensis* actually represents two distinct species, including a new one. The new species is described on the basis of 10 specimens collected from Chiang Mai, Thailand. It is the largest species of the *pearsoni* group of the genus, with a large skull and long ears. *Rhinolophus yunanensis* is redescribed on the basis of specimens collected from China. In Principal Component Analyses of the cranial morphometric data, the new species was completely separated from the redescribed *R. yunanensis* and *R. pearsoni*.

*Key words:* new species, *Rhinolophus*, taxonomy, morphology, karyotype, Thailand

## **Phylogeny of *Eumops* Miller, 1906 (Chiroptera: Molossidae) using morphological data**

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Mastiff bats (genus *Eumops*, family Molossidae) are widely distributed in the neotropics and southern parts of the United States, and form the most taxonomically diverse genus of the family Molossidae with 14 species and six subspecies. The taxonomy of *Eumops* was treated in two broad studies, and recently, minor taxonomic changes were proposed. Relationships among taxa were historically proposed based on phenetic analyses using biochemical and morphometric data, but a phylogenetic analysis of all species within the genus is lacking. This study proposes a new hypothesis of relationships among most species and subspecies using morphological data and employing cladistic methods. Morphological complexes examined include skull, dentition, tongue, and external morphology; penial data were compiled from literature. The topology of a strict consensus cladogram revealed that one clade is composed of *E. perotis* + *E. trumbulli*, and is sister to (*E. bonariensis* + *E. delticus* + *E. patagonicus* + *E. nanus* + *E. hansae* in an unresolved polytomy). A second clade is composed of *E. underwoodi* + *E. dabbenei*, and a third consists of *E. auripendulus* and *E. maurus*, and both are sister to each other. *Eumops glaucinus* occupies a separate branch in an unresolved polytomy among clades defined above or as sister to *E. perotis*, *E. hansae* and *E. bonariensis*-complex. Results from this study contradict the relationships proposed by previous studies which considered *E. auripendulus* closer to *E. glaucinus*, and also disagree with previous outcomes that suggested the non-monophyly of the genus. Results from this study corroborate affinities of *E. dabbenei* with *E. underwoodi*, and the uncertain monophyly of *E. bonariensis* as a polytypic species, supporting the specific status of *E. nanus* and *E. delticus* as recently proposed.

*Key words:* Molossidae, *Eumops*, phylogenetic analysis, morphological characters, cladistics

## **Phylogeography of *Musonycteris harrisoni* along the Pacific coast of Mexico**

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The goal of this study was to assess the phylogeography of the trumpet nosed-bat (*Musonycteris harrisoni*) through an analysis of the phylogeographic relationship among populations over its entire distributional range along the Pacific coast of Mexico. We used nucleotide sequence data from the mitochondrial cytochrome-*b* (≈ 950 bp) and D-loop to assess levels of intraspecific variation in the species. DNA-samples of *M. harrisoni* were obtained from museums, own field collections and bats provided by other researchers. We analyzed samples collected from 21 different localities. Molecular sequence data were analyzed using neighbour-joining, maximum likelihood and Bayesian studies. Nested clades analyses were used to assess the cladistic arrangement of haplotypes. Across the 21 distinct localities, we found nine haplotypes using cytochrome-*b* data, and 11 different haplotypes using the D-loop. Nested clade analysis revealed a moderate level of molecular variance among localities. Localities were grouped into two clades, composed of individuals from either the northern or southern portion of the species' range that accounted for 41% of the genetic variance. The northern clade shows little phylogenetic structure and distribution seems to be restricted by the Sierra Madre mountain range. Our results suggest a pattern consistent with the vicariant allopatric divergence/speciation model, influenced by habitat loss and fragmentation.

