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Bat mortality at wind turbines in northwestern Europe

Jens Rydell[1, 5], Lothar Bach[2], Marie-Jo Dubourg-Savage[3], Martin Green[1], Luisa Rodrigues[4],
and Anders Hedenström[1]

[1]*Ecology Building, Lund University, SE-223 62 Lund, Sweden*
[2]*Freilandforschung, zool. Gutachten, Hamfhofsweg 125b, D-28357 Bremen, Germany*
[3]*Société pour l'Etude et la Protection des Mammifères, c/o Muséum d'Histoire Naturelle de Bourges, Les Rives d'Auron, F-18000 Bourges, France*
[4]*Instituto da Conservação da Natureza e da Biodiversidade, Rua de Santa Marta 55, P-1150-294 Lisboa, Portugal*
[5]*Corresponding author: E-mail: jens.rydell@telia.com*

We reviewed published and unpublished written reports on bat mortality at wind farms in northwestern Europe. The estimated number of bats killed per turbine annually was relatively low (0–3) on flat, open farmland away from the coast, higher (2–5) in more complex agricultural landscapes, and highest (5–20) at the coast and on forested hills and ridges. The species killed almost exclusively (98%) belonged to a group (*Nyctalus*, *Pipistrellus*, *Vespertilio* and *Eptesicus* spp.) adapted for open-air foraging. The bats were killed by the moving rotor blades as they hunted insects attracted to the turbines. This occurred independently of sex and age. Peak mortality varied considerably in frequency and timing among years, but the events usually (90%) occurred on nights with low wind speeds in late July to early October and to a lesser extent (10%) also in April-June. The mortality increased with turbine tower height and rotor diameter but was independent of the distance from the ground to the lowest rotor point. It was also independent of the size of the wind park (1–18 turbines). Bat species other than the open-air suite referred to above are usually not at risk at wind turbines, because they fly below the rotors, but are still killed occasionally (2%).

Key words: aerial ecology, aeroecology, bat conservation, high-altitude feeding, killing factors, renewable energy, wind farming

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Do current vampire bat (*Desmodus rotundus*) population control practices pose a threat to Dekeyser's nectar bat's (*Lonchophylla dekeyseri*) long-term persistence in the Cerrado?

LUDMILLA M. S. AGUIAR[1], DANIEL BRITO[2, 3, 4], and RICARDO B. MACHADO[1]

[1]*Universidade de Brasília, Instituto de Biologia, Departamento de Zoologia, Campus Universitário Darcy Ribeiro, Brasília, Distrito Federal 70910-900, Brazil*
[2]*Universidade Federal de Goiás, Instituto de Ciências Biológicas, Departamento de Ecologia, Caixa Postal 131, Goiânia, Goiás 74001-970, Brazil*
[3]*Universidade Estadual de Santa Cruz, Programa de Pós-Graduação em Ecologia e Conservação da Biodiversidade, Rodovia Ilhéus-Itabuna km 16, Ilhéus, Bahia 45662-000, Brazil*
[4]*Corresponding author: brito.dan@gmail.com*

The Cerrado is rapidly losing space to agriculture, pastures and urbanization. Current management practices to control rabies outbreaks through the eradication of vampire bat populations may put other bat species in peril. Our objective is to evaluate if the current vampire bat population control practices could pose a threat to *Lonchophylla dekeyseri*'s persistence, an endemic bat of the Cerrado. We used the VORTEX program to model different vampire bat management scenarios, causing low (25%), medium (50%) or high (75%) incidental mortality to *L. dekeyseri* populations. Inbreeding depression has been identified as a threat to the species, therefore we also modeled scenarios evaluating such effects. Results show that current vampire bat management practices have serious impacts on populations of *L. dekeyseri*. In all cases marked declines in population sizes were observed (even when there was no decline in survival probabilities). For medium and high incidental mortality management scenarios, we also observed decreases in survival probability and in genetic diversity. In those scenarios evaluating vampire bat management and inbreeding depression together, the models suggest that such interaction results in more pronounced declines. Habitat loss and fragmentation in the Cerrado are severe threats and have already negatively impacted *L. dekeyseri*. Unfortunately, if currentpopulation control practices dealing with vampire bats are not changed, inappropriate rabies management may be the coup de grace to the long-term persistence of this species.

Key words: Cerrado, *Desmodus*, *Lonchophylla*, population viability analysis, rabies, roost

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Nocturnal activity patterns of lactating silver-haired bats (*Lasionycteris noctivagans*): the influence of roost-switching behavior

Maarten J. Vonhof[1, 3] and Burr J. Betts[2]

[1]*Department of Biological Sciences and Environmental Studies Program, Western Michigan University, Kalamazoo, MI 49008-5410, USA*
[2]*Eastern Oregon University, One University Blvd., La Grande, OR 97850-2899, USA*
[3]*Corresponding author: E-mail: maarten.vonhof@wmich.edu*

