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

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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

INTRODUCTION

Rather little is known about bats in the British Tertiary, owing to the rarity of their remains in deposits laid down in open environments. Below is a summary of records to date.

The oldest British bat is Eppsinycteris, a genus erected by Hooker (1996) for the ‘insectivoran’ species Adapisorex? anglicus Cooper, 1932, originally described from a near complete right dentary with P3–M3 from the early Ypresian (earliest Eocene) of Abbey Wood, London. The specimen, transferred by Hooker (1996) to the Chiroptera, was referred to the Emballonuridae. Although indisputably a bat, its familial affinities have been disputed (Simmons and Geisler, 1998). Hooker and Insole (1980) were only able to list an undetermined chiropteran from the English Paleogene at that time. Hooker (1989) in addition to earlier records of bat teeth from Creechbarrow, recorded Stehlinia ?gracilis and S. ?minor from the Late Eocene and Early Oligocene of the Isle of Wight. Hooker (1986) described isolated teeth of Chiroptera from Creechbarrow. These he dated as Bartonian and from the type Bartonian at Barton, Hampshire and thus late Middle Eocene (Robian European Land Mammal Age). Hooker and Weidmann (2000: 126–127) provided an updated partial faunal list for the site, including a number of distinctively Bartonian species, such as Lophiotherium siderolithicum (Perissodactyla) and Ailuravus stehlinschaeubi (Rodentia) and revised the definition of the lautricense-siderolithicum zone. Hooker (1986: 241, figs. 16–17) reported four chiropteran taxa from Creechbarrow. Microchiroptera gen. et sp. indet. 1 was considered most likely to represent Archaeonycteris. Microchiroptera gen. et sp. indet. 2 is a lower molar trigonid, which is reidentified here as Rhinolophidae gen. et sp. indet. 3 consists of the basal part of an upper canine (M36790 — Hooker, 1986: fig. 17e–g) that has rhinolophid characters and is here referred to Pseudorhinolophus schlosseri. Microchiroptera gen. et sp. indet. 4 of Hooker (1986: fig. 17h–j) is a fragmentary basal part of a lower canine, too incomplete to identify further. Creechbarrow is an open site of freshwater origin and this is probably the reason that isolated teeth of Chiroptera are rare and fragmentary.

MATERIALS AND METHODS

Additional teeth of Chiroptera were recovered from Creechbarrow during the past decade of research at the Harrison Institute.
INTRODUCTION

Although the Order Chiroptera is one of the most diversified in number of species (Koopman, 1993; Barquez et al., 1999), its fossil record is scant. In South America, there are Quaternary records from Peru (two species — Czaplewski, 1990; Morgan and Czaplewski, 1999), Argentina (two species — Ameghino, 1880; Tonni et al., 1988; Pardiñas and Tonni, 2000; Iudica et al., 2003), Venezuela (± 21 taxa — Linares, 1968; Morgan et al., 1988; Czaplewski et al., 2005), Ecuador (Galápagos island; 1 species — Steadman, 1986), and Brazil (± 59 taxa — Lund, 1840; Winge, 1893; Ameghino, 1907; Paula-Couto, 1946; Souza-Cunha and Guimarães, 1982; Trajano and de Vivo, 1991; Cartelle and Abu-hid, 1994; Czaplewski and Cartelle, 1998; Salles et al., 1999; Queiroz, 2004; Fracasso and Salles, 2005). To date, the only known records of Chiroptera for the Quaternary of Rio Grande do Sul include two genera: Mimon Gray, and Molossus Saint-Hilaire, found in RS-TQ-58 Site (Queiroz, 2004).

Despite not having an extensive fossil record when compared to other mammal groups, it is possible to conclude that Chiroptera were taxonomically very diversified during Quaternary times, at least in Brazil. Unfortunately, most of the previously published records from Brazil are not dated or are poorly dated, and the records from caves often lack stratigraphic provenience data. This work deals with remains of Chiroptera from the Holocene of Rio Grande do Sul, and the inferences that can be drawn concerning paleobiogeography.

MATERIALS AND METHODS

The study material comes from two archaeological sites of Rio Grande do Sul State, dating from ± 9,400 yrs BP to ± 4,250 yrs BP. The taxa recorded were: Chrotopterus auritus, Pygoderma bilabiatum (Phyllostomidae); Eptesicus brasiliensis, E. fuscus, Myotis cf. Myotis ruber, Vespertilionidae aff. Lasius (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
A taxonomic review of *Hipposideros halophyllus*, with additional information on *H. ater* and *H. cineraceus* (Chiroptera: Hipposideridae) from Thailand and Myanmar

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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

INTRODUCTION

As recently noted by Guillén-Servent and Francis (2006), the taxonomy of bats in the genus *Hipposideros* has been complicated by the morphological similarity of many species and the lack of adequate field collections in many regions of the Old World tropics. This is particularly the case with respect to the *H. bicolor* group, where despite a series of papers since Tate (1941) and Hill (1963) describing several new species (Khajuria, 1970; Hill and Yenbutra, 1984; Kock and Bhat, 1994; Francis et al., 1999; Guillén-Servent and Francis, 2006; Bates et al., 2007) and a number of additional publications which have contributed to an understanding of the taxonomy and phylogeny of this group, for example Jenkins and Hill (1981) and Bogdanowicz and Owen (1998), there remains considerable taxonomic confusion. This in turn has led to a lack of authoritative information on species diagnosis, distributions, ecology, and population status.