**Key words:** cytochrome-*b*, D-loop, endemism, *Musonycteris harrisoni*, Pacific coast of Mexico, phylogeography, tropical dry forest

## ***Vampyravus orientalis* Schlosser (Chiroptera) from the Early Oligocene (Rupelian), Fayum, Egypt — body mass, humeral morphology and affinities**

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*Vampyravus orientalis*, from the Oligocene of Fayum, Egypt was the first fossil bat described from Africa. It is represented by a single, relatively large humerus from an unknown horizon in the Jebel Qatrani Formation. Based on regression analyses of skeletal proportions of modern bats, we developed a set of equations to estimate body mass of fossil bats from known skeletal elements in order to test the hypothesis that *Vampyravus* could have been within the body size range of other Fayum bats, including several recently described taxa from the Jebel Qatrani and underlying Birket Qarun Formations. Our findings indicate that only *Witwatia* could have had a body mass similar to *Vampyravus*. *Witwatia* is known only from Quarry BQ-2 (Late Eocene, Priabonian) in the Birket Qarun Formation. Therefore *Vampyravus* is between 2 and 7 million years younger, depending on where within the Jebel Qatrani Formation it was found. Also, a recently discovered distal humerus of *Witwatia* from BQ-2 demonstrates that this taxon differs substantially from *Vampyravus* in comparable morphology. *Vampyravus* is distinct from all other Fayum fossil bats. *Vampyravus* shares characteristics of the proximal and distal humerus with several extant bat groups including phyllostomids, some rhinolophoids, natalids, emballonurids, and rhinopomatids. The latter two families are represented by fossil forms in the Fayum. Although *Vampyravus* is much larger than either the Fayum emballonurid or rhinopomatid, relatively large size typifies many taxa representing modern bat groups in the Fayum, making it all the more conceivable that *Vampyravus* could belong to one of these families.

*Key words:* Africa, bats, Paleogene, fossils, *Vampyravus orientalis*, body size

## **Operational criteria for genetically defined species: analysis of the diversification of the small fruit-eating bats, *Dermanura* (Phyllostomidae: Stenodermatinae)**

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Species diversity and species limits of the small fruit-eating bats, genus *Dermanura* (Phyllostomidae: Stenodermatinae) were examined. Estimates of species diversity based on classical morphological criteria (current taxonomy) were compared to diversity estimates based on monophyly and cytochrome-*b* sequence divergence. The most recent taxonomic list included nine species, whereas the genetic based list contained 11: *anderseni*, *azteca*, *bogotensis*, *cinerea*, *glauca*, *gnoma*, *phaeotis*, *rava*, *rosenbergi*, *tolteca*, and *watsoni*, of which three (*bogotensis* Andersen, *rava* Miller, and *rosenbergi* Thomas) have been considered synonyms of *cinerea*, *glauca*, *phaeotis*, and *tolteca* by previous authors. In addition, we consider *incomitata* to be a synonym of *watsoni*. Phylogenetic analyses of mtDNA sequences resolved the interrelationships among taxa and prompted us to re-evaluate some morphological characters that support the distinction of all the recognized taxa, therefore providing a robust estimate of species status. A phylogenetic tree revealed a geographic component to the diversification of *Dermanura*, including a historical connection between western Andean and Middle American biota. In South America, no species has been recorded from both sides of the Andes Mountains, and at least one clade (*glauca*, *gnoma*, and *bogotensis*) is restricted to the eastern versant of the Andes. Using genetic data (monophyly and genetic distance) to identify species we were able to produce testable genealogical and biogeographic hypotheses to facilitate further studies.

*Key words:* *Dermanura*, Genetic Species Concept, monophyletic lineages, morphology, phylogenetics, species boundaries