A characteristic feature of forest-dwelling bats is that they regularly switch day roosts. The additional time associated with finding or assessing the availability of a new roost, moving offspring to the new roost, coordinating with other group members, and meeting any increased energetic demands that may be associated with these behaviors may influence the number and duration of feeding bouts of reproductive females. To examine the influence of roost-switching on nocturnal activity patterns we radio-tagged lactating female silver-haired bats (*Lasionycteris noctivagans*) and monitored them on nights when they moved to a new roost site and nights when no roost shift occurred. The typical activity pattern on a non-move night consisted of an initial long bout away from the day roost (median length: 177.4 min) followed by alternating bouts in (50.6 min) and away (57.0 min) from the roost for the rest of the night. On move nights bats reduced the length of their first absent period (82.7 min) and increased the number of trips from the roost, although neither the length of these subsequent absent periods nor the total time absent from the roosts differed from non-move nights. Similarly, total time spent in roosts did not differ between move and non-move nights, but bats made more and shorter visits on move nights. Visits to original and new roosts were not synchronous among colony members, and the length of time for individuals from the same colony to move to a new roost varied from 1 to 4 h. Our results indicate that roost switching did not influence the total time spent in or away from day roosts. Rather, bats moved between the original roost, the new roost, and foraging areas with much greater frequency on move nights.

Key words: activity patterns, lactation, *Lasionycteris noctivagans*, roost switching, silver-haired bat, time budget, tree-roosting

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Foraging behavior of a desert dwelling arthropod-gleaning bat (*Otonycteris hemprichii*) during pregnancy and nursing

SHAI DANIEL[1, 2], CARMI KORINE[2, 3, 4], and BERRY PINSHOW[1, 2]

[1]*Department of Life Sciences, Ben-Gurion University of the Negev, P.O.B. 653, 84105 Beer Sheva, Israel*
[2]*Mitrani Department of Desert Ecology, Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, 84990 Midreshet Ben-Gurion, Israel*
[3]*Present address: Ramon Science Center, P.O.B. 194, 80600 Mitzpe Ramon, Israel*
[4]*Corresponding author: E-mail: ckorine@bgu.ac.il*

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.

Key words: desert, emergence behavior, *Otonycteris hemprichii*, reproduction

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The implications of sympatry in the spectacled and grey headed flying-fox, *Pteropus conspicillatus* and *P. poliocephalus* (Chiroptera: Pteropodidae)

JENNIFER G. PARSONS[1, 4], JEREMY VAN DER WAL[1, 2], SIMON K. A. ROBSON[1], and LOUISE A. SHILTON[1, 3]

[1]*School of Marine and Tropical Biology, James Cook University, Qld, Australia, 4811*
[2]*Centre for Tropical Biodiversity and Climate Change, James Cook University, Qld, Australia, 4811*
[3] *Spatial Conservation, P.O. Box 511, Edge Hill, Qld, Australia, 4870*
[4]*Corresponding author: jennifer.parsons@jcu.edu.au*

Sympatry in flying-foxes is common and it occurs throughout coastal Australia, however *Pteropus conspicillatus* and *P. poliocephalus* are thought to have allopatric populations. We examine the distribution of these two flying-fox species and report on the first flying-fox camp (day roost) with all four species of Australian mainland *Pteropus* co-occurring. Climatic models were developed from previous records to determine if the location of this new camp is climatically suitable for these species. We found that this location is climatically suitable to some degree for both *P. conspicillatus* and *P. poliocephalus* but that the latter had a higher climatic suitability at this site. Historical records exist for *P. poliocephalus* close to this location but not for *P. conspicillatus*. The location of this mixed-species flying-fox camp is the most southerly distribution for *P. conspicillatus*, being 500 km further south than previous records. This area of overlap creates potential opportunities for interbreeding between *P. conspicillatus* and *P. poliocephalus*. Therefore, monitoring of this region for the location of further mixed-species camps and the degree of panmixia at those locations is highly desirable.

Key words: distribution, flying-fox, *Pteropus*, spatial modeling, sympatry

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Echolocation call analysis and presence-only modelling as conservation monitoring tools for rhinolophoid bats in Thailand

ALICE C. HUGHES[1, 4], CHUTAMAS SATASOOK[2], PAUL J. J. BATES[3], PIPAT SOISOOK[2], TUANJIT SRITONGCHUAY[2], GARETH JONES[1], and SARA BUMRUNGSRI[2]

[1]*School of Biological Sciences, University of Bristol, Woodland Road, Bristol, BS8 1UG, United Kingdom*
[2]*Princess Maha Chakri Sirindhorn Natural History Museum, Faculty of Science, Prince of Songkla University, 15 Karnjanavanit Road, Hat Yai, Songkhla 90112, Thailand*
[3]*Harrison Institute, Centre for Systematics and Biodiversity Research, Bowerwood House, 15 St Botolph's Road, Sevenoaks, Kent, TN13 3AQ, United Kingdom*
[4]*Corresponding author: E-mail: AH3881@bristol.ac.uk*