In this study, three species of small hipposiderid from the *bicolor* subgroup of the *bicolor* group (sensu Corbet and Hill, 1992) were studied, primarily in Thailand but with additional information from Myanmar and northern Malaysia. The species are *Hipposideros halophyllus* Hill and Yenbutra, 1984, which is essentially restricted to Thailand but with one additional record from northern Malaysia (Francis, 2008), and two geographically widespread taxa, *H. cineraceus* Blyth, 1853 and *H. ater* Templeton, 1848. The study was based on a thorough review of the existing literature and extensive recent field work in Thailand (2006–2009), and some previous field work in Myanmar (2000–2003, 2006) and northern Malaysia (2002–2004).

MATERIALS AND METHODS

**Study Areas**

New material for this study was collected from 28 localities in 17 provinces of Thailand, four localities in three states in...
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Glacial refugia, where species or their component populations persisted through multiple glacial as well as interglacial periods, are probably the main causal factors for the presence of divergent genetic lineages associated with distinct geographical patterns found within many European taxa (Hewitt, 1999, 2004). The onset of the major Northern Hemisphere glaciations, which started at ca. 2.8 Myr before present (BP), intensified after 0.9 Myr BP, and culminated at ca. 650 kyr BP, 430 kyr BP, 140 kyr BP, and 20 kyr BP (Shackleton, 1987), forced most of the surviving populations into a number of refugia, scattered across Europe and Asia Minor. Every time the climate warmed during interglacial periods, those populations would expand only to contract again with the next glaciation. Extensive periods of allopatric differentiation in refugia accompanied by expansion-contraction phases and secondary contacts, would regularly reshape genetic structure of the existing populations (Avise, 2000). The most important refugia, in which ancestors of the present European populations could survive the glacial conditions, were situated in the Iberian and Italian peninsulas, the Balkans (including Thrace and north-western Anatolia), and in the lowlands of western Georgia (Hewitt, 1999; Krebs et al., 2004; Connor et al., 2007; Randi, 2007). Many smaller refugia were dispersed along the coastal zones of the Mediterranean region (Medail and Diadema, 2009).

The most recent repopulation of Europe started ca. 16 kyr BP, when the process of perpetual expansion-contraction cycles paused at the end of the last glacial maximum (LGM) (Hewitt, 1999). Postglacial expansion patterns, which were shaped by the number of contributing refugial populations and the incidence of geographical barriers, set a foundation for the current geographical distribution of species and their genetic differentiations (Taberlet et al., 1998; Hewitt, 2004). Indeed, many molecular studies, which sampled populations at the European scale, confirmed the presence of phylogeographic patterns that were congruent with the locations of glacial refugia (for selected examples see Seddon et al., 2001 or Brito, 2005). Similarly, phylogeographic studies of bats linked the distribution of extant populations and their genetic divergences to...
INTRODUCTION

DNA sequencing plays nowadays a major role in the research of bats. Molecular markers were successfully employed to investigate effects of temporary geographical separation, philopatry, or sedentary behaviour (Worthington Wilmer et al., 1994; Cardinal and Christidis, 2000; Miller-Butterworth et al., 2003). Furthermore, DNA sequence analyses proved to be particularly useful in detection of cryptic taxa, as exemplified by the recent discovery of 14 previously unrecognized bat species in western Palaearctic (Ibáñez et al., 2006; Mayer et al., 2007).

As a consequence of facilitated identification of cryptic taxa, many species, such as Miniopterus schreibersii, previously considered to be cosmopolitan are presently recognized as species complexes.

The bent-wing bat, Miniopterus schreibersii (Kuhl, 1817) is a species complex with a vast distributional range, which includes the European, African, Asian, and Australian biogeographic zones (Koopman, 1994; Nowak, 1994; Simmons, 2005). The complex consists of two major lineages; one assembling Palaearctic-Ethiopian and other Oriental-Australasian taxa (Appleton et al., 2004; Miller-Butterworth et al., 2005). The nominotypical M. schreibersii, however, occurs only in Europe, northern Africa, and Asia Minor (Hutson et al., 2008). In Asia Minor, M. schreibersii is represented by two subspecies: M. s. schreibersii (type locality: Kolumbacs cave, Romania — Kuhl, 1817) and M. s. pallidus (type locality: South coast of Caspian Sea, Iran — Thomas, 1907).

Miniopterus s. schreibersii and M. s. pallidus are morphologically very similar to each other and had been traditionally distinguished only by a slight difference in dorsal coloration. The reliability of such distinction, however, has been questioned (Etemad, 1967; Albayrak and Coşkun, 2000; Karataş and Sözen, 2004; Gazaryan, 2005), and its ambiguity led to disagreements regarding distribution or even the presence of M. s. pallidus in Asia Minor. Steiner and Gaisler (1994), for example, placed M. s. schreibersii in western Anatolia and M. s. pallidus in north-eastern Anatolia, whereas Albayrak and Coşkun (2000) assigned Thrace (European part of Turkey) to M. s. schreibersii and Anatolia to M. s. pallidus. Still another distribution was suggested by Karataş and Sözen (2004), who proposed that Thrace and western Anatolia were occupied by M. s. schreibersii and central and eastern Anatolia by M. s. pallidus. Furthermore, Karataş and Sözen (2004) defined

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

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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 Palaearctic-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

INTRODUCTION

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INTRODUCTION

Molecular data are widely used to assess recent and historical processes that formed genetic structure of contemporary species. Factors that have been shown to affect genetic architecture of populations include social systems or expansions and fragmentation of habitats (Avise, 2000; Beebee and Rowe, 2004). There is much interest in determining whether these factors are historical either caused by natural changes in the environment (glaciations — Taberlet et al., 1998) or by activity of ancient people (deforestation, urbanisation — Horáček, 1984). The main difference is the age of the population process, such as population differentiation or expansion. Where older events are attributable to climatic and associated vegetation changes in Pleistocene glacial cycles, more recent events might be influenced by increasing human impact on environment in historical times. Genetic structure of populations that colonise new areas after range expansion is influenced either by genetic drift due to a founder effect that usually causes the decrease of genetic polymorphism (Ibrahim et al., 1996) and/or by genetic variation of original populations from which the expansion started (Avise, 2000).