## Ancient and contemporary DNA sheds light on the history of mouse-eared bats in Europe and the Caucasus

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Nietoperzowa Cave in southern Poland has more than 30 subfossils of mouse-eared bats of known age ( $820 \pm 25$  years BP). If DNA has been preserved in a useable fashion in these fossils, they will provide unique opportunities for studying historic population genetics of these animals. We sequenced the entire cytochrome *b* gene (1,140 bp) from seven subfossil and 56 contemporary individuals of mouse-eared bats from Europe and the Caucasus Mts. Our phylogenetic estimates, combined with a low level of genetic differentiation (2.7%) suggest that *M. myotis* and *M. oxygnathus* recently diverged and are distinct at the subspecies level. We also included a fragment of mitochondrial hypervariable region (292 bp) from contemporary mouse-eared bats in our analyses, and noted that among eight haplogroups recorded in Europe and the Caucasian Mts., haplogroup D (recognized as *oxygnathus*) probably arose in the Crimean refugium and evolved in a steppe landscape. The Balkan stock (haplogroup F) was also successful and dispersed over extended areas. Individuals possessing this haplogroup can be found from the northern part of Apennine Peninsula to southern Poland. On the other hand, during the last ice age, individuals with haplogroup A (described as *myotis*) most likely found refugia in Iberia. As the glaciers retreated north, these individuals migrated north of the Alps to central Europe (and then to the Balkans). As this group has much stronger affinities with forests than mouse-eared bats from southern parts of Europe, the dispersal of these individuals would have followed the northern migration of deciduous trees in this area. The Carpathian Basin is an area of mixing for several haplogroups from different refugia, including those in Iberia, Apennine Peninsula, Balkans, and the Crimea. Nuclear RAG2 sequence data revealed reciprocal hybridization events of both historic and recent origins. Our results document for the first time that both taxa were present north of the Carpathian Mts. for at least the past 800 years (ca. 400 generations). These are the first subfossil bats from which DNA has been extracted and sequenced, opening new possibilities for future research. Finally, these data highlight the importance of large phylogeographic surveys even among very common taxa.

**Key words:** mouse-eared bats, *Myotis* spp., ancient DNA, mtDNA and nDNA, Europe, refugia, migratory routes, hybridization

## **Bat activity and genetic diversity at Long Point, Ontario, an important bird stopover site**

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Long Point, Ontario is an important stopover site for a variety of migrating birds and it may also serve migrating bats. While bats often have been caught during mist netting for birds at Long Point, there have been no quantitative studies of migrating (or resident) bats at this location. We monitored bat activity at Long Point using mist-net captures and recordings of echolocation calls in June and August 2006. Bat activity was significantly higher in August than in June, suggesting a peak in bat activity coincident with when migration would be expected to occur. *Lasionycteris noctivagans* was the only species known from Ontario not present at Long Point in June, but it was the second most abundant bat in August. An increase in *L. noctivagans* and *Lasiurus cinereus* abundance between June and August, suggests that Long Point serves as a migratory flyway for both species. Feeding activity of *L. noctivagans* increased towards the end of August, suggesting that it and not others use Long Point as a stopover and refuelling site. Mitochondrial haplotypes of *Myotis lucifugus* were more diverse at Long Point than at a swarming site in Ontario, indicating that Long Point is important for bats, regardless of its function as a stopover site during migration.

*Key words:* bat migration, stopover site, bat activity, genetic diversity, echolocation, acoustic monitoring, mist-netting

## **A first assessment of home range and foraging behaviour of the African long-tongued bat *Megaloglossus woermanni* (Chiroptera: Pteropodidae) in a heterogeneous landscape within the Lama Forest Reserve, Benin**

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We investigated spatial use and foraging behaviour of the nectarivorous African long-tongued bat, *Megaloglossus woermanni* (Chiroptera: Pteropodidae), in the Lama Forest Reserve, southern Benin, West Africa. We monitored movement and activity patterns of two males and two females that were fitted with position-sensitive radio transmitters for five to nine nights within a three-month study period. The study site comprised the central patch of relatively undisturbed forest ('Noyau Central'), and a mosaic of orchards, agroforestry plantations, and degraded forests surrounding the central patch. Spatial use of *M. woermanni* was characterized by small home ranges and high site-fidelity. Mean home range sizes (minimum convex polygon) were larger in females (139.0 and 146.8 ha) than in males (99.8 and 102.9 ha). Throughout the study period, long-tongued bats were frequently observed visiting flowers of cultivated bananas. The mean foraging areas (95% density kernel) of females (39.0 and 109.4 ha) were much larger than in males (12.3 and 14.1 ha). Difference in core areas (50% density kernel) between the sexes was less marked (both females: 6.8 ha, males: 2.7 and 2.9 hectares). Core areas constituted only a small part of home ranges (2.6–4.9%). Large segments of the home ranges were only used for commuting flights between discrete resource patches. Our study provides, for the first time, information on home ranges and foraging behaviour of the sole obligate nectar-drinking bat in Africa.

