Acta Chiropterologica, 12(1): 1–18, 2010

PL ISSN 1508-1109 $\ensuremath{\mathbb{C}}$ Museum and Institute of Zoology PAS doi: 10.3161/150811010X504554

Late Middle Eocene bats from the Creechbarrow Limestone Formation, Dorset, southern England with description of a new species of *Archaeonycteris* (Chiroptera: Archaeonycteridae)

DAVID L. HARRISON^{1, 3} and JEREMY J. HOOKER²

¹Harrison Institute, Centre for Systematics and Biodiversity Research, Bowerwood House, St. Botolph's Road, Sevenoaks, Kent TN13 3AQ, Great Britain
²Department of Palaeontology, The Natural History Museum, Cromwell Road, London, SW7 5BD, Great Britain
³Corresponding author: E-mail: hzm@btinternet.com

Isolated teeth of Chiroptera from the Creechbarrow Limestone Formation of late Middle Eocene age are reported. Five distinct chiropteran taxa are present. A new species of *Archaeonycteris* is described, representing the last survivor of this archaic genus. Two rhinolophoid species include the hipposiderid *Pseudorhinolophus schlosseri* and Rhinolophidae gen. et sp. indet. Vespertilionoid bats are represented by one species *Stehlinia quercyi*. A single trigonid represents a small species, which could have affinity with the genus *Ageina*.

Key words: Late Middle Eocene, Archaeonycteris n.sp., Hipposideridae, Rhinolophidae, Vespertilionidae, Ageina

Acta Chiropterologica, 12(1): 19–27, 2010 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/150811010X504563

Chiroptera (Mammalia) from the Holocene of Rio Grande do Sul state, Brazil

PATRÍCIA HADLER^{1, 3}, JORGE FERIGOLO², and ANA MARIA RIBEIRO²

¹Universidade Federal Rural de Pernambuco, Unidade Acadêmica de Serra Talhada, Fazenda Saco, s/n, Serra Talhada, PE, Brazil, CEP 56900-000 ²Secção de Paleontologia, Museu de Ciências Naturais, Fundação Zoobotânica do Rio Grande do Sul, Av. Dr. Salvador França, 1427, Porto Alegre, RS, Brazil, CEP 90690-000 ³Corresponding author: E-mail: hadlerpa@gmail.com

The Chiroptera do not have an extensive fossil record. To date, for the Quaternary of Brazil, only material from Minas Gerais, São Paulo, Bahia and Goiás States are known. For Rio Grande do Sul State, in contrast to the studies about the Pleistocene megafauna, little is known about Holocene small mammals, this being the first contribution about the Chiroptera of this age found in Rio Grande do Sul. The material was excavated from two archaeological sites, dating from \pm 9,400 yrs BP to \pm 4,250 yrs BP. The taxa recorded were: *Chrotopterus auritus, Pygoderma bilabiatum* (Phyllostomidae); *Eptesicus brasiliensis, E. fuscus, Myotis* cf. *Myotis ruber*, Vespertilionidae aff. *Lasiurus* (Vespertilionidae); *Tadarida brasiliensis*, and *Molossus molossus* (Molossidae). The presence of *E. fuscus* extends its Holocene distribution far southwards into the south temperate zone; its previous Quaternary occurrences were in Bahia State, Brazil, as well as in Venezuela, Mexico and the USA.

Key words: Chiroptera, Holocene, paleobiogeography, Rio Grande do Sul state, Brazil

Acta Chiropterologica, 12(1): 29–50, 2010 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/150811010X504572

A taxonomic review of *Hipposideros halophyllus*, with additional information on *H. ater* and *H. cineraceus* (Chiroptera: Hipposideridae) from Thailand and Myanmar

BOUNSAVANE DOUANGBOUBPHA^{1, 2, 8}, SARA BUMRUNGSRI², PIPAT SOISOOK³, SUSAN W. MURRAY⁴, SÉBASTIEN J. PUECHMAILLE⁵, CHUTAMAS SATASOOK^{2, 3}, SI SI HLA BU⁶, DAVID L. HARRISON⁷, and PAUL J. J. BATES⁷

 ¹Faculty of Environmental Sciences, National University of Laos, Dong Dok Campus, Xaythany District, Vientiane Capital, Lao PDR
 ²Department of Biology, Faculty of Science, Prince of Songkla University, Hat Yai 90112, Thailand
 ³Princess Maha Chakri Sirindhorn Natural History Museum, Faculty of Science, Prince of Songkla University, Hat Yai 90112, Thailand
 ⁴Department of Biology, Boston University, 5 Cummington Street, Boston, MA 02215, USA
 ⁵School of Biological and Environmental Sciences, University College Dublin, Belfield, Dublin 4, Ireland
 ⁶Department of Zoology, Mandalay University, Research, Bowerwood House, St. Botolph's Road, Sevenoaks, Kent, TN13 3AQ, Great Britain
 ⁸Corresponding author: E-mail: bounsavanhd@yahoo.com

Based on recent field surveys in Thailand, Myanmar, and northern peninsular Malaysia, this paper reviews the taxonomy, morphometric and acoustic characters, distribution and ecology of the little known, globally endangered species *Hipposideros halophyllus*. It lists nine new localities records, including the first from northern and peninsular Thailand, which represent a substantial increase in the species' known range; it confirms the record from northern peninsular Malaysia. In addition, it provides further information on two other small species of the *Hipposideros bicolor* group, *H. ater* and *H. cineraceus*.