In the last two decades, bats became one of the model groups for analysis of historical and contemporary factors affecting genetic structure of populations. Genetic studies of bat populations indicated that patterns of geographic genetic differentiation can be affected by a variety of factors — seasonal migration, geographical barriers, and past demographic processes (Burland and Wortington-Wilmer, 2001). Migratory species exhibited little genetic structure across the study range (McCracken et al., 1994; Petit and Mayer, 1999, 2000), while the gene flow in sedentary species was more restricted and

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

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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*
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

**INTRODUCTION**

The plecotine genus *Otonycteris* Peters, 1859 is a Saharo-Sindian faunal element which inhabits arid and semi-arid areas of the central and southwestern Palaeartic (Fig. 1 — cf. Gharaibeh and Qumsiyeh, 1995; Simmons, 2005). In Africa, it occurs in Saharan countries from Morocco, southern Algeria and Niger to Egypt and Sudan; the Asian range comprises almost the whole Middle East and Central Asia to Afghanistan and northwestern India (Hayman and Hill, 1971; Corbet, 1978; Nader and Kock, 1983; Horáček, 1991; Bates and Harrison, 1997; Benda et al., 2006). *Otonycteris* is a large bat reported to forage in two different ways; very close to the ground or at the height of some 4–8 metres (Horáček, 1991). According to the studies from different parts of its range, its prey includes mainly large ground arthropods, like Coleoptera, Blattodea, Orthoptera, Solpugida, and Scorpionida (Horáček, 1991; Whitaker et al., 1994; Arlettaz et al., 1995; Fenton et al., 1999; Benda et al., 2001, 2006).

A single species is currently recognised within the genus, *Otonycteris hemprichii* Peters, 1859 (Koopman, 1993, 1994; Simmons, 2005). However, five subspecies can be found within its rank according to Koopman (1994) and Gharaibeh and Qumsiyeh (1995). The nominotypical form, *O. h. hemprichii*, from the North-African part of the range, was described by Peters (1859) who gave no type locality (TL). Based on the material collected by F. W. Hemprich and C. G. Ehrenberg, Ellerman and Morrison-Scott (1951: 180) suggested “NE Africa” as TL, but Kock (1969: 184) reasonably restricted TL to “the Nile valley between Assuan, Egypt, and Chondek, N-Sudan”. *Otonycteris h. leucophaea* (Severcov, 1873) from Turkmenistan to Kirghizstan and India, was described from western Tajikistan; TL: near Djan-Bulak, between Tashkent and Hodjent (= western promontory of the Kursinskiy Range — see Ognev, 1927; Rossolimo and
Recent surveys of bats (Mammalia: Chiroptera) from China II. Pteropodidae

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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 formerly found in Taiwan and now restricted to its neighbouring islands), Marginal (three species), Questionable (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

INTRODUCTION

Forty-two extant genera and 186 species of Old World fruit bats (Pteropodidae) are recognized in the world (Simmons, 2005). Pteropodids are restricted to tropical and subtropical regions of the Old World, including Australia, southern Asia, southeast Europe, Africa and many oceanic islands (Hill and Smith, 1984; Nowak, 1999). “The 2008 IUCN Red List of Threatened Species” assessed the status of 187 pteropodid bat species, listing four species as Extinct (EX), nine species as Critically Endangered (CR), 18 species as Endangered (EN), 38 species as Vulnerable (VU), 14 species as Near Threatened (NT), 82 species as Least Concern (LC), as well as 22 species as Data Deficient (DD) (IUCN, 2008). It is likely that at least 44% of species in the family Pteropodidae are threatened by various factors that are largely anthropogenic in nature. Population trends for most species are decreasing or unknown.

The status of fruit bats in China is still little known, because (1) the initiation of a scientific approach to mammalogy, including bat research, in China was late (only really beginning in the early 1950s) and (2) it experienced a long-term hiatus at a critical period (during the Cultural Revolution, 1966–1976), (3) the current situation (from the late 1970s to the present) has improved (see details in “History of Chinese mammalogy” by Smith and Xie, 2008) but has been slow, especially because very few zoologists studied bats in China. The Bat Research Group at the Institute of Zoology, Chinese Academy of Sciences, Beijing (now moved to the East China Normal University, Shanghai) and the Guangdong Entomological Institute, Guangzhou initiated a series of bat surveys in the late 1990s. Although these investigations (sometimes involving international researchers) were conducted over a decade, further surveys are still needed to understand the diversity and status of Chinese bats including the fruit bats. Moreover, very few Chinese references are available in English for western scientists to read, and some of these older references deserve a wider audience. Consequently, this paper also reviews the Chinese literature on the distribution and status of fruit bats. Because some of the
A review of the bat fauna of the Comoro Archipelago

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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 anjoanensis. 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