*Key words:* animal-plant interactions, Dahomey Gap, foraging area, nectarivory, radio-tracking, spatial use, West Africa

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## **Habitat occupancy and detection of the Pacific sheath-tailed bat (*Emballonura semicaudata*) on Aguiguan, Commonwealth of the Northern Mariana Islands**

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Occupancy analysis was used to quantify Pacific sheath-tailed bat (*Emballonura semicaudata*) foraging activity and its relationship to forest structure and proximity to cave roosts on Aguiguan Island in the Commonwealth of the Northern Mariana Islands. Bat occurrence was most closely associated with canopy cover, vegetation stature and distance to known roosts. The metrics generated by this study can serve as a quantitative baseline for future assessments of the status of this endangered species following changes in habitat due to management activities (e.g., feral goat control) or other factors (e.g., typhoon impacts). Additionally, we provide quantitative descriptions of the echolocation calls of *E. semicaudata*. Search-phase calls were characterized by a relatively narrow bandwidth and short pulse duration typical of insectivores that forage within vegetative clutter. Two distinctly characteristic frequencies were recorded:  $30.97 \pm 1.08$  kHz and  $63.15 \pm 2.20$  kHz

*Key words:* Anabat, bat detector, echolocation calls, endangered species, Emballonuridae, Mariana Islands, occupancy analysis

## **Differences in bat activity in relation to bat detector height: implications for bat surveys at proposed windfarm sites**

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We recorded bat activity simultaneously at ground level and 30 m height using Anabat II bat detectors and Anabat ZCAIM recording units mounted on masts at seven sites of varying habitat type in eastern England. At the lower detectors 6194 passes were recorded; 90.02% of calls were from *Pipistrellus*; 6.91% were from *Nyctalus/Eptesicus*; 1.70% were *Myotis/Plecotus*; 0.13% were *Barbastella* and 1.24% could not be determined to species. At the higher detectors 484 passes were recorded from *Pipistrellus* (65.08%) and *Nyctalus/Eptesicus* (34.09%) and 0.83% were not determined to species. Total bat passes and the number of *Pipistrellus* passes were significantly higher on the lower detectors compared with the upper detectors. The difference between numbers of passes of *Nyctalus/Eptesicus* at the upper and lower detectors was not significant, despite proportionally more passes of these species being recorded at height. No extra species groups were recorded at height than were recorded at ground level except at one site where closed canopy broadleaved woodland surrounded the mast. Here, *Nyctalus/Eptesicus* species were recorded only at height. Overall, 28% of *Nyctalus/Eptesicus* passes and 5% of *Pipistrellus* passes were recorded exclusively at height, and not at ground level. Assessing bat activity levels from ground level detectors only can therefore be misleading, particularly when surveying high-flying species that are most likely to be at risk from wind turbine developments.