Key words: Hipposideros halophyllus, H. ater, H. cineraceus, distribution, ecology, echolocation, baculum, Southeast Asia

Acta Chiropterologica, 12(1): 51–59, 2010

PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/150811010X504581

Shallow genetic differentiation in *Miniopterus schreibersii* (Chiroptera: Vespertilionidae) indicates a relatively recent re-colonization of Europe from a single glacial refugium

ANDRZEJ FURMAN^{1, 3}, TUNÇ ÖZTUNÇ¹, TOMASZ POSTAWA², and EMRAH ÇORAMAN¹

¹Institute of Environmental Sciences, Boğaziçi University, Istanbul, Turkey ²Institute of Systematics and Evolution of Animals, Polish Academy of Science, Slawkowska 17, 31-016 Kraków, Poland ³Corresponding author: E-mail: furman@boun.edu.tr

In this study we analyzed 547 sequences of the first hypervariable domain of the control region of *Miniopterus schreibersii* sampled in colonies located in the western- and eastern-most borders of its distribution. We assessed genetic diversity of these colonies, quantified differences between them, and pointed out to their putative ancestral origin. Our results suggest that the extant European populations of *M. schreibersii* are descendants of the ancestors that survived the last glacial maximum in a single glacial refugium, probably located in the north-western Anatolia. According to our model, a rapid population expansion and major re-colonization events started after the climatic change that followed the end of the last glacial maximum. Our suggestions are supported by the shallow genetic differentiation between the eastern and western colonies of *M. schreibersii*, high genetic diversity observed in the eastern colonies, and population expansion time estimated for ca. 15.6 kyr BP.

Key words: glacial refugia, mtDNA, Miniopterus schreibersii, postglacial re-colonization

Acta Chiropterologica, 12(1): 61-72, 2010

PL ISSN 1508-1109 $\ensuremath{\mathbb{C}}$ Museum and Institute of Zoology PAS doi: 10.3161/150811010X504590

On the phylogeny of *Miniopterus schreibersii schreibersii* and *Miniopterus schreibersii pallidus* from Asia Minor in reference to other *Miniopterus* taxa (Chiroptera: Vespertilionidae)

ANDRZEJ FURMAN^{1, 2}, TUNÇ ÖZTUNÇ¹, and EMRAH ÇORAMAN¹

¹Institute of Environmental Sciences, Boğaziçi University, 34342 Bebek, Istanbul, Turkey ²Corresponding author: E-mail: furman@boun.edu.tr

In this study we investigated phylogenetics of *Miniopterus schreibersii schreibersii* and *M. s. pallidus* from Asia Minor by means of two mitochondrial DNA markers, NADH dehydrogenase subunit 2 (ND2) and cytochrome-*b* (*Cytb*). The average genetic divergence between reciprocally monophyletic *M. s. schreibersii* and *M. s. pallidus* was 5.6% on ND2 and 3.5% on *Cytb*. In all phylogenetic trees, the clade with *M. s. schreibersii* and *M. s. pallidus* was placed within Palearctic-Ethiopian *Miniopterus* taxa. There was a considerable genetic divergence (ca. 8% in *Cytb*) between *M. s. pallidus* from Israel and *M. s. pallidus* from Turkey, Iran, and Nagorno-Karabakh, indicating that they probably are not the same taxon. Time to the most recent common ancestor of *M. s. schreibersii* and *M. s. pallidus* was estimated to be between 1.98 to 0.60 Myr BP (ND2 data) and between 1.95 to 0.45 Myr BP (*Cytb* data).

Key words: Asia Minor, cytochrome-b, Miniopterus schreibersii schreibersii, M. s. pallidus, NADH subunit 2

Acta Chiropterologica, 12(1): 73–81, 2010 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/150811010X504608

Mitochondrial DNA confirms low genetic variation of the greater mouse-eared bats, *Myotis myotis*, in Central Europe

JOSEF BRYJA^{1, 2, 7}, MARCEL UHRIN^{3, 4}, PETER KAŇUCH⁵, PETRA BÉMOVÁ¹, NATÁLIA MARTÍNKOVÁ^{1, 6}, and JAN ZUKAL^{1, 2}