Bats are an important component of biodiversity in Southeast Asia, and are key indicators of habitat quality. Acoustic analysis of echolocation calls not only allows the identification of bat species that are difficult to capture, but also allows for rapid and standardised ways to survey and monitor bats over large areas. However keys based on call parameters must also account for geographic variation in call parameters, and consider any effects of morphology and sex on call frequency. Presence-only modelling can predict likely geographic locations of specific taxa, and can used to refine decision making so that species unlikely to occur in a specific region can be omitted from more localised acoustic libraries. Here we develop an acoustic library for the echolocation calls of rhinolophoid bats in Thailand, and use presence-only modelling (Maxent) to explore how species with similar calls in a library developed at the national level can sometimes be largely allopatric, and hence identifiable, once geographic range is predicted. Presence-only modelling can also be used to explore whether species with similar calls adjust call frequency in likely areas of sympatry. We analysed calls from fourteen species of rhinolophid and twelve hipposiderid species from Thailand. Calls from a further three rhinolophid and one hipposiderid species are also described but not analysed statistically because of small sample sizes. Even without considering geographic variation, 69% of rhinolophid (14 species with a minimum of five individuals/ species) and 91% of hipposiderid calls (12 species) could be classified successfully to species using two call parameters (frequency of most energy (*FMAXE*) and duration) in a discriminant function analysis. Most of the discrimination was achieved because species often utilised different frequency bands. Morphology can also affect call frequency both across and within species. In both rhinolophids and hipposiderid families there was a negative relationship between *FMAXE* and forearm length. Within species, *FMAXE* was negatively related to forearm length in *Rhinolophus microglobosus*, *R. pusillus* and *R. thomasi*, and positively related to forearm length in *R. affinis* and *R. pearsonii*. Male *R. pusillus* called at higher frequencies than females, although there was no sexual size dimorphism in forearm length. Call frequency was negatively related to relative humidity in *R. pusillus*, suggesting that bats called at lower frequencies in humid environments to counter increases in atmospheric attenuation. Presence-only modelling was used to show that some species with similar call frequencies (e.g., *R. lepidus* and *R. microglobosus*; *R. yunanensis* and *R. trifoliatus* are predicted to occur largely in allopatry, and so could be identified reliably in particular parts of the country. Presence-only modeling can assist in predicting areas of overlap between species with similar call frequencies. Other species (e.g., *R. malayanus*, *R. coelophyllus*) overlap in frequency when data from all of Thailand are combined, but seem to avoid call overlap when syntopic. Hence acoustic identification can be improved by taking into account local distribution patterns and patterns of species coexistence. The creation of call libraries at a local scale would have extensive potential as a resource to monitor changes in species distributions through time.

Key words: constant frequency, acoustic identification, horseshoe bats, Old World leaf-nosed bats, Southeast Asia

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Intra- and interspecific responses to Rafinesque's big-eared bat (*Corynorhinus rafinesquii*) social calls

SUSAN C. LOEB[1, 3] and ERIC R. BRITZKE[2]

[1]*USDA Forest Service, Southern Research Station, Department of Forestry and Natural Resources, Clemson University, Clemson, SC 29634, USA*
[2]*US Army Engineer Research and Development Center, 3909 Halls Ferry Road, Vicksburg, MS 39180, USA*
[3]*Corresponding author: E-mail: sloeb@fs.fed.us*

Bats respond to the calls of conspecifics as well as to calls of other species; however, few studies have attempted to quantify these responses or understand the functions of these calls. We tested the response of Rafinesque's big-eared bats (*Corynorhinus rafinesquii*) to social calls as a possible method to increase capture success and to understand the function of social calls. We also tested if calls of bats within the range of the previously designated subspecies differed, if the responses of Rafinesque's big-eared bats varied with geographic origin of the calls, and if other species responded to the calls of *C. rafinesquii*. We recorded calls of Rafinesque's big-eared bats at two colony roost sites in South Carolina, USA. Calls were recorded while bats were in the roosts and as they exited. Playback sequences for each site were created by copying typical pulses into the playback file. Two mist nets were placed approximately 50–500 m from known roost sites; the net with the playback equipment served as the Experimental net and the one without the equipment served as the Control net. Call structures differed significantly between the Mountain and Coastal Plains populations with calls from the Mountains being of higher frequency and longer duration. Ten of 11 Rafinesque's big-eared bats were caught in the Control nets and, 13 of 19 bats of other species were captured at Experimental nets even though overall bat activity did not differ significantly between Control and Experimental nets. Our results suggest that Rafinesque's big-eared bats are not attracted to conspecifics' calls and that these calls may act as an intraspecific spacing mechanism during foraging.

Key words: call playback, *Corynorhinus rafinesquii*, eavesdropping, echolocation, social calls

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Why the bat did not cross the road?