*Key words:* flight height, Anabat, survey, wind turbine

## **Habitat selection and activity patterns in the greater mouse-eared bat *Myotis myotis***

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The habitat preferences and activity of greater mouse-eared bats were investigated by means of radio-telemetry in two regions in Upper Franconia (Bavaria, Germany) that are characterized by a mosaic of deciduous forests, coniferous forests and woodless areas. In one case bats roosted in a maternity colony from which they visited foraging habitats up to 10.8 km away; in the second, the bats started in a cave which served as a night roost. These bats foraged around the cave up to 2.5 km away. Mean size of foraging areas was  $13.1 \pm 4.6$  ha. Most of the bats used several foraging areas per night (mean 5.1, range 1–10). Hunting time per foraging site ranged from 5 to 224 (median 25) minutes. Foraging habitats in some individuals remained constant over two consecutive years. The bats hunted almost exclusively in woodland (98% of the hunting time) with a significant preference for deciduous forests as opposed to coniferous forests. The preference for deciduous forests as foraging habitats is likely to be caused by: (1) a higher density of suitable prey animals and (2) a better accessibility of the ground-dwelling prey due to the lack of ground vegetation. The mean time span between emergence from the roost and return lasted about 5.5 hours. On average,  $79.9 \pm 9.0\%$  of that time the bats spent flying. They behaved like other gleaning bats and did not show distinct activity peaks. The proportion of commuting flights (between roost and foraging area and between different foraging sites) added up to about 19% of the flight activity whereas the rest of the time in flight was spent hunting. Interruptions in the hunting activity occurred regularly, about five times per night and bat. These breaks lasted 1 to 130 (median 10) minutes and were spent in temporarily used night roosts and on perches. The bats hunted mainly during slow flight, but we also found evidence for hunting from perches on tree trunks as an additional foraging strategy.

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## **Use of underground hibernacula by the barbastelle (*Barbastella barbastellus*) outside the hibernation season**

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Barbastelles are commonly recorded in the vicinity of their wintering underground sites outside the hibernation season. It is uncertain why barbastelles visit hibernacula at this time of the year. Possible functions include feeding, resting, rearing of young, mating or stop-over sites during migration. To determine which of these functions are important I carried out observations at six large (max. 1,870 individuals) barbastelle hibernacula in SW Poland. To characterize daily and seasonal patterns of shelter use behaviour surveys were carried out at regular intervals throughout 2003 to 2005. Bats were mist-netted (73 nights) at hibernacula entrances and their age, sex and the development of caudae epididymides in the males were determined. Their behaviour was sampled by recording (315 hours) their calls with a time-expansion bat detector in combination with direct observation and infrared filming. Hibernacula were not used as colony roosts, foraging places, day resting places or temporary night shelters. The hibernacula served primarily as mating sites. Both females and sexually active males (with fully developed caudae epididymides) were seen in the highest numbers in August/September, when display flights, chases of individuals, low frequency social calling and copulations were observed. As the number of bats visiting hibernacula in the mating period was much higher than that observed in winter, the underground shelters appear to be at least as important for them in the mating period as in the winter. Barbastelle hibernation sites should therefore be protected from the beginning of mating period (August) till the end of hibernation.

*Key words:* *Barbastella barbastellus*, swarming, hibernacula, mating, BCI

## **Forest bats of Madagascar: results of acoustic surveys**

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Spectral and temporal features of echolocation calls produced by 15 insectivorous bat species in three families from Madagascar are described. In addition we provide a library of bat vocalizations that can be used for acoustic inventories involving heterodyne and time-expansion bat detectors. Time-expanded recordings of calls from 153 bats from 15 species were analyzed using five commonly used temporal and frequency variables measured from spectrographs. Echolocation calls for six species (*Scotophilus tandrefana*, *S. marovaza*, *Emballonura tiavato*, *Neoromicia* spp., *N. malagasyensis* and *Triaenops auritus*) are described for the first time. A discriminant function analysis revealed that a function based on the five measured variables provided a correct overall classification of 82.2%. Three groups of echolocation calls based upon the temporal and frequency characteristics of calls are recognized. The Constant Frequency group consists of hipposiderids and *Emballonura* spp., the Frequency Modulated/Quasi-Constant Frequency group is dominated by vespertilionids, and one species, *Myotis goudoti*, is in the Frequency Modulated group. Further we describe the utility of using acoustic sampling in inventory and monitoring studies, and in investigations of habitat use.