¹Institute of Vertebrate Biology, Academy of Sciences of the Czech Republic, Květná 8, CZ-603 65 Brno, Czech Republic ²Institute of Botany and Zoology, Faculty of Science, Masaryk University, Kotlářská 2, CZ-637 01 Brno, Czech Republic ³Institute of Biology and Ecology, Faculty of Science, P. J. Šafárik University, Moyzesova 11, SK–040 01 Košice, Slovakia ⁴Department of Zoology, Faculty of Science, Charles University, Viničná 7, CZ–128 44 Praha 2, Czech Republic ⁵Institute of Forest Ecology, Slovak Academy of Sciences, Štúrova 2, SK-960 53 Zvolen, Slovakia ⁶Institute of Biostatistics and Analyses, Masaryk University, Kamenice 3, CZ-625 00 Brno, Czech Republic ⁷Corresponding author: E-mail: bryja@brno.cas.cz

Recent data shows that range expansion of the greater mouse-eared bat *Myotis myotis* (Borkhausen, 1797) to Central Europe occurred mainly from the Iberian glacial refugium and in a lesser extent from South-eastern Europe. Here we present sequences of the mitochondrial control region obtained from 16 localities in the Czech Republic, Slovakia, and NW Romania. From the 97 sequences, 87 were identical with the haplotype H1, the most frequent one of haplogroup A occurring throughout Western Europe, and nine sequences (eight haplotypes) differed from H1 only by one substitution. This confirms decrease of genetic variability from south to north and colonisation of Central Europe from the Iberian Peninsula. However, we found a new haplotype, which is closely related to sequences from haplogroup D so far described in the nominative form of this species only from Greece and Bulgaria, which suggests two possible scenarios. First, colonization route from the Balkan refugium existed in this species as well, which is supported also by recently published analyses of historical DNA. Second, the Balkan haplotype entered Central Europe via interspecific hybridisation with *M. blythii*, a species, in which the haplogroup D is the most frequent in Europe and which is known to have colonised Europe from south-east.

Key words: genetic structure, mtDNA, control region, phylogeography, Myotis myotis

Acta Chiropterologica, 12(1): 83–102, 2010 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/150811010X504617

Taxonomy of the genus *Otonycteris* (Chiroptera: Vespertilionidae: Plecotini) as inferred from morphological and mtDNA data

PETR BENDA^{1, 2, 4} and VÁCLAV GVOŽDÍK^{1, 3}

¹Department of Zoology, National Museum (Natural History), Václavské nám. 68, CZ–115 79 Praha 1, Czech Republic ²Department of Zoology, Faculty of Science, Charles University, Viničná 7, CZ–128 44 Praha 2, Czech Republic ³Department of Vertebrate Evolutionary Biology and Genetics, Institute of Animal Physiology and Genetics, Academy of Sciences of the Czech Republic, CZ–277 21 Liběchov, Czech Republic ⁴Corresponding author: E-mail: petr.benda@nm.cz

Two alternative opinions on geographic variation and taxonomy of the genus *Otonycteris* are available in the literature; (1) the genus is rather invariable and includes one monotypic species, or (2) local populations of the genus are rather diverse and create up to five subspecies and/or represent a complex of more species. We analysed a relatively extensive material of *Otonycteris* from all essential parts of its distribution range, using both morphological and molecular genetic approaches to revise taxonomic status of the genus. Results of our analysis suggest rather manifold taxonomic arrangement of the genus. Morphological comparisons of cranial and bacular characters revealed three distinct geographically separated morphotypes in the set of examined bats; (1) in North Africa and in the western part of the Middle East (Levant and Mesopotamia), (2) in the eastern part of the Middle East (E Arabia and Iran) and (3) in Central Asia (incl. NE Iran, Afghanistan and Pakistan). Molecular genetic comparisons of two mitochondrial genes revealed two deeply separated clades differing in uncorrected *p*-distances at > 11.8% (cytochrome *b*) and > 9.3% (ND1), respectively. These clades correspond with two groups of morphotypes, (1+2) and (3), and we therefore regard the respective populations as two separate species, *O. hemprichii* and *O. leucophaea*. Within the species rank of *O. hemprichii* sensu stricto, three sublineages were found, each tentatively considered to be a separate subspecies.

Key words: Otonycteris, morphology, morphometry, mtDNA, phylogeography, taxonomy

Acta Chiropterologica, 12(1): 103–116, 2010 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/150811010X504626

Recent surveys of bats (Mammalia: Chiroptera) from China II. Pteropodidae

JIN-SHUO ZHANG¹, GARETH JONES^{2, 5}, LI-BIAO ZHANG³, GUANG-JIAN ZHU³, and SHU-YI ZHANG⁴

¹Institute of Zoology, and Graduate University of Chinese Academy of Sciences, Beijing, 100101, China ²School of Biological Sciences, University of Bristol, Bristol, United Kingdom ³Guangdong Entomological Institute, Guangzhou, Guangdong, 510260, China ⁴School of Life Science, East China Normal University, Shanghai, 200062, China ⁵Corresponding author: E-mail: gareth.jones@bristol.ac.uk