ARTHUR A. ZURCHER[1, 4], DALE W. SPARKS[2], and VICTORIA J. BENNETT[3]

[1] *Center for North American Bat Research and Conservation, Department of Biology, Indiana State University, Terre Haute, IN 47809, USA*
[2] *Environmental Solutions and Innovations, 781 Neeb Road, Cinncinati, OH 45233, USA*
[3] *Department of Forestry and Natural Resources, Purdue University, West Lafayette, IN 47907, USA*
[4] *Corresponding author: E-mail: azurcher1@indstate.edu*

Roadways are nearly ubiquitous parts of the modern landscape, but their impact on bats remain relatively unknown. We studied the influence of vehicular traffic on the behaviour of commuting bats near the Indianapolis International Airport. A previous study at this site documented that Indiana bats (*Myotis sodalis*) were much more likely to cross roads with low traffic volumes. One potential interpretation of this result is that bats perceive motor vehicles as a threat and exhibit avoidance behaviour whether or not the bats are in immediate danger. To test this hypothesis, we observed 211 cases of bats approaching roads that bisected their commuting routes. Information recorded at the time included the presence or absence of vehicles, the height the bat was flying, whether a bat reversed course prior to crossing the road and if so the distance from the road or vehicle (if present) when it altered its direction, and finally the speed, type and relative level of noise emitted by vehicles. Results revealed that bats were more than twice as likely to reverse course when vehicles were present as opposed to their absence. When automobiles were present 60% of bats exhibited avoidance behaviour, reversing course at an average of 10 m from a vehicle. Conversely, when no automobiles were present, only 32% of bats reversed their course and 68% crossed the road. The height a bat flew, speed of the vehicle, type of vehicle or level of noise emitted by vehicles had no effect on the likelihood of bats reversing course. These data support the hypothesis that bats perceive vehicles as a threat and display anti-predator avoidance behaviour in response to their presence.

Key words: anti-predator behaviour, automobiles, bats, behavioural modification, commuting, roadways

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The diet of Indian flying-foxes (*Pteropus giganteus*) in urban habitats of Pakistan

MUHAMMAD MAHMOOD-UL-HASSAN[1, 3], TAYIBA L. GULRAIZ[1], SHAHNAZ A. RANA[2], and ARSHAD JAVID[1]

[1]*Department of Wildlife and Ecology, University of Veterinary and Animal Sciences, Syed Abdul Qadir Jilani Raod, Lahore, Pakistan*
[2]*Department of Zoology, University of Agriculture, Faisalabad, Pakistan*
[3]*Corresponding author: E-mail: drmmhassan@gmail.com*

We studied the diet of the Indian flying fox (*Pteropus giganteus*) in Pakistan from March 2008 to February 2009 and found that the bats fed on 20 species belonging to 11 plant families. Of these, four families (Anacardiaceae, Bignonaceae, Malvaceae, and Sapotaceae) were identified from remnants of flower petals in food boluses while the remaining families (Annonaceae, Arecaceae, Ebenaceae, Meliaceae, Moraceae, Myrtaceae, and Sapindaceae) were identified from the seeds in the boluses and from guano samples. Plants in the family Moraceae (50.7%) comprised most of the bat's diet. Fruit of *Ficus retusa* (27.5%) and *F. carica* (23.0%) during winter, *F. glomerata* (30.9%) and *F. religiosa* (28.1%) during spring, *Psidium guajava* (19.6%), *F. bengalensis* (18.7%) and *Diospyros peregrina* (17.8%) during summer, and *D. peregrina* (71.9%) during autumn, were the most frequently identified items. The four seasonal diets varied significantly ($\chi^2 = 435$, $d.f. = 18$, $P < 0.01$). Results confirm that the ecological services rendered by *P. giganteus*, such as pollination and seed dispersal, outweigh its losses, such as damage to the ripe fruit. Hence, the species should not be regarded as a pest; rather efforts should be made to ensure its conservation.

Key words: conservation, *Ficus*, fruit bat, Pakistan, pest, seed dispersal, urban habitat

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Do bats forage over cattle dung or over cattle?

NICK C. DOWNS[1, 3] and LAURA J. SANDERSON[1,2]

[1]*Hyder Consulting Limited, Cresswell Associates, The Mill, Brimscombe Port, Stroud, Gloucestershire, GL5 2QG, United Kingdom*
[2]*School of Animal and Microbial Sciences, University of Reading, Whiteknights, P.O. Box 228, Reading, Berkshire, RG6 6AJ, United Kingdom*
[3]*Corresponding author: E-mail: nhi768@yahoo.co.uk*

Although the importance of cattle grazed pasture to foraging bats has already been well documented, the relative importance of cattle dung compared with the cattle themselves is largely unknown. This was investigated by comparing two adjacent fields: a current and a recent area of organic cattle-grazed pasture in England. The cattle were exchanged between fields during each of two separate observation periods in June and July 2005, one of eight evenings and the other of ten. Hand-held detectors were used to record time-expanded bat passes simultaneously from comparable positions within each field for 150 minutes after sunset. In addition, two separate observation periods (one of three evenings and the other of four) was used to investigate bat activity over and away from cattle within the same field. In general, bat activity was statistically greater within the field containing cattle than in the field without cattle (paired t-test, $t_{21} = 3.97$, $P < 0.001$). Within the field containing cattle, bat activity was greater over cows than away from them (paired t-test, $t_6 = 2.48$, $P < 0.05$). It is therefore suggested that cattle, rather than dung are the primary attractant for foraging bats. Specifically, the difference in bat activity between the fields with and without cattle was statistically significant for *Eptesicus serotinus* (paired t-test, $t_{21} = 4.14$, $P < 0.001$), *Pipistrellus pipistrellus* (paired t-test, $t_{21} = 3.23$, $P < 0.01$) and *Myotis* (Dunn's test, $Z = 2.99$, $P < 0.01$) bats. Management recommendations include keeping cattle within bat foraging areas, minimizing the use of anthelminthic avermectin-based drugs for cattle, and maintaining woodland/trees within and around cattle-grazed pasture.