INTRODUCTION

Islands and archipelagos provide interesting models to examine the biogeographical history of bats (see papers in Fleming and Racey, 2010). Given their varying distances to potential mainland source areas, geological history and age, and diverse ecosystems, island bat faunas provide fascinating natural experiments in evolutionary biology with regards to the dispersal and colonization ability of these volant organisms (e.g., Heaney, 1991; Juste and Ibañez, 1994; Heaney et al., 2005). One outstanding area of the world where these different parameters show considerable variation and allow stratification of biogeographical and dispersal patterns is the islands of the western Indian Ocean (Fig. 1). The principal islands or island groups important for this current review are as follows:

1) The ancient Madagascar block has been isolated from other portions of Gondwana for 170 to 155 million years (de Wit, 2003), long before the evolution of bats estimated at 71 to 58 million years ago (Teeling et al., 2005). Madagascar has remarkably different and complex biomes and topography (Gautier and Goodman, 2003), which have had important bearing on species diversification (Vences et al., 2009). Madagascar is separated from Africa by 415 km distance across the Mozambique Channel and by about 300 km to the nearest island (Mayotte) in the Comoro Archipelago.
2) The in situ volcanic Mascarene Islands (La Réunion and Mauritius) of at least five million years (Gillot et al., 1994), with varying topography and natural habitats, and separated from Madagascar by 680 km and from the Indian subcontinent (the nearest portion of Asia) by 3,800 km.
Cranial differentiation of fruit-eating bats (genus *Artibeus*) based on size-standardized data

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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 basioccipitum. 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

INTRODUCTION

More than 20% of all bat species occur in the Neotropics. One of the most abundant are the fruit-eating bats of the genus *Artibeus*, which are members of the subfamily Stenodermatinae — the most diverse and recently evolved radiation of the New World leaf nosed bats (Baker et al., 2003). This genus is widely distributed from Mexico through northern Argentina, including the Antillean islands in the Caribbean (Simmons, 2005; Larsen et al., 2007). Members of this genus play key roles in forest dynamics by dispersing seeds, mostly of figs (one of the most species rich and habitat-diverse genera in the Neotropics — Harrison, 2005); promoting forest regeneration (Gorchov, 1993); and contributing to the maintenance of floristic and faunal diversity (Emmons and Feer, 1990). Because of this, *Artibeus* has served as a model for several studies in various fields such as ecology (Muscarella and Fleming, 2007), conservation (Medellín et al., 2000), behavioral analysis (Ortega et al., 2008), and phylogeography (Larsen et al., 2007; Redondo et al., 2008). However, all these studies have relied on a still contentious taxonomy of the genus (Lim et al., 2004; Larsen et al., 2007), which may provide a limited interpretation of results based on taxa relationships. Thus, a more thorough understanding of the natural history of this genus and of its importance in Neotropical ecosystems requires comprehensive analyses of the variability among species to improve the taxonomy of this group.

Traditionally, *Artibeus* (sensu lato) has been split into two main groups based on body size. The
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The time during which a young mammal develops appropriate sensory and locomotor skills necessary to become independent from its mother is defined as the postnatal growth period (Baptista et al., 2000). Many researchers have studied this period with respect to changes in behavior, physiology and ecology to investigate life history traits and to estimate maternal investment (Kunz and Hood, 2000).

There have been numerous studies on postnatal development of bats under both natural (Hoying and Kunz, 1998; McLean and Speakman, 2000; Chaverni and Kunz, 2006; Liu et al., 2009; Wei et al., 2009) and captive conditions (Boyd and Myhill 1987; Rajan and Marimuthu, 1999; Elangovan et al., 2003, 2007; Raghuram and Marimuthu, 2007). It has been shown that measurements of body mass, forearm length, the total length of the epiphyseal gap of the fourth metacarpal-phalangeal joint (De Fanis and Jones, 1995; Hoying and Kunz, 1998; Liu et al., 2009), and changes in tooth development (Anthony, 1988) can all be used to estimate the age of bats during the early postnatal period. Forearm length is the most accurately measured and reliable character for estimating age during the early linear growth period of bats. However, the length of the epiphyseal gap is best for estimating age at later stages of postnatal growth (Kunz and Anthony, 1982; Krochmal and Sparks, 2007). Body mass is less reliable for estimating the age of growing bats because it is highly sensitive to variations in nutritional intake and energy expenditure over the short term, and to daily water flux (Kunz, 1987; Stern and Kunz, 1998).

Accurate age determination is important for behavioral, physiological and ecological studies (Kunz and Hood, 2000). In the absence of age estimates, it is impossible to determine growth rates, the timing of sexual maturity, the periodicity of reproduction, the development of various behavioral repertoires, or the longevity of an animal (Elangovan et al., 2003). In addition, patterns of growth and development vary among species and families of bats.

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

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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
INTRODUCTION

The timing of reproductive events in bat populations is an important parameter in ecological studies, because the reproductive state of individuals within a population is closely linked to migration, torpor (Lausen and Barclay, 2003), roosting habits (Anthony et al., 1981; Kerth et al., 2001) and feeding behavior (Racey and Swift, 1985). Such information is also essential for studies of embryonic development in wild bat populations, as knowledge of the timing and progression of pregnancy allows the efficient collection of embryos at different stages in development (Hockman et al., 2008, 2009). This information is especially critical when working with small populations where sampling should be limited so as not to decrease population viability. As part of our studies on pre-natal wing development in the insectivorous bat, Miniopterus natalensis (Hockman et al., 2008, 2009) in the Western Cape Province of South Africa (De Hoop Nature Reserve). We needed to determine the timing of embryonic growth and we required a method that used maternal features to provide an estimate of the stage of pregnancy and thus the stage of embryonic development for Miniopterus natalensis prior to sampling of pregnant bats to minimize the number of bats killed in future studies. Here, we report on the progression of embryonic development in the De Hoop population and provide evidence that abdominal palpation can be used in the field as a reliable, non-invasive method to facilitate sampling of embryos at the appropriate stage of development from a wild population of bats.