*Key words:* Chiroptera, echolocation calls, discrimination, Madagascar

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## **Food and feeding habits of some bats from Turkey**

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Food habits data were obtained from 26 species of bats from Turkey. *Barbastella barbastellus*, *Myotis capaccinii*, *M. mystacinus*, *Plecotus auritus*, *P. austriacus*, *P. kolombatovici*, *P. macrobullaris*, and *Rhinolophus euryale* were primarily moth feeders. *Eptesicus bottae*, *E. serotinus*, *Myotis myotis*, and *Taphozous nudiventris* fed heavily on beetles. *Myotis aurascens* and, *M. brandtii* fed heavily on Diptera. *Myotis blythii* and *Tadarida teniotis* were tentatively classified as cricket feeders at least in Turkey. *Hypsugo savii*, *Miniopterus schreibersii*, *Myotis emarginatus*, *M. nattereri*, *Pipistrellus kuhlii*, *P. pipistrellus*, *P. pygmaeus*, *Rhinolophus ferrumequinum*, *R. hipposideros*, and *R. mehelyi* preyed on a variety of insects and may be treated as generalists. In 17 species, the foods found paralleled those previously reported in the literature, but in nine (some with notably small samples) they did not. These are apparently the first data on the food of *Plecotus macrobullaris*, *P. kolombatovici*, *M. schreibersii*, and *M. aurascens*.

*Key words:* Chiroptera, Turkey, fecal analysis, food habits

## **Calls of a bird-eater: the echolocation behaviour of the enigmatic greater noctule, *Nyctalus lasiopterus***

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The greater noctule (*Nyctalus lasiopterus*) is one of the rarest, least studied and the largest European bat. It feeds on large flying insects and also preys extensively on small night-migrating songbirds that it presumably intercepts at high altitude. The present study provides the first systematic account of echolocation behaviour and call design in the greater noctule. We documented variability in call duration from 1.4 to 25 ms and an associated strong variation in frequency parameters of echolocation calls. Greater noctules adapted call structure and repetition rate to the current perceptual task. In open space, they used calls with very low peak and terminal frequencies; generally below 15 kHz. We recorded echolocation calls from the sympatric — at least in Eastern Europe — smaller congener *N. noctula*. Our data suggest that acoustic separation of the two species is feasible. Therefore, acoustic monitoring could prove useful to survey distribution and habitat use of the enigmatic greater noctule. Using still lower call frequency than *N. lasiopterus* would yield larger detection ranges for large echolocation targets such as migratory birds for the greater noctule, while it might be constrained by the upper hearing threshold of passerines and thus the predator's potential conspicuousness to its prey. However, in a within-genus comparison, allometric scaling explained the greater noctules' call frequency to a very large extent, i.e., we found no evidence for specific adaptations of call frequency to bird hunting.

*Key words:* echolocation, foraging, migratory bird, *Nyctalus*, Vespertilionidae

## **Characterization of the echolocation calls of bats from Exuma, Bahamas**

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The islands of the West Indies are home to 56 species of bats, half of which are endemic to the region. Recently, researchers have begun to characterize the echolocation calls of the bat fauna of the West Indies. However, the majority of species have not yet been characterized and no studies have been conducted on most West Indian islands, including the islands of the Bahamas. Exuma, a small island in the Bahamas, has six species of bats classified in four families (Molossidae, Natalidae, Phyllostomidae, and Vespertilionidae). We used an ultrasonic detector (Avisoft UltraSoundGate 116) to study the echolocation calls of these bats, focusing on three species whose calls have not been previously described, *Erophylla sezekorni*, *Macrotus waterhousii*, and *Nyctiellus lepidus*. Each of these species uses low-intensity, frequency modulated echolocation calls and exhibits intraspecific call variation both among individuals and within individual call sequences. Despite this variation, we were able to accurately classify each species using discriminant function analysis. Accuracy rates varied from 94% (*M. waterhousii*) to 100% (*E. sezekorni*, *N. lepidus*). We also provide a preliminary description of the echolocation calls of two additional Exuman bat species, *Lasiurus borealis* and *Tadarida brasiliensis*. The echolocation calls of *L. borealis* and *T. brasiliensis* appear similar to their mainland counterparts; however, more study is needed to characterize the calls of these two species on Exuma.