Key words: Chiroptera, farming, foraging, management, England

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Predation by free-roaming cats on an insular population of bats

ARMANDO RODRÍGUEZ-DURÁN[1, 2], JANSEL PÉREZ[1], MARI ANA MONTALBÁN[1], and JEAN M. SANDOVAL[1]

[1]*Universidad Interamericana, 500 John W. Harris Ave., Bayamón, PR 00957, USA*
[2]*Corresponding author: E-mail: arodriguez@bc.inter.edu*

Free-roaming cats are known to adversely impact native faunas in the areas where they have been introduced, an impact that is even greater on islands. We examine the predation of bats by cats at Culebrones cave, Puerto Rico, West Indies. Culebrones cave is a hot cave located in the karst region of northern Puerto Rico. The temperature gradient inside the cave sustains a multi-species assemblage of bats consisting of approximately 300,000 individuals of six species, namely: *Brachyphylla cavernarum*, *Erophylla bombifrons*, *Monophyllus redmani*, *Mormoops blainvillei*, *Pteronotus quadridens* and *Pteronotus parnellii*. Even though rats are often their primary prey, cats will use alternative prey, which enables them to maintain their abundance when one prey is not available. In Puerto Rico, birds and reptiles are known to be preyed upon by cats. Although cats are commonly observed in or around bat caves in Puerto Rico, this is the first systematic attempt to evaluate their role as bat predators. We made observations of the hunting strategy of cats using an infrared camera and recorded the number of wings left as remains of these hunting bouts. Wings were identified to species. Cat scats were also recovered and examined to identify prey species. Our results suggest that captures of different species of bats is not a function of their abundance in the cave. While *M. blainvillei* (11 g) and *P. quadridens* (5 g) are the most abundant species in the cave, *B. cavernarum* (50 g) and *M. redmani* (11 g) are captured in greater numbers by the cats.

Key words: islands, tropical bats, predation, cats, foraging behavior

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A test of mist-net configurations in capturing bats over stream corridors

L. MICHELLE GILLEY[1, 3] and MICHAEL L. KENNEDY[2]

[1]*Department of Biological Sciences, 331 Funchess Hall, Auburn University, Alabama 36849, USA*
[2]*Department of Biology, Ellington Hall 307, The University of Memphis, Tennessee 38152, USA*
[3]*Corresponding author*: *E-mail: gillelm@auburn.edu*

Most surveys for bats are conducted using mist nets in riparian areas along stream corridors. Various methods exist for deploying mist nets, but success of using different configurations has not been assessed. We tested efficiency of three configurations of mist nets during summers of 2000 and 2001 at the Milan Army Ammunition Plant (Carroll and Gibson counties) in western Tennessee. Configurations of mist nets included: I (one net placed transverse to stream), T (one net placed transverse to stream, and one net positioned perpendicular to first net in midstream), and Z (two nets positioned parallel to stream, and a center net positioned diagonally between the two nets). The study consisted of 347 net nights and 220 captures of bats (85 I, 62 T, 73 Z). Four species were captured including: 133 *Lasiurus borealis*, 63 *Perimyotis subflavus*, 15 *Nycticeius humeralis*, and nine *Myotis austroriparius*. Sex-ratios for adults were female biased, while juvenile sex-ratios were near equal. Netting results suggest that traditional I-configurations were statistically equal to T- and Z-configurations for all analyses of total captures and for the two dominant species captured: *L. borealis* and *P. subflavus*. Because the I-configuration requires less equipment and time for set-up, capturing bats in linear corridors could be optimized by using more I-nets rather than multiple net configurations.

Key words: bats, capture techniques, *Lasiurus borealis*, mist-net configuration, *Perimyotis subflavus*, Tennessee

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A recent inventory of the bats of Mozambique with documentation of seven new species for the country

ARA MONADJEM[1, 13], M. CORRIE SCHOEMAN[2], APRIL RESIDE[3], DOROTHEA V. PIO[4], SAMANTHA STOFFBERG[5], JULIAN BAYLISS[6, 7], F. P. D. (WOODY) COTTERILL[8], MICHAEL CURRAN[9, 10], MIRJAM KOPP[9], and PETER J. TAYLOR[11, 12]