The Natal long-fingered bat, M. natalensis (Smith, 1936), belongs to the recently recognized family, Miniopteridae (Miller-Butterworth et al., 2007). This species was originally designated as being a subspecies of Schreibers’ long-fingered bat (Miniopterus schreibersii) but is now considered as distinct (Simmons, 2005). It is a small bat with body...
Divergent microclimates in artificial and natural roosts of the large-footed myotis
(Myotis macropus)

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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

INTRODUCTION

The amount of energy available to an animal influences a wide range of essential processes including growth, development and reproduction (Thomas and Speakman, 2006). For small, endothermic mammals, with large surface areas relative to their volume, energy budgets are closely associated with body temperature (Tb) and metabolic rates (MR). Metabolic costs for endotherms increase with both increasing and decreasing environmental temperatures outside of their thermal neutral zone (TNZ; which defines the range of temperatures within which basal, or resting, MR can be maintained passively — Speakman and Thomas, 2003). Such costs can be regulated behaviourally, by seeking suitable microclimates, and also physiologically, by relaxing the degree of endothermy and allowing Tb to conform to environmental temperature.

Regular food intake is the main energy source of daily heterotherms in temperate regions, including insectivorous bats (Geiser, 2004). Therefore, relaxing endothermic control is particularly important for microbats and other small mammals for which endogenous fat reserves are often not substantial enough to constantly maintain a high Tb during periods of low ambient temperatures (Ta) and limited food supply. At temperate latitudes, such food shortages for insectivorous bats occur every winter when invertebrate activity is notably reduced (Turbill, 2008; McGuire et al., 2009). Seasonal changes in energy demands and food availability therefore need to be met either by increasing the frequency and/or duration of foraging bouts (e.g., Kunz, 1974; Chruszcz and Barclay, 2003), adjusting the diet (e.g., Anthony and Kunz, 1977; Kunz et al., 1995; Agosta et al., 2003), conserving energy by clustering (e.g., Roverud and Chappell, 1991; Sano, 2000;
Introduction

Bats have specific requirements for foraging grounds, hibernacula and summer roosts. Roosts play a crucial role for bats, because they provide shelter for single animals and reproductive groups (maternity colonies) from predators and unfavourable weather conditions. Roost quality (e.g., microclimate, space) and the structural composition of the roosting habitat influence the reproductive success of individuals and even shape patterns of behaviour in populations of bats (Lewis, 1995, 1996). Forest-dwelling bats often have high demands on roost quality (e.g., cavity size, ambient temperature, humidity), but as these types of roosts are less permanent compared to others (e.g., caves) the bats have to compensate by roost-switching and exploitation of new roosts (Lewis, 1995; Kerth et al., 2006; Barclay and Kurta, 2007).

The western barbastelle bat (Barbastella barbastellus) is one of the most endangered forest-dwelling bat species in Europe (Temple and Terry, 2007). Numerous roosts of western barbastelle bats have been located in man-made structures as they can easily be observed in crevices in walls, in old barns or behind wooden window shutters. Today, radio-telemetry enables researchers to study the roosting behaviour of the western barbastelle under more natural conditions. Through radio-telemetry studies, this species has been identified as a forest-dweller relying on old-growth forests that provide a high density of potential roosts and maternity colonies have mainly been found behind the loose bark of trees or, in exceptional cases, in rock crevices (Steinhauser, 2002; Russo et al., 2004, 2005). Such qualitative findings have been implemented in practice guidelines for woodland management that consider the qualitative roosting requirements of bat colonies and other wildlife (Boye and Dietz, 2005).

Unfortunately, quantitative data about the structure of roost areas of western barbastelle bats as well as other forest-dwelling bats, e.g., the existence of core areas and the intra- and interannual fidelity to these core areas are lacking, although these data would improve existing conservation strategies. Despite the fact that the degree of connectivity between the habitat patches (e.g., roost areas) drives the spatial distribution of bat populations (Racey and Entwistle, 2003), there are still but a few studies that reveal long-term fidelity to linking landscape elements, e.g., forest tracks or hedgerows. These
INTRODUCTION

In order to make optimal decisions and hence increase fitness, individuals rely on information about the outcomes of various alternative decisions. Individuals can use two forms of information: personal information (by using trial and error tactics to interact with the physical environment) or social information (by monitoring other organisms’ interactions with the environment — Danchin et al., 2004). Social information can be made available intentionally (signals) or inadvertently (cues). Inadvertent social information may contain information about the location of resources. However, it may also contain information about the quality of the resource when it is revealed by the performance of other individuals sharing the same requirements: so called public information. By making use of public information individuals might reduce costs associated with trial and error learning. Furthermore, public information could provide additional information that could lead, for instance, to a more accurate estimation of the location of forage patches or resource quality (Danchin et al., 2004). Studies on the use of public information provided mixed results (for reviews, see Valone and Templeton, 2002; Valone, 2007).

Bats use echolocation to detect information about airborne prey (Griffin, 1958). The echolocation is divided into three different stages: a search phase for detecting prey, an approach phase in which the bats approach the prey, and a final stage, also known as the catch buzz, terminal buzz or feeding buzz. During these phases, the call duration decreases but the repetition rate increases (Schnitzler and Kalko, 2001). With the terminal buzz, the prey is located more precisely, by the production of more frequent, shorter sonar sounds, followed by a moment of silence if the prey is caught, caused by the handling of the prey (Griffin, 1958). Racey and Swift (1985) found that the number of buzzes and prey density were strongly related.