*Key words:* acoustic identification, Avisoft, echolocation, *Erophylla*, Exuma, *Macrotus*, *Nyctiellus*, ultrasonic detector

## **Selection of maternity roosts by *Myotis bechsteinii* (Kuhl, 1817) in the Southwestern Iberian Peninsula**

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Bechstein's bat (*Myotis bechsteinii*) is a European species, restricted to woodlands with preference for mature deciduous forests in lowlands. It is considered rare throughout its range, although it may be common in optimal habitats. Roosts play crucial roles in the ecology of bats, and survival is partially dependant on the extent to which roosts protect bats from environmental extremes and predators. Roost selection is especially important for reproductive females, due to the higher energetic demands imposed by reproduction so understanding roost selection by maternity colonies is important for conservation. We investigated maternity roost selection by *M. bechsteinii* in southwestern Spain as a hierarchical process that proceeds from broad landscape scales to fine-scale local habitat characteristics. Radio-tracking of 28 lactating females allowed location and census of 13 maternity roost sites. Roosts were characterised at four detail scales (cavity, tree, stand, and landscape). All the roosts occurred in *Quercus pyrenaica* trees, within stands of the same species of very diverse structure. Ten of the roosts were former woodpecker holes, among which seven had their entrance modified by nuthatch. Roosts were located inside the forest and close (< 620 m) to permanent water sources. Roost trees were characterised by a higher proportion of dead branches. Other explored variables such as tree height, orientation, foliar cover, and elevation did not explain distribution of roosts at any scale. The species' breeding roost selection is described for the first time in a Mediterranean area.

*Key words:* *Myotis bechsteinii*, Mediterranean, maternity roost selection, *Quercus pyrenaica*, forest bats, tree cavities, secondary cavity users

## **Bat foraging strategies and pollination of *Madhuca latifolia* (Sapotaceae) in southern India**

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The sympatrically occurring Indian short-nosed fruit bat *Cynopterus sphinx* and Indian flying fox *Pteropus giganteus* visit *Madhuca latifolia* (Sapotaceae), which offers fleshy corollas ( $\approx 300$  mg) to pollinating bats. The flowers are white, tiny and in dense fascicles. The foraging activities of the two bat species were segregated in space and time. *Cynopterus sphinx* fed on resources at lower heights in the trees than *P. giganteus* and its peak foraging activity occurred at 19:30 h, before that of *P. giganteus*. Foraging activities involved short searching flights followed by landing and removal of the corolla by mouth. *Cynopterus sphinx* detached single corollas from fascicles and carried them to nearby feeding roosts, where it sucked the juice and spat out the fibrous remains. *Pteropus giganteus* landed on top of the trees and fed on the corollas in situ; its peak activity occurred at 20:30 h. This species glided and crawled between the branches and held the branches with claws and forearms when removing fleshy corollas with its mouth. Both *C. sphinx* and *P. giganteus* consumed fleshy corollas with attached stamens and left the gynoecium intact. Bagging experiments showed that fruit-set in bat-visited flowers was significantly higher ( $P < 0.001$ ) than in self-pollinated flowers.

*Key words:* *Cynopterus sphinx*, *Pteropus giganteus*, bat pollination, *Madhuca latifolia*, fleshy corolla, fruit-set

## **Does variation in cranial morphology of *Myotis occultus* (Chiroptera: Vespertilionidae) reflect a greater reliance on certain prey types?**

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Few studies have investigated the relationship between morphological variation and local feeding habits of bats in the United States. We used discriminant function analysis (DFA) to compare cranial morphology of *Myotis occultus* from southern Colorado, and central, and southern New Mexico. We analyzed guano collected from maternity colonies in southern Colorado and central New Mexico to compare food habits. Bats from southern Colorado had the smallest values on the first canonical variate (CV1) that also reflected the smallest measurements of key cranial and dental variables, including height of coronoid process, width of molar, and dentary thickness. Bats from central and southern New Mexico had intermediate and large CV1 values, respectively. Overall, CV1 discriminated individuals occurring in southern Colorado and central New Mexico from those in southern New Mexico. CV2 served best at discriminating bats of southern Colorado from those of central New Mexico. Comparison of food habits revealed that individuals from southern Colorado ate more soft-bodied prey items (e.g., flies) whereas bats from central New Mexico ate more hard-bodied prey items (e.g., beetles). As shown in earlier studies that investigated relationships between morphology and diet of insectivorous bats, we found differences in skull morphology of *M. occultus* that were correlated with differences in food habits.