We review the distribution and conservation status of Old World fruit bats (Pteropodidae) in tropical and subtropical China. Our results are based on a series of surveys conducted between 1999 and 2008 by Chinese researchers and international collaborators, spanning almost the entire range of pteropodids within China over nine provinces. Additionally we provide new information on morphometrics and notes on ecology. We also review earlier Chinese literature on fruit bats because much of this has previously been inaccessible to western scientists, and we evaluate the reliability of some of these older records. Thirteen species of fruit bats have been reputed to occur in China, including one species restricted to Taiwan. We classified Chinese fruit bats according to distribution and status as follows: Resident (six species, including one species) and Alien (three species). Consequently, only five species are encountered with any regularity in mainland China and Hainan Island: *Cynopterus sphinx, Eonycteris spelaea, Macroglossus sobrinus, Rousettus leschenaultii*, and *Sphaerias blanfordi*. Three species in the genus *Pteropus* are referred to in old records, but these bats are clearly not native to mainland China.

Key words: Old World fruit bats, fauna, distribution, ecology, conservation status, Asia

Acta Chiropterologica, 12(1): 117–141, 2010 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/150811010X504635

A review of the bat fauna of the Comoro Archipelago

STEVEN M. GOODMAN^{1, 2, 6}, NICOLE WEYENETH³, YAHAYA IBRAHIM⁴, ISHAKA SAÏD⁵, and MANUEL RUEDI³

¹Field Museum of Natural History, 1400 South Lake Shore Drive, Chicago, Illinois 60605, USA ²Vahatra, BP 738, Antananarivo (101), Madagascar

³Department of Mammalogy and Ornithology, Natural History Museum of Geneva, Route de Malagnou 1, BP 6434, 1211 Geneva (6), Switzerland

⁴Centre National de Documentation et de Recherche Scientifique, Musée National des Comores (CNDRS), BP 169, Moroni, Union des Comores
⁵Action Comores, BP 279, Mutsamudu, Union des Comores

⁶Action Comores, BP 279, Mutsamudu, Union des Comores ⁶Corresponding author: E-mail: sgoodman@vahata.mg

Recent fieldwork and associated molecular and systematic studies on the bat fauna of the Comoro Archipelago (Grande Comore, Anjouan, Mohéli, and Mayotte) have provided new insights into the locally occurring species, their origins, and evolutionary history. Based on museum specimens, published studies, and our fieldwork, we provide a review of the Chiroptera of this archipelago. The Comoros, composed of in situ formed volcanic islands of recent geological age, occur midway between Madagascar and the African continent, and approximately 300 km of sea separate this island group from these two potential source areas for bat colonization. Ten species are documented in the Comoro Archipelago and the occurrence of one other species remains uncertain. Of these 10 taxa, one was new to science (*Miniopterus aelleni*) and two were new for the archipelago (*Mops leucostigma* and *Chaerephon leucogaster*), and all three of these taxa are shared with Madagascar. The only endemics to the Comoros are the fruit bats *Pteropus livingstonii* and *Rousettus obliviosus*, and the vespertilionid *Myotis anjouanensis*. Certain species occur on all four islands, while others have more limited distributions. Of the species known from the archipelago, five taxa or sister species occur on Madagascar, which appears to be the source of colonization, rather than the African continent. Based on current phylogeographic information, only one taxon, *Miniopterus griveaudi*, shows a clear pattern of genetic differentiation between different islands in the archipelago. Hence, in most cases a distance of 40–80 km separating the different islands does not form a measurable dispersal barrier to gene flow.

Key words: Chiroptera, Comoro Archipelago, checklist, occurrence, endemics, genetics, morphology

Acta Chiropterologica, 12(1): 143–154, 2010 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/150811010X504644

Cranial differentiation of fruit-eating bats (genus Artibeus) based on size-standardized data

MARÍA R. MARCHÁN-RIVADENEIRA^{1, 2, 5}, CARLETON J. PHILLIPS¹, RICHARD E. STRAUSS¹, JOSÉ ANTONIO GUERRERO³, CARLOS A. MANCINA⁴, and ROBERT J. BAKER^{1, 2}

¹Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409-3131, USA ²Natural Science Research Laboratory, Museum Texas Tech University Lubbock, TX 79409-3191, USA ³Laboratorio de Sistemática y Morfología. Facultad de Ciencias Biológicas, Universidad Autónoma del Estado de Morelos Av. Universidad 1001, C.P. 62210, Cuernavaca, Morelos, México ⁴División de Zoología, Instituto de Ecología y Sistemática, CITMA, Carretera de Varona, km 3 1/2, Capdevila, Boyeros, Ciudad de La Habana, Cuba ⁵Corresponding author: raquel.marchan@ttu.edu