Although catch buzzes and echolocation are not explicitly meant for communication, these sounds might inform other bats about the quality of different feeding patches. So far, five studies have found evidence in favour of this.
INTRODUCTION

Despite a growing interest in social vocalizations of bats (Fenton, 1985, 2003; Siemers, 2006), detailed descriptions of species-specific vocalizations other than echolocation pulses are still fairly scarce. While the vocal repertoire of some species has been described in impressive detail in its behavioural context (Antrozous pallidus — Brown, 1976; Myotis lucifugus — Barclay et al., 1979; Saccopteryx bilineata — Davidson and Wilkinson, 2002; Behr and von Helversen, 2004; Knörnschild et al., 2006; Knörnschild and von Helversen, 2008; Tadarida brasiliensis — Bohn et al., 2008a, 2008b), other species have received far less attention, either because studies focussed specifically on selected vocalizations (isolation calls — Esser and Schmidt, 1989; Scherrer and Wilkinson, 1993; Bohn et al., 2007; Knörnschild et al., 2007; contact calls — Boughman, 1997; Carter et al., 2008; Janšen and Schmidt, 2009; male displays — Barclay and Thomas, 1979; Zagmajster, 2003; Russ and Racey, 2007; Jahelková et al., 2008; aggression calls — Bastian and Schmidt, 2008) or because the social context in which vocalizations were produced remained mostly unclear (Brown et al., 1983; Kanwal et al., 1994; Andrews et al., 2006; Ma et al., 2006). It is now well established that bats eavesdrop on the echolocation pulses or social calls of conspecifics (Fenton et al., 1976; Barclay, 1982; Ryan et al., 1985; Barlow and Jones, 1997; Russ et al., 2005; Gillam, 2007) or other species (Barclay, 1982; Russ et al., 2004). Eavesdropping may allow bats to better find rich patches of food (Barclay, 1982; Gillam, 2007), to maintain contact with group members (Wilkinson and Boughman, 1998) or to locate and prey on the calling bat (Fenton, 2003). Echolocation pulses are normally produced for the purpose of orientation, despite the fact that they often serve an additional communicative function (Wilkinson, 1995; Fenton, 2003). Social calls, however, are not mandatory for orientation and hence their utterance is likely to have some advantage for the vocalizing bat (Wilkinson, 1995), e.g., attracting other bats to repel a predator by mobbing (Russ et al., 2004, 2005) or defending a food patch against conspecifics (Barlow and Jones, 1997).

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

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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

INTRODUCTION

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

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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

INTRODUCTION

Echolocation in bats is characterised by variation in call intensity, frequency, shape, and patterns of pulse emission (Fenton et al., 1998). These differences are sufficiently large in some bat species to facilitate species identification among sympatric species (Rydell et al., 2002). Recently more and more studies of bat echolocation are attempting to assess how accurately species in different bat communities can be identified by their echolocation calls (MacDonald et al., 1994; Fenton et al., 2001; Pretoni et al., 2005; Murray et al., 2009). This is linked to the wider question of whether bat detectors provide a reliable means of sampling a bat community without capturing individuals, or whether they can be used as an adjunct method to inventory the community more completely (Fenton and Griffin, 1997; Vaughan et al., 1997; Ahlen and Baagøe, 1999; Barclay, 1999; Rydell et al., 2002). Capturing bats can be difficult, time consuming and relatively costly in terms of manpower. Moreover, many bat species in tropical forests are undersampled by mist nets and harp traps as they rely almost exclusively on echolocation for orientation in space and when foraging are able to avoid nets and traps (Kalko, 1998; Simmons and Voss, 1998).

Echolocation studies are also used to investigate resource partitioning and guild assemblies (Schnitzler and Kalko, 1998; Siemers and Schnitzler, 2004), as echolocation call characteristics reflect habitat and dietary partitioning (Aldridge and Rautenbach, 1987; Jones et al., 1992; Vaughan et al., 1997; Fenton and Ratcliffe, 2004). Bats can be divided into guilds according to their wing morphology, preferred habitat, diet and foraging behaviour, which are thought to coincide with distinct adaptations in signal structure (Schnitzler and Kalko, 1998). Although coarse partitioning of niche space is generally accepted, it is not clear how niches differ within guilds, or whether fine-grained niche differentiation is reflected in echolocation signal structure (Siemers and Schnitzler, 2004).

Bat assemblages in the forests of the Old World are typically characterised by many species with strong and distinct calls of high intensity. In the families
Reliable automation of bat call identification for eastern New South Wales, Australia, using classification trees and AnaScheme software

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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% (≥ 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

INTRODUCTION

The success of microchiropteran call surveys depends on the ability of surveyors to detect and recognise all target species resident in the study area. Identification of bat call recordings is possible quantitatively and qualitatively, but such methods are controversial if they are based on subjective decisions (e.g., visual inspection of call sonograms; Barclay, 1999; O’Farrell et al., 1999a, 1999b). The calls of different bat species often overlap in frequency and shape (pattern of frequency change over time), making subjective identification problematic, especially when a large number of sympatric species are present (Fenton and Bell, 1981). However, calls that overlap between species could be misidentified regardless of whether identification is done objectively or subjectively. Misidentification is more likely to occur when insufficient reference call data are available for comparison with survey calls (Duffy et al., 2000; Gannon et al., 2004). A lack of reference calls limits our knowledge of the extent of intraspecific call variability, due to factors such as individual identity (Masters et al., 1995), age (Jones and Kokurewicz, 1994), flight situation (Berger-Tal et al., 2008), foraging mode (Griffin et al., 1960), presence of conspecifics (Chiu et al., 2009), acoustic clutter (Broders et al., 2004) and ambient noise (Gillam and McCracken, 2007). This situation is further complicated by the possibility of regional variation in call types for a species (Thomas et al., 1987; Parsons, 1997; Barclay et al., 1999; O’Farrell et al., 2000; Murray et al., 2001; Reinhold et al., 2001a; Law et al., 2002).