*Key words:* Colorado, diet, morphology, *Myotis occultus*, New Mexico

## Variation in serum 25-hydroxyvitamin D in free-ranging New-World tropical bats

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Vitamin D (represented by D<sub>2</sub> or D<sub>3</sub>) is considered essential for normal calcium homeostasis. It is either synthesized in the skin following ultraviolet-B irradiation of provitamin D<sub>3</sub> (7-dehydrocholesterol), or ingested in the diet as vitamin D<sub>2</sub> or vitamin D<sub>3</sub>. Most neotropical bats are nocturnal, roost in dark places, and consume diets that lack vitamin D and thus have no other known source of this important nutrient. A few species, namely fish-eating (piscivores) and blood-eating (sanguivores), however, have the potential to ingest large quantities of dietary vitamin D. In this study, blood serum collected from five nocturnal, neotropical bats (including three plant-visiting species, one fish-eating species and one blood-eating species), was analyzed using a competitive protein binding assay (CPBA) to determine concentrations of 25-hydroxyvitamin D [25(OH)D], the major circulating vitamin D metabolite. Cave-roosting (absence of sunlight), plant-visiting species (*Artibeus jamaicensis*, *Brachyphylla cavernarum*, and *Monophyllus redmani*) had a mean serum concentration of 25(OH)D between 7–15 ng/ml, values that are less than sufficient for humans. By contrast, cave-roosting, sanguivorous *Desmodus rotundus* and piscivorous *Noctilio leporinus*, species which have access to dietary vitamin D, had a mean serum concentration of 25(OH)D between 236–247 ng/ml, with high values to 400 ng/ml, the highest recorded for any vertebrate taxon. These findings support the hypothesis that circulating 25(OH)D concentrations in bats are strongly influenced by dietary habits.

*Key words:* calcium, cave-roosting, neotropical bats, UV-B light, vitamin D

## **White-nose syndrome inflicts lasting injuries to the wings of little brown myotis (*Myotis lucifugus*)**

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White-nose syndrome (WNS) is an emerging disease causing massive mortality of hibernating bats in the northeastern United States. At hibernacula, bats affected with WNS typically exhibit growth of a white psychrophilic fungus (*Geomyces destructans*) on the nose, wings and ears; many individuals seem to prematurely die of starvation owing to depleted fat reserves. Conspicuous scarring and necrosis of the wings on WNS-affected bats that survive hibernation may have lasting consequences for survival and reproductive success during the active season. We monitored two maternity colonies of little brown myotis, *Myotis lucifugus*, in Massachusetts and New Hampshire from 14 May to 8 August 2008 to assess body conditions after expected exposure to WNS over the previous winter. We developed a 4-point wing damage index (WDI = 0 to 3) to assess the incidence and severity of wing damage in the months following emergence from hibernation. Severe wing damage was observed up to 4 June and moderate damage was observed through 9 July. Light wing damage was observed on both adult and juvenile bats throughout the study period, but was not exclusively attributed to WNS. The most severe wing damage was associated with a lower body mass index which may reflect reduced foraging success. Overall, reproductive rate was 85.1% in 2008; slightly lower than reported in previous studies. The incidence, timing, and geographic range of wing damage observed on little brown myotis in 2008 correspond to the occurrence of WNS at hibernacula. Monitoring wing conditions of affected and healthy bats will be important tool for assessing the spread of this disease and for establishing baseline data for unaffected bats. The simple scale we propose should be useful for monitoring wing conditions in any bat species.

*Key words:* disease monitoring, flight performance, white-nose syndrome, wing damage index, WNS