Size-standardized craniometric variation was investigated among species of the genus *Artibeus*. Eleven extant and one extinct species were examined using geometric and linear morphometric analyses to evaluate morphological differences among species. Based on 19 landmarks located in the ventral side of the cranium, 29 size-standardized linear measurements were calculated and used for statistical multivariate analyses. Discriminant Function Analysis showed major interspecific differences in shape between *A. anthonyi* and *A. concolor* with respect to the remaining extant species of *Artibeus*. These two species are described as morphologically unique morphotypes with a broader rostrum, enlarged squamosal region, and wider basicranium. Specifically, a broader premaxilla is the character that better discriminates *A. anthonyi* from all other species, whereas a broader squamosal region (particularly the deep mandibular fossa, and elongated squamosal) and wider braincase are the main characters differentiating *A. concolor*. All other species of the genus overlap to varying extents in their morphology showing high shape similarities. The least variant shape features include the pterygoid fossa, the glenoid (mandibular) fossa, the maxillae, and the occipital region; these regions in all cases contribute to mechanical aspects of jaw function and bite. The fact that the least variant aspects of skull shape all involve feeding is consistent with the hypothesis that selection has favored a specific diet-associated morphology rather than divergence or character displacement in *Artibeus*.

Key words: extinct and extant taxa, Neotropics, geometric and linear morphometrics

Acta Chiropterologica, 12(1): 155–160, 2010 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/150811010X504653

Postnatal growth and age estimation in the ashy leaf-nosed bat, *Hipposideros cineraceus*

LONGRU JIN^{1, 2}, AIQING LIN^{1, 2}, KEPING SUN^{1, 2}, YING LIU^{1, 2}, and JIANG FENG^{1, 2, 3}

¹Key Laboratory for Wetland Ecology and Vegetation Restoration of National Environmental Protection, Northeast Normal University, Changchun 130024, China
²Key Laboratory of Vegetation Ecology of Education Ministry, Institute of Grassland Science, Northeast Normal University, Changchun 130024, China
³Corresponding author: E-mail: fengj@nenu.edu.cn

We quantified changes in body mass, forearm length, and the total length of the epiphyseal gap of the fourth metacarpal-phalangeal joint of the ashy leaf-nosed bat (*Hipposideros cineraceus*) based on mark-recapture data obtained in Fangkong Cave in Hekou, Yunnan Province, China. We used these data to develop empirical growth curves, to derive growth rates, to establish age-predictive equations, and to compare growth parameters based on three nonlinear growth models. Forearm length and body mass of pups followed a linear pattern of growth until day 17, with mean growth rates of 0.81 mm/day and 0.09 g/day, respectively and thereafter their growth rates increased more slowly. The length of the epiphyseal gap initially increased linearly up to day 13 and then decreased linearly at a mean rate of 0.07 mm/day until day 37. An equation for estimating age based on forearm length was valid when this dimension was ≤ 27.6 mm, whereas the equation based on the length of the epiphyseal gap was valid for forearm lengths ≥ 24.3 mm. Together, these two equations permit estimation of the age of *H. cineraceus* pups between 1 and 37 days. Of the three nonlinear growth models (logistic, Gompertz, and von Bertalanffy), the logistic equation provided the best fit to the empirical curves for body mass and forearm length.

Key words: Hipposideros cineraceus, postnatal growth, age estimation, nonlinear growth models

Acta Chiropterologica, 12(1): 161–171, 2010 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/150811010X504662

Evaluation of maternal features as indicators of asynchronous embryonic development in *Miniopterus natalensis*

MANDY K. MASON¹, DORIT HOCKMAN², DAVID S. JACOBS¹, and NICOLA ILLING^{2, 3}

¹Department of Zoology, University of Cape Town, Rondebosch, 7701, South Africa ²Department of Molecular and Cell Biology, University of Cape Town, Rondebosch, 7701, South Africa ³Corresponding author: E-mail: Nicola.Illing@uct.ac.za

The timing of early reproductive events for the Natal long-fingered bat, *Miniopterus natalensis*, was examined during its breeding season (August to December) in its maternity roost at the De Hoop Nature Reserve (South Africa). This migrating species is monoestrous with copulation occurring around April in South African populations. Embryonic development is stalled during hibernation by delayed implantation of the blastocyst. As a result, limb bud stage embryos (CS13) are first noted in other South African populations in mid-September. The timing of these reproductive events for the De Hoop population is similar with bats arriving at the maternity roosts in September and embryos at the limb bud stage (CS13) being noted in this month. Pregnancy was not synchronous in the population with bats dissected on the same day exhibiting differences in the stage of development of their young (CS11 to CS21 being the largest range). Maternal features (progesterone concentration, body mass and abdominal distension) were analysed to determine if they provided a reliable estimate of embryonic stage. The progesterone concentrations of pregnant bats showed a similar profile to the Kwa-Zulu Natal and the Eastern Cape populations. Though progesterone concentration did increase as pregnancy progressed, it was not an accurate predictor of embryonic stage. Maternal body mass did not correlate with the stage of embryonic development. However, abdominal distension determined by palpation is an accurate field based predictor of the stages of pregnancy: no abdominal distension, small to medium abdominal distension and large abdominal distension distinguished between non-pregnant bats and those carrying either early (CS11–CS15) or mid-developmental stages (CS16–CS21), respectively.