[1]*All Out Africa Research Unit, Department of Biological Sciences, University of Swaziland, Private Bag 4, Kwaluseni, Swaziland*
[2]*School of Biological and Conservation Sciences, University of KwaZulu-Natal, Durban, Republic of South Africa*
[3]*All Out Africa, P.O. Box 153, Lobamba, Swaziland*
[4]*Département d'Ecologie et Evolution, Université de Lausanne, Biophore 1015, Lausanne, Switzerland*
[5]*Evolutionary Genomics Group, Department of Botany and Zoology, University of Stellenbosch, Private Bag X1, Matieland, Stellenbosch, Republic of South Africa*
[6]*Mulanje Mountain Conservation Trust (MMCT), P.O. Box 139, Mulanje, Malawi*
[7]*Conservation Science Group, Department of Zoology, University of Cambridge, Cambridge, UK*
[8]*AEON – Africa Earth Observatory Network, Departments of Geological Sciences, and Molecular and Cell Biology, University of Cape Town, Rondebosch 7701, Republic of South Africa*
[9]*Institute of Biogeography, University of Basel, St. Johanns-Vorstadt 10, CH-4056, Switzerland*
[10]*Institute of Environmental Engineering, ETH Zurich, HIF C 13, Wolfgang-Pauli-Str. 15, CH-8093 Zurich, Switzerland*
[11]*Durban Natural Science Museum, P. O. Box 4085, Durban, Republic of South Africa*
[12]*Department of Ecology and Resource Management, School of Environmental Sciences, University of Venda, Private Bag X5050, Thohoyandou, 0950, Republic of South Africa*
[13]*Corresponding author: E-mail: ara@uniswacc.uniswa.sz*

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.

Key words: Mozambique, Chiroptera, distribution, check-list, conservation

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Karyotypic variation in rhinolophid and hipposiderid bats (Chiroptera: Rhinolophidae, Hipposideridae)

DARINA KOUBÍNOVÁ[1, 4], K. S. SREEPADA[2], PETR KOUBEK[3], and JAN ZIMA[3]

[1]*Department of Zoology, Faculty of Science, Charles University, Viničná 7, CZ-12844 Praha 2, Czech Republic*
[2]*Department of Applied Zoology, Mangalore University, Mangalagangotri - 574 199, Karnataka, India*
[3]*Institute of Vertebrate Biology, Academy of Sciences, Květná 8, CZ-60365 Brno, Czech Republic*
[4]*Corresponding author: E-mail: darina.koubinova@gmail.com*

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 (2*n*) 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 2*n* 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 2*n* of 32, 36, 52, 56, 58, and 62, and with relatively stable number of autosomal arms (FNa = 60, 62, 64) were recorded.

Key words: chromosomal evolution, karyosystematics, Robertsonian translocations

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Range-wide population genetic structure of the pallid bat (*Antrozous pallidus*) — incongruent results from nuclear and mitochondrial DNA

JUSTIN B. LACK[1, 2], JEREMY E. WILKINSON[1], and RONALD A. VAN DEN BUSSCHE[1]

[1]*Department of Zoology, 501 Life Sciences West, Oklahoma State University, Stillwater, OK 74078, USA*
[2]*Corresponding author: E-mail: justin.lack@okstate.edu*

Male-biased dispersal with female philopatry is a common pattern for many mammals. Because mtDNA is inherited maternally, biparentally inherited nuclear markers are often utilized to estimate population structure and gene flow. The pallid bat (*Antrozous pallidus*) exhibits a relatively continuous distribution across arid western North America. A previous mtDNA study suggested little gene flow among populations and identified three distinct phylogroups. We examined population structure of *A. pallidus* using amplified fragment length polymorphisms (AFLP) in 187 individuals from 29 localities across the distribution of the species. Eight primer pairs identified 797 polymorphic loci. All analyses indicated that populations in California, British Columbia, and the Baja Peninsula were relatively distinct. Cluster analysis indicated gene flow has been occurring between the Baja Peninsula population and populations to the north and east. The pallid bat appears to be characterized by male-mediated dispersal and gene flow, while females are largely philopatric. While several populations appear to be somewhat distinct, the overall pattern of divergence for *A. pallidus* is indicative of isolation by distance throughout the majority its range, suggesting significant gene flow has been occurring since populations diverged during Pliocene desert formation and mountain building.

Key words: *Antrozous pallidus*, philopatry, phylogeography, AFLP, sex-biased dispersal, Pliocene

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A taxonomic review of the *Hipposideros bicolor* species complex and *H. pomona* (Chiroptera: Hipposideridae) in Thailand

BOUNSAVANE DOUANGBOUBPHA[1, 2, 5], SARA BUMRUNGSRI[2], PIPAT SOISOOK[3], CHUTAMAS SATASOOK[3],
NIKKY M. THOMAS[4], and PAUL J. J. BATES[4]

[1]*Faculty of Environmental Sciences, National University of Laos, Dong Dok Campus, Xaythany District, Vientiane Capital, Lao PDR*
[2]*Department of Biology, Faculty of Science, Prince of Songkla University, Hat Yai 90112, Thailand*
[3]*Princess Maha Chakri Sirindhorn Natural History Museum, Faculty of Science, Prince of Songkla University, Hat Yai 90112, Thailand*
[4]*Harrison Institute, Centre for Systematics and Biodiversity Research, Bowerwood House, St. Botolph's Road, Sevenoaks, Kent, TN13 3AQ, Great Britain*
[5]*Corresponding author: E-mail: bounsavanhd@yahoo.com*