Although manual keys (e.g. Reinhold et al., 2001b) increase the objectivity of call identification,
Hitting the wall: light affects the obstacle avoidance ability of free-flying little brown bats
(Myotis lucifugus)

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

INTRODUCTION

Echolocation allows flying bats to avoid obstacles (e.g., Griffin and Galambos, 1941; Galambos and Griffin, 1942; Grummon and Novick, 1963; Bradbury and Nottehohm, 1969; Gustafson and Schnitzler 1979; Jen 1982; Schnitzler et al., 2003; and many others), in some cases targets as small as 0.065 mm diameter wires (Gustafson and Schnitzler, 1979). We were thus surprised to observe free-flying little brown bats (Myotis lucifugus) crashing into the side of a 10 m long by 3.8 m tall trailer. Here we present these observations and the results of our preliminary experiments to determine the cause.

In August and September 2007, we studied the feeding behaviour of M. lucifugus at a swarming site (an abandoned mine) in eastern Ontario, Canada (see Fenton, 1969, 1970 for a description of the site). Our standard procedure was to capture bats in a harp trap placed at the entrance of the mine, transfer the bats to a cylindrical Hitchcock holding cage and bring them to a trailer we used as a mobile laboratory for processing.

One night, while processing bats outside on the doorstep of the trailer, we noticed that free-flying bats attracted to the distress calls of the bats in the holding cage (as described in Fenton, 1969; Thomas et al., 1979) sometimes flew into the side of the trailer. These collisions occurred when the exterior lights were on. As the trailer provided a large surface that should have been detected easily by bats using echolocation, we hypothesized that the lights were somehow involved in the collisions and conducted experiments to gain further insight into this occurrence.

MATERIALS AND METHODS

All experiments were performed at a swarming site near Renfrew, Ontario, Canada (see Fenton, 1970 for details). We parked the trailer (Fig. 1) at the intersection of two one-lane dirt roads approximately 100 m from the mine entrance, and conducted experiments between 3 and 8 September 2007.

We placed a harp trap at the mine entrance and checked it at 30-minute intervals. We transferred all captured bats to a cylindrical Hitchcock holding cage and brought them to the trailer. We placed the holding cage at the foot of the steps outside the trailer while the senior author and another observer sat on the steps where the sounds of bats colliding with the side of the trailer were clearly audible. No bats appeared to be injured or otherwise negatively affected by the collision. After colliding, the bats simply flew off without hitting the ground.

We conducted 12 trials over three nights. Trials commenced between 2 and 5 h after sunset (activity begins to increase approximately 1 h after sunset — Fenton, 1969; authors’ personal observation). For each trial, we counted the number of audible collisions with the trailer in two five-minute intervals, one with the exterior lights (two-12 V lights) on (Fig. 1) and the other with lights off. We alternated the order of light presentation between trials (i.e., lights on first one trial, off first the next trial) to control for any effect that presentation order might have. Following the second five-minute interval, we counted the number of bats in the holding cage and released them. A new collection of bats was used for each trial.

We used mixed effects modeling in R (version 2.9.2 — R Development Core Team, 2009) to test the effects of light, number of bats in the holding cage, and time of night (minutes after sunset) on the number of collisions. The distribution for the number of bats in the holding cage was bimodal and could not be transformed to a normal distribution. Consequently, we classified the number of bats in the holding cage as either ‘low’ (9–13 bats) or ‘high’ (17–24 bats). In the same model, we also tested for any effect of time of night (minutes after sunset). We chose a mixed effects model because the same stimulus (holding cage of bats) was used for a paired trial, once with lights on and once with lights off. A mixed effects model accounts for random variations that may arise from the repeated use of the same cage of bats.

We recorded the echolocation calls of free-flying bats for seven of 12 experiments using an Avisoft UltraSoundGate 116 system (Avisoft Bioacoustics, Berlin, Germany) equipped with a single condenser microphone. We mounted the microphone on a tripod next to the holding cage, approximately 0.75 m from the ground, facing perpendicularly away from the trailer. Recordings...
Hard pellets from bats of Turkey

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

INTRODUCTION

The original purpose of this project was to examine guano from 28 species of bats from Turkey to obtain information on their foods (Whitaker and Karataş, 2009). However, many fecal pellets examined did not contain fresh food remnants. Rather, they were black, shiny, very hard, and could not easily be broken up with dissecting needles. They looked like pieces of coal or obsidian, and when put in water or alcohol, they often exuded a greenish color. Similar pellets were previously observed by J. O. Whitaker, Jr. (unpublished) in big brown bats, Eptesicus fuscus, from Indiana, and recently also in bats from Missouri (Dunbar et al., 2007) during winter when bats were not feeding. We have previously referred to these as ‘winter’ pellets, but since they have now been found in this study throughout the active period of bats, they will be referred to as ‘hard’ pellets.