Key words: Chiroptera, abdominal palpation, embryo staging, body mass, plasma progesterone concentration, reproduction

Acta Chiropterologica, 12(1): 173-185, 2010

PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/150811010X504671

Divergent microclimates in artificial and natural roosts of the large-footed myotis (Myotis macropus)

SUSAN CAMPBELL^{1, 2, 4}, GRAEME COULSON¹, and LINDA F. LUMSDEN³

¹Department of Zoology, The University of Melbourne, Parkville, Victoria, 3010, Australia ²Current address: Vertebrate Pest Research Section, Department of Agriculture and Food, Forrestfield, Western Australia, 6058, Australia ³Arthur Rylah Institute for Environmental Research, Department of Sustainability and Environment, PO Box 137, Heidelberg, Victoria, 3084, Australia ⁴Corresponding author: E-mail: s.campbell@zoology.unimelb.edu.au

The thermal environment of day roosts is considered one of the most influential factors affecting the survival, growth and reproduction of microbats. The use of torpor is a common energy saving strategy employed by microbats in temperate regions. The efficiency of entry into, and arousal from, torpor is governed by roost microclimate, primarily roost temperature. The large-footed myotis *Myotis macropus* roosts in both tree cavities and a man-made tunnel at Yan Yean reservoir in Victoria, Australia. We investigated the thermal properties of both roost types in comparison to available tree cavities and ambient temperature over four time periods from October 2003 to May 2005. Tree cavities and tunnel roosts remained significantly warmer at night, cooler during the day, and were more stable than ambient temperatures. In addition, roost tree cavities were significantly cooler between 10:00–13:00 h compared to available tree cavities, and there was a trend for roost tree cavities to be slightly warmer at night and slower to reach maximum temperature relative to available tree cavities during the breeding season (October–January). In contrast, there was little difference in roost and available tree cavity temperatures outside of the breeding season (April–May). Temperatures inside tunnel roosts were more stable and were significantly cooler during the afternoon compared to roost tree cavities during both the breeding and non-breeding seasons. *Myotis macropus* may actively trade-off the enhanced thermoregulatory benefits of warm roosts for reduced predation risk associated with the tunnel roosting environment.

Key words: Australia, bat, microclimate, Myotis macropus, roost selection

Acta Chiropterologica, 12(1): 187–195, 2010

PL ISSN 1508-1109 $\ensuremath{\mathbb{C}}$ Museum and Institute of Zoology PAS doi: 10.3161/150811010X504680

Interannual fidelity to roosting habitat and flight paths by female western barbastelle bats

JESSICA HILLEN^{1, 3}, ANDREAS KIEFER¹, and MICHAEL VEITH²

¹Institute of Zoology, Department of Ecology, University of Mainz, J. J. Becherweg 13, D-55128 Mainz, Germany ²Faculty of Geography and Geosciences, Department of Biogeography, University of Trier, Am Wissenschaftspark 25-27, D-54296 Trier, Germany ³Corresponding author: E-mail: hillenj@uni-trier.de

The roost area selection of reproductive female western barbastelles was examined throughout four study seasons (2004–2007) via radio-tracking and automated acoustic monitoring. We specifically analysed the spatial structure of the roosting habitat and roost fidelity including a flight path connecting the roosts. We radio-tracked 13 colony members to 46 natural roosts, mainly dead oaks with large pieces of loose bark. Simultaneous tracking of four pairs of females revealed the existence of subgroups and fission-fusion-behaviour in *Barbastella barbastellus*. The colony displayed fidelity to the roost area rather than to single roost trees, although some trees were reused in two or three study seasons. Bimodal activity patterns obtained from acoustic monitoring indicated that the flight path connecting two core roosting areas functioned as a commuting corridor.

Key words: roosting preferences; site fidelity; radio-tracking; kernel density estimation; commuting corridor; Anabat

Acta Chiropterologica, 12(1): 197–203, 2010 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/150811010X504699

Foraging and public information use in common pipistrelle bats (*Pipistrellus pipistrellus*): a field experiment

MARLOTTE N. JONKER¹, WILLEM F. DE BOER¹, RALF H. J. M. KURVERS¹, and JASJA J. A. DEKKER^{2, 3}

¹Wageningen University, Resource Ecology Group, Droevendaalsesteeg 3a, 6708 PB Wageningen, The Netherlands ²Dutch Mammal Society, P.O. Box 6531, 6503 GA, Nijmegen, The Netherlands ³Corresponding author: E-mail: jasja.dekker@zoogdiervereniging.nl

Decision making by animals is likely to be influenced strongly by the behaviour of conspecifics. In this study we tested whether public information affected the foraging behaviour of common pipistrelles (*Pipistrellus pipistrellus*) by manipulating public information about the quality of foraging patches. Capture attempts during foraging are revealed by terminal buzzes, which are a potential source of public information about prey abundance for other foraging bats. We tested whether the estimation of food patch quality was affected by the number of terminal buzzes emitted by conspecifics. We conducted an experiment at 12 different locations in an urban habitat in the Netherlands. At each location we played back recordings of echolocation sounds of hunting bats with different terminal buzz rates and scored the bat activity. No significant differences between treatments were found. Our results do not support the hypothesis that bat activity increases in response to an increase in simulated terminal buzzes, suggesting that public information does not influence the choice of foraging patches in *P. pipistrellus*. We propose that *P. pipistrellus* does not use this kind of information because of either the high reliability of personal information or of the low collection costs associated with personal information.