Following extensive field work in Thailand (2006–2008), this paper reviews the taxonomic status of the three species of the *Hipposideros bicolor* group. Based on morphometric characters and acoustic data, the two phonic types, *H. bicolor* (131 kHz) and *H. bicolor* (142 kHz) are treated as distinct species. *Hipposideros bicolor* (131 kHz) is designated as *H. bicolor*; *H. bicolor* (142 kHz) is provisionally designated as *H. atrox*. The morphometric characters, acoustic data, and geographical distribution of *H. pomona* are also reviewed. The diagnostic characters of these frequently confused taxa are discussed, with a detailed study of the external, cranio-dental, and bacular morphology, and acoustic features. New data on the conservation status, distribution and ecology of these three species are included.

Key words: *Hipposideros bicolor* group, *H. atrox*, *H. pomona*, taxonomy, distribution, Thailand

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Morphological evidence for hybridization in the sister species *Myotis myotis* and *Myotis oxygnathus* (Chiroptera: Vespertilionidae) in the Carpathian Basin

JUSTYNA BACHANEK[1, 2] and TOMASZ POSTAWA[1]

[1]*Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Sławkowska 17, 31-016 Kraków, Poland*
[2]*Corresponding author: E-mail: jbachan@gmail.com*

A recent molecular-based study suggested that two sister species of mouse-eared bats (*Myotis myotis* and *M. oxygnathus*) share some mtDNA haplotypes when they occur in sympatry. We used traditional morphometric methods in order to find potential hybrid specimens. Multivariate morphometric analysis of 22 cranial and dental characters was applied to a sample of 298 adult specimens of mouse-eared bats (*Myotis myotis* and *M. oxygnathus*) from their sympatric range in the Carpathian Basin. Additionally, we included several juvenile exemplars of both species in order to exclude the treatment of juvenile specimens as individuals with intermediate characteristics. Principal Component Analyses (PCA) and Discriminant Function Analysis (DFA) revealed a distinct separation between specimens of *M. myotis* and *M. oxygnathus*, with 6 specimens in an intermediate position. All intermediate specimens come from the contact area of *M. myotis* and *M. oxygnathus*. A subsequent detailed analysis showed that intermediate specimens are similar to *M. myotis* in skull and mandible size, but with tooth-row size similar to *M. oxygnathus*. An analogous situation has been described in several species of small mammals. Bats designated as intermediate are probable hybrids, i.e. their phenotypes lay between the parental forms.

Key words: Mouse-eared bat, cranial measurements, intermediate individuals, morphological analysis, Carpathian Basin

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Revalidation of *Myotis taiwanensis* Ärnbäck-Christie-Linde 1908 and its molecular relationship with *M. adversus* (Horsfield 1824) (Vespertilionidae, Chiroptera)

NAI-JIAN HAN[1], JIN-SHUO ZHANG[1], TERRY REARDON[2], LIANG-KONG LIN[3], JUN-PENG ZHANG[4], and SHU-YI ZHANG[4, 5]

[1]*Institute of Zoology, and Graduate University of Chinese Academy of Sciences, 100101, Beijing, China*
[2]*Evolutionary Biology Unit/Vertebrates, South Australian Museum, North Terrace, Adelaide SA 5000, Australia*
[3]*Department of Life Science, Tunghai University, Taichung, 40704, Taiwan, China*
[4]*School of Life Science, East China Normal University, 200062, Shanghai, China*
[5]*Corresponding author: E-mail: syzhang@bio.ecnu.edu.cn*

A combined approach using molecular and morphological data has revealed that the taxon *Myotis taiwanensis*, which until now has been usually considered as a subspecies of *Myotis adversus*, should be reinstated as a full species, as originally described by Ärnbäck-Christie-Linde (1908) from Takao, Anping, Tainan, Formosa (= southern Taiwan). In our genetic analysis using two nuclear DNA segments of protein kinase C iota (PRKCI) and ubiquitin specific peptidase 9 (Usp9x), X-linked genes, together with two mitochondrial genes, i.e., nicotinamide adenine dinucleotide dehydrogenase subunit 1 (ND1) and cytochrome *b* (Cyt *b*), we demonstrate that *M. taiwanensis* is closely related to *M. pilosus*, and largely divergent from two subspecies of *M. adversus*. Our analysis further shows that *M. taiwanensis* differs considerably from *M. adversus* in external and dental features. New records of *M. taiwanensis* from Shandong and Anhui provinces in eastern China are presented.