Most insectivorous bats do not feed during winter even when insects are present for short periods. We suggest that this is because the cost of bringing the digestive tract up to full function is not efficient in view of the amount of energy obtained. Whitaker and Rissler (1993) collected Myotis lucifugus and Myotis septentrionalis throughout the winter outside a mine serving as a hibernaculum in Vermillion County, Indiana. They captured 61 bats and examined their entire digestive tracts, and although these bats had stopped feeding, there were fragments of chitin in their intestines. These fragments became smaller as the winter progressed, which suggested that chitinase was present (produced by bacteria), and that it was slowly digesting the pieces of chitin. Whitaker et al. (2004) showed that chitinase-producing bacteria and chitinase were present in these species as well as in Eptesicus fuscus, Nycticeius humeralis, Lasiurus cinereus, Lasiurus borealis, Pipistrellus subflavus, and Lasionycteris noctivagans, all from Indiana. Chitinase and chitinase-producing bacteria also were found in these bats in summer, and the chitinase was in greater concentration in summer than in winter (Whitaker et al., 2004). We suggest that chitinase has little time to act on chitin in summer in Indiana since food passage time is so short.

Some bats, for example, L. borealis, clearly do feed in winter (Whitaker et al., 1997; Dunbar et al., 2007). Ransome (1968) has shown that Rhinolophus ferrumequinum has at least limited feeding in winter in England. A. Fairbairn (unpublished data) studied hibernating E. fuscus in Indiana during winter. She found a few normal feeding pellets, as well as hard pellets. The few normal pellets indicate that some of these bats now practice limited feeding in winter whereas they had not 15–20 years earlier (Sutter, 1995). During the present work, we have also found normal food pellets that appeared to be changing to hard pellets and called these ‘transitional’ pellets.

The purpose of this paper was to determine which bats produce hard pellets, when, how many, and to present hypotheses as to how hard pellets might relate to the biology of the species.

MATERIALS AND METHODS

Turkey is a relatively large country (784,000 km²) with a great amount of environmental variation, ranging from cold to hot and wet to dry in different areas. Summers are hot and dry, with temperatures in summer generally above 30°C during the day. Annual precipitation averages about 400 mm. May is generally the wettest month whereas July and August are the driest (Turkish State Meteorological Service, 2006).

The bats for this study were captured during the active season for bats, March through November (but mostly July through
Sampling small quantities of blood from microbats

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

INTRODUCTION

Sampling blood from bats can be valuable for a range of studies including antibody detection for disease surveillance (Young et al., 1996; Johara et al., 2001; Li et al., 2005), analysis of blood biochemistry (McLaughlin et al., 2007) and populations genetics (Cardinal and Christidis, 2000; Appleton et al., 2004). However, sampling sufficient volumes of blood, plasma or serum to satisfy a study’s requirements from microbats can be challenging.

In the past, a range of techniques have been used including cardiac puncture (La Motte, 1958), bleeding from the orbital sinus (Baer, 1966), nicking a brachial or jugular vein with a scalpel (Baer and McLean, 1972) and puncture of the propatagial or uropatagial vein (Gustafson and Damassa, 1985; Entwistle et al., 1994; Wimsatt et al., 2005; Ellison et al., 2006). Cardiac puncture yields good quantities of blood, however considerable mortality is often experienced (La Motte, 1958; Baer, 1966). Bleeding from the orbital sinus has commonly been used to sample bats, however yielding sufficient volumes of blood can sometimes be difficult (Baer and McLean, 1972) and puncture of the propatagial or uropatagial vein identified that the technique may have an adverse affect on the survival of some species of rodents. As such, cardiac puncture and orbital bleeding are no longer recommended as appropriate techniques for bleeding animals that are intended for release, however, cardiac puncture is still appropriate when exsanguination under anaesthesia is required (Morton et al., 1993). Morton (1993) also recommended that a scalpel blade should not be used as it was imprecise and may lead to accidental mutilation of the animal, or operator if the animal was not adequately restrained. Several studies have described the sampling of blood via venipuncture using a heparinised haematocrit tube or glass micropipette and were able to yield sufficient volumes of blood (10–200 µl) to satisfy the study’s requirements. They also identified that neither bleeding nor the use of anaesthesia had an effect on survival (Baer and McLean, 1972; Gustafson and Damassa, 1985; Wimsatt et al., 2005; Ellison et al., 2006). It is important that bleeding techniques are continually refined (Morton et al., 1993) and so we describe a technique for sampling small quantities of blood from microbats and report the volumes taken from 1,129 bats.

MATERIALS AND METHODS

Bats were caught between 2006 and 2009 using a handnet or hartrap and placed individually into light-weight cloth bags (10 cm × 15 cm) secured with a drawstring (Hall, 1979). These cloth bags were then suspended from plastic tubing inside a polythene cooler using plastic clothes pegs (Hall, 1979). A thermometer and hygrometer were used to monitor the internal environment of the cooler so that it could be maintained at a temperature and humidity similar to that of the bats roost. The coolers’ lid was left slightly ajar to allow adequate ventilation and to prevent excess humidity.

 Morphometric measurements were taken from the bats before being bled. The bats’ mass was measured to the nearest 0.5 g using a spring balance and its forearm length was measured to the nearest 0.1 mm using callipers. For bleeding, bats were manually restrained between the thumb and palm of the non-preferred hand. The bats’ wing was extended until its fore and upper arm formed a 90° angle and then restrained between the fore and middle finger (Fig. 1A). The venipuncture site was prepared with a 70% ethanol swab and a sterile 25 g needle was used to puncture either the brachial (Fig. 1B) or the propatagial vein. Venous blood would then bead on the surface of the skin (Fig. 1C) and could be collected in 12 µl aliquots using a 20 µl micropipette and sterile tip (Fig. 1D). The first aliquot of blood
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 equipped with all standard facilities including inexpensive accommodation in student residences.

The organizers expect a 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.