Key words: catch buzzes, competition, facilitation, food availability, bat activity, public information, Pipistrellus pipistrellus

Acta Chiropterologica, 12(1): 205–215, 2010 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/150811010X504707

The vocal repertoire of two sympatric species of nectar-feeding bats (Glossophaga soricina and G. commissarisi)

MIRJAM KNÖRNSCHILD^{1, 4}, VOLKER GLÖCKNER², and Otto von Helversen³

¹Institute of Experimental Ecology, University of Ulm, Albert-Einstein Allee 11, 89069 Ulm, Germany ²Institute of Zoology, University of Erlangen-Nuremberg, Staudtstr. 5, 91058 Erlangen, Germany ³Chair of Botany II, University of Wuerzburg, Julius-von-Sachs-Plaz 3, 97082 Wuerzburg, Germany ⁴Corresponding author: E-mail: mirjam.knoernschild@uni-ulm.de

We recorded social vocalizations from two sympatric species of glossophagine bats, *Glossophaga soricina* and *G. commissarisi*, using habituated captive groups that were housed in separate flight cages. Whenever possible, the species-specific vocalization types were described in the light of the social context in which they were produced. Several vocalization types within each species' repertoire had remarkable similarities to vocalization types in the other species' repertoire. Out of these, four vocalization types with interspecific acoustic similarities (approach pulses, distress calls, aggressive trills, and alert calls) were used in similar behavioral contexts in both species. Approach pulses were produced whenever a bat was flying towards an already occupied roost. Distress calls were uttered whenever a bat was attacked by conspecifics or restrained by the observer, whereas aggressive trills were produced during aggressive encounters prior to physical contact. Alert calls were uttered when bats were disturbed or when several individuals were circling the same location. The interspecific similarity of both the social context and the acoustic structure of vocalization types suggest that the potential for interspecific communication is high in *G. soricina* and *G. commissarisi*.

Key words: acoustic similarity, distress calls, eavesdropping, interspecific communication, social calls, repertoire size

Acta Chiropterologica, 12(1): 217–229, 2010 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/150811010X504716

Echolocation calls of the bats of Trinidad, West Indies: is guild membership reflected in echolocation signal design?

DOROTHEA V. PIO^{1, 3}, FRANK M. CLARKE², IAIN MACKIE², and PAUL A. RACEY²

¹Department of Ecology and Evolution, University of Lausanne, CH-1015, Lausanne, Switzerland ²School of Biological Sciences, University of Aberdeen, AB24 2TZ, Scotland, United Kingdom ³Corresponding author: E-mail: dorotheapio@yahoo.com

Time-expanded echolocation calls were recorded from 29 species of Neotropical bats in lowland moist tropical forest in Trinidad, West Indies with three aims: (1) to describe the echolocation calls of the members of a diverse Neotropical bat community, especially members of the family Phyllostomidae, whose calls are not well documented (2) to investigate whether multivariate analysis of calls allows species and foraging guilds to be identified and (3) to evaluate the use of bat detectors in surveying the phyllostomids of Neotropical forests. The calls of 12 species of the family Phyllostomidae are described here for the first time and a total of 29 species, belonging to five families (Emballonuridae, Mormoopidae, Phyllostomidae, Molossidae and Vespertilionidae) were recorded. Quadratic discriminant function analysis (DFA) was used to obtain classification rates for each one of 11 individual species and for six guilds (based on diet, foraging mode and habitat) comprising 26 species. Overall classification rates were low compared to similar studies conducted in the Palaeotropics. We suggest that this may be due to a combination of ecological plasticity for certain species and a loose relationship between echolocation call shape, fine-grained resource partitioning and resource acquisition in phyllostomids.

Key words: bats, Chiroptera, echolocation, guilds, Phyllostomidae, Trinidad

Acta Chiropterologica, 12(1): 231–245, 2010 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/150811010X504725

Reliable automation of bat call identification for eastern New South Wales, Australia, using classification trees and AnaScheme software

MARIA D. ADAMS^{1, 3}, BRADLEY S. LAW¹, and MATTHEW S. GIBSON²

¹Forest Science Centre, Industry and Investment NSW, PO Box 100, Beecroft NSW 2119, Australia ²Centre for Environmental Management, School of Science and Engineering, University of Ballarat, PO Box 663, Ballarat Victoria 3353, Australia ³Corresponding author: E-mail: maria.adams@y7mail.com