Key words: *Myotis adversus*, *M. taiwanensis*, molecular phylogeny, morphology

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The status of the cryptic bat species, *Myotis mystacinus* and *Myotis brandtii* in Ireland

EMMA S. M. BOSTON[1], DANIEL J. BUCKLEY[1], MICHAËL BEKAERT[1], YANN GAGER[1], MATHIEU G. LUNDY[2], DAVID D. SCOTT[2], PAULO A. PRODÖHL[2], W. IAN MONTGOMERY[2], FERDIA MARNELL[3], and EMMA C. TEELING[1, 4]

[1]*Centre for Irish Bat Research, University College Dublin, School of Biology and Environmental Science, Belfield, Dublin 4, Ireland*
[2]*Centre for Irish Bat Research, Queen's University Belfast, Medical and Biological Centre, 97 Lisburn Road, Belfast, Northern Ireland, United Kingdom*
[3]*National Parks and Wildlife Service, 7 Ely Place, Dublin 2, Ireland*
[4]*Corresponding author: E-mail: emma.teeling@ucd.ie*

The recent identification of *Myotis brandtii* in Ireland raised the possibility that many roosts previously identified as *M. mystacinus* had the potential of being misidentified *M. brandtii*. Thus, the distribution and population estimates for *M. mystacinus* may have been over-estimated, while *M. brandtii* may have been under-estimated. Results from an all Ireland genetic survey of known *M. mystacinus* maternity roosts confirm that no long term misidentification has taken place. All specimens caught and sampled were *M. mystacinus*. Additonally, no further records of *M. brandtii* were found during six nights of woodland trapping using the acoustic lure. While the status of *M. mystacinus* in Ireland is now listed as 'least concern' in the Irish Red List, *M. brandtii* is listed as 'data deficient' and cannot currently be considered a resident species

Key words: Vespertilionidae, *Myotis*, cryptic species, Irish mammals

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Vespertilio murinus Linnaeus, 1758 confirmed in Japan from morphology and mitochondrial DNA

KUNIKO KAWAI[1, 2, 7], DAI FUKUI[3], MASAHIKO SATÔ[4], MASASHI HARADA[5], and KISHIO MAEDA[6]

[1]*Field Science Center for Northern Biosphere, Hokkaido University, Sapporo, Hokkaido, Japan*
[2]*Division of Mammals, National Museum of Natural History, Smithsonian Institution, Washington, D.C., USA*
[3]*Hokkaido Research Center, Forestry and Forest Products Research Institute, Sapporo, Hokkaido, Japan*
[4]*Rishiri Town Museum, Senhoshi, Rishiri Island, Hokkaido, Japan*
[5]*Laboratory Animal Center, Osaka City University, Graduate School of Medicine, Abeno, Osaka, Japan*
[6]*Center for Natural Environment Education, Nara University of Education, Takabatake, Nara-City, Japan*
[7]*Corresponding author: E-mail: kkawai@fsc.hokudai.ac.jp*

In December 2005, three bats of indeterminate identity were captured in northern Japan. Their forearm lengths were slightly smaller than the average for *Vespertilio sinensis*. We identified these three individuals as *V. murinus* using both morphological and molecular approaches, and discussed their possible migration or vagrancy routes. Prior to the first record of *V. murinus* on Rebun Island near Hokkaido in 2002, there was no record of this species in Japan. These new occurrences illustrate the importance of determining possible migration or vagrancy routes of bats for understanding and preventing the spread of zoonotic diseases.

Key words: *Vespertilio murinus*, mtDNA, cytochrome-*b*, ND1, migration, occurrence, Japan

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Myotis alcathoe confirmed in the UK from mitochondrial and microsatellite DNA

CAMILLE M. I. JAN[1, 3], KATIE FRITH[2, 3], ANITA M. GLOVER[1], ROGER K. BUTLIN[2], CHRIS D. SCOTT[1],
FRANK GREENAWAY[1], MANUEL RUEDI[4], ALAIN C. FRANTZ[3], DEBORAH A. DAWSON[3], and JOHN D. ALTRINGHAM[1, 5]

[1] *IICB, Faculty of Biological Sciences, University of Leeds, Leeds, LS2 9JT, United Kingdom*
[2] *Animal and Plant Sciences, University of Sheffield, Sheffield, S10 2TN, United Kingdom*
[3] *NERC Biomolecular Analysis Facility, Department of Animal and Plant Sciences, University of Sheffield, Sheffield, S10 2TN, United Kingdom*
[4] *Muséum d'Histoire Naturelle, 1 route de Malagnou, CH-1208 Genève, Suisse*
[5] *Corresponding author: E-mail: j.d.altringham@leeds.ac.uk*

We describe the recent discovery of Alcathoe bat, *Myotis alcathoe*, at locations in the south and north of England. First described in 2001 from individuals caught in Greece, the species' known range has steadily been extended across much of Europe. Its presence in the UK was confirmed by mtDNA (ND1) and microsatellite analysis of wing biopsy samples collected between 2003–2009, primarily at swarming sites. Morphological and echolocation call data are consistent with the genetic interpretation. The presence of *M. alcathoe* at sites 350 km apart, and the probability that it makes up a significant proportion of the small *Myotis* bats at these sites, suggest it is a resident species. Preliminary assessment of its distribution in the UK will be facilitated by its distinctive echolocation call, an FM sweep that typically terminates at 43–46 kHz, above those of other *Myotis* species.

Key words: *Myotis alcathoe*, UK, mtDNA, microsatellite genotyping, swarming