Accurate and efficient identification of bat (Microchiroptera) echolocation calls has been hampered by poor knowledge of the intraspecific variability in calls (including regional variation), a lack of call parameters for use in separating species and the amount of time required to manually identify individual calls or call sequences. We constructed and tested automated bat call identification keys for three regions in New South Wales, Australia, using over 4,000 reference calls in ≈300 call sequences per region. We used the program AnaScheme to extract time, frequency and shape parameters from calls recorded with the Anabat system. Classification trees were built to separate species using these parameters and provided the decision rules for construction of the keys. An 'Unknown' category was included in the keys for sequences that could not be confidently identified to species. The reliability of the keys was tested automatically with AnaScheme, using independent sets of reference call sequences, and keys were refined before further testing on additional test sequences. Regional keys contained 18–19 species or included species groups. We report rates of sequence misidentification (accuracy) and correct identification (detection) relative to all sequences (including 'unknowns') used to test each version of a key. Refined versions of the keys were accurate, with total misidentification rates of 0.5–5.3% for the three regions. Additionally, total correct identifications for regions were 56-75% ($\geq 50\%$ for most species), an overall high rate of detection. When 'unknowns' were ignored, as is common in many published studies, correct identification for regions increased to 91-99%, rates which compare favourably to the most successful classifiers tested to date. The future use of AnaScheme for automated bat call identification is promising, especially for the large-scale temporal and spatial acoustic sampling to which Anabat is particularly suited.

Key words: Anabat, echolocation, habitat use, identification keys, monitoring, regional variation

Acta Chiropterologica, 12(1): 247–250, 2010 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/150811010X504734

SHORT NOTES

Hitting the wall: light affects the obstacle avoidance ability of free-flying little brown bats (Myotis lucifugus)

LIAM P. MCGUIRE^{1, 2} and M. BROCK FENTON¹

¹Department of Biology University of Western Ontario,1151 Richmond Rd London, ON, Canada, N6A 5B7 ²Corresponding author: E-mail: lmcguir5@uwo.ca

Key words: distress calls, echolocation, collision, light, Myotis lucifugus, obstacle avoidance

Acta Chiropterologica, 12(1): 251–254, 2010 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/150811010X504743

SHORT NOTES

Hard pellets from bats of Turkey

JOHN O. WHITAKER, JR.^{1, 3} and AHMET KARATAŞ²

¹Department of Ecology and Organismal Biology, Indiana State University, Terre Haute, Indiana 47809, USA ²Niğde Üniversitesi, Zübeyde Hanım Sağlık Yüksekokulu, 51100 Niğde, Turkey ³Corresponding author: E-mail: jwhitaker3@isugw.indstate.edu

Key words: Chiroptera, Turkey, fecal analysis, hard pellets

Acta Chiropterologica, 12(1): 255–258, 2010 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/150811010X504752

SHORT NOTES

Sampling small quantities of blood from microbats

CRAIG S. SMITH^{1, 2, 3, 4}, CAROL E. DE JONG^{2, 3}, and HUME E. FIELD^{2, 3}

¹School of Veterinary Science, University of Queensland, St. Lucia, Queensland 4072, Australia
²Australian Biosecurity Cooperative Research Centre for Emerging Infectious Diseases, St. Lucia, Queensland 4072, Australia
³Biosecurity Queensland, Queensland Primary Industries and Fisheries, Department of Employment, Economic Development and Innovation, Yeerongpilly, Queensland 4105, Australia
⁴Corresponding author: E-mail: craig.smith@deedi.qld.gov.au

Key words: bats, bleeding, blood, mammals, plasma, sampling, serum

Acta Chiropterologica, 12(1): 259, 2010 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS

THE 15TH INTERNATIONAL BAT RESEARCH CONFERENCE

The Conference will be held in Prague, the Czech Republic, from 22 to 27 August 2010. It will take place in a modern campus of the Czech University of Life Science equiped with all standard facilities including inexpensive accommodation in student residences.

The organizers expect large number of participants including almost most of the top researchers in bat biology. Nine plenary keynote lectures by leading experts in current bat research will provide detailed overviews of the current state of knowledge and future research perspectives in bat biology. Sixteen symposia, mostly composed of invited lectures by prominent specialists, have already been formally announced. A large number of free contributions is expected, both oral presentations and posters, either included in the particular symposia or in specialized parallel sessions. Moreover, the program will also include an evening talk by Merlin Tuttle on Bats and Bat Conservation, workshops on bat monitoring and white nose syndrome, three post-conference excursions and a rich social program during the Conference. All this promises that, in accord with the organizers' wishes, the Prague Conference will succeed in providing an invaluable synthesis of the current state of bat science, covering both its major achievements and latest perspectives and also its broad diversity of methods and techniques.

The 15th IBRC is essentially designed as an open meeting: the organizers do not wish to restrict either the number of symposia or the number of contributions and invite both oral and poster presentations. Everybody who is interested in any topic of bat research and bat conservation will be gladly welcome at the Conference. Detailed information on the 15th IBRC (including all technicalities and online forms for registration, accommodation, post-conference excursions, etc.) is available at www.conference.cz/IBRC.