New species of bonneted bat, genus *Eumops* (Chiroptera: Molossidae) from the lowlands of western Ecuador and Peru

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We describe and formally name a species of bonneted bat (genus *Eumops*), which is a member of the *E. glaucinus* complex. Closely related species are *E. glaucinus*, *E. ferox*, and *E. floridanus*. The conceptual basis for the description of this species is the Genetic Species Concept with speciation by the Bateson-Dobzhansky-Muller model. The new species is distinguished from all other species of bats by its unique karyotype (2N = 38, FN = 54), sequence of the mitochondrial cytochrome-*b* gene, and genetic markers revealed through analysis of Amplified Fragment Length Polymorphisms. The series from the type locality (Ecuador, Guayas) is comprised of seven specimens. Morphologically, the new species is smaller than *E. floridanus* and *E. glaucinus*, but is indistinguishable from *E. ferox*. The new species is significantly smaller in size than *E. glaucinus* in six out of eight measurements and is distinguishable from *E. glaucinus* based on length of maxillary toothrow and zygomatic breadth. The geographic range of *E. wilsoni*, as currently documented, is the dry forests of southwestern Ecuador and adjacent northwestern Peru. We propose the common name for this species be Wilson’s bonneted bat.

**Key words**: Genetic Species Concept, AFLPs, cytochrome-*b*, karyotypes, bonneted bats, *Eumops*, operational species criteria

**INTRODUCTION**

In addition to the 5,416 species of mammals recognized in Wilson and Reeder (2005) there remains in nature a substantial number of unrecognized mammalian species (Baker and Bradley, 2006). In a recent review of Wagner’s bonneted bat using genetic [mitochondrial cytochrome-*b*, nuclear Amplified Fragment Length Polymorphisms (AFLPs), and karyotypic] and morphological data, McDonough et al. (2008) concluded that within *Eumops glaucinus*/*floridanus* (sensu Timm and Genoways, 2004) there were four species: *E. ferox*, *E. floridanus*, *E. glaucinus*, and an undescribed species. *Eumops ferox* is distributed in the Caribbean, Mexico, and Central America (Eger, 1977; McDonough et al., 2008), *E. floridanus* in southern Florida, *E. glaucinus* in South America east of the Andes, and the undescribed taxon is distributed in the western lowlands of the Andes in Ecuador and Peru. The purpose of this paper is to describe that taxon.

It is appropriate in describing a previously unrecognized species, in elevating a subspecies to the species level, or in synonymizing a currently recognized species, to define the conceptual and operational standard applied for specific recognition. There are over 20 species concepts (Mayden, 1997) and the criteria for recognition of species vary according to the conceptual application chosen. In the following description we are applying the Genetic Species Concept following Bradley and Baker (2001) and Baker and Bradley (2006). These authors define a genetic species as “a group of genetically compatible interbreeding natural populations that is genetically isolated from other such groups” (Baker and Bradley, 2006: 645). Further, they define speciation as the accumulation of genetic changes in two lineages (Bateson, 1909) that produce genetic isolation and protection of the integrity of the two respective gene pools resulting in each having independent evolutionary fates (Baker and Bradley, 2006).

Classically, morphological data have been used (Corbet, 1997; see Baker and Bradley, 2006) to recognize and describe species and even now the magnitude of morphological difference is the standard...
A relaxed molecular clock places an evolutionary timescale on the origins of North American big-eared bats (Vespertilionidae: Corynorhinus)

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The notoriously fragmented nature of the chiropteran fossil record has made it extremely difficult to resolve issues of evolutionary history based solely on morphological data. Placing estimates on dates of divergence for taxa, as well as developing a reliable calibration for a molecular clock, has been problematic due to a deficiency in reliable fossil calibration points, and a lack of statistical power in the analyses available, as well as the mistreatment of the available data. We obtained sequence data from the hypervariable D-loop of the mitochondrial DNA control region of Corynorhinus rafinesqui, C. mexicanus, and the five recognized subspecies of C. townsendii and employed a relaxed molecular clock model to test competing hypotheses of evolution for big-eared bats in North America. Our analyses indicate interspecific divergences occurred during the Pliocene, with C. rafinesquit diverging from the other Corynorhinus relatively early, during periods of increased warmth and significantly higher sea levels, and C. townsendii and C. mexicanus diverging relatively late, possibly during the cooler periods leading up to the Pleistocene. Intraspecific divergences within C. townsendii appear to have occurred as a result of repeated glacial advances during the Pleistocene, with the C. t. ingens and C. t. virginians lineages arising at relatively the same time as C. t. pallescens and C. t. australis, and recent rapid population decline producing the disjunct distribution of C. t. ingens and C. t. virginians. Dating and demographic analyses indicate all species of Corynorhinus are likely undergoing population decline.

Key words: Corynorhinus, big-eared bats, mtDNA, molecular clock, Pliocene, Pleistocene

INTRODUCTION

The molecular clock hypothesis has been a topic of significant debate beginning with the original work by Zuckerkandl and Pauling (1962). The early theory surrounding the molecular clock hypothesis led to the development of the neutral theory of evolution (Kimura, 1968, 1983; Kimura and Ohta, 1971), which states that the vast majority of mutations are selectively neutral, producing a potentially useful linear (or curvilinear) relationship between nucleotide substitution rates and time. However, as more molecular clock data accumulates, it is becoming increasingly clear that significant deviation from the molecular clock assumption (and, therefore, neutrality) exists, with rates varying not only among portions of the genome within individuals (i.e., Dickerson, 1971), but also among branches of phylogenies consisting of relatively closely related taxa (Gillespie, 1991; Bickel, 2000; Drummond et al., 2006). In addition to the uncertainty due to violations of the molecular clock assumption, mishandling of fossil calibration points can further reduce confidence in estimating rates of evolution and divergence dates. A fossil calibration represents the first known appearance of a particular group in the fossil record. However, the divergence from the common ancestor of two groups in question undoubtedly occurred before the appearance of the fossilized taxon. There can be extremely large degrees of uncertainty involved with dating fossils, and if these calibrations are not handled with a certain amount of objectivity, divergence estimates can have deceptively ‘narrow’ confidence intervals and yield incorrect estimates (Ho et al., 2005; Drummond et al., 2006; Ho, 2007).

The combination of the above factors has led to many instances where there is a lack of concordance between paleontological-based and molecular clock-based estimates for times of divergence (Bromham and Penny, 2003). However, in spite of the numerous difficulties that accompany producing reliable estimates of divergence dates and evolutionary rates of change, such estimates are...
INTRODUCTION

The islands of the western Indian Ocean are excellent natural laboratories to examine the history of over-water dispersal and the colonization of bats, because of their varying size and position with respect to continental Africa and Asia, and very different geological ages. Given that Madagascar has been separated from the African mainland for 170–155 million years (de Wit, 2003), which pre-dates the origin of Chiroptera estimated to be 71–58 Mya (Teeling et al., 2005), there is little doubt that the modern bat fauna colonized this island over water. In contrast, the land masses making up the Comoro Archipelago are in situ volcanic islands that range in age from 0.5 to 10–15 million years (Nougier et al., 1986); given the lack of land connections since their formation, over water colonization is the only tangible explanation for the presence of bats on these islands. There is some debate as to the history of isolation of Pemba from mainland Africa, and estimates range from as early as the Miocene (roughly 10 million years BP) to as recently as the Pleistocene (1 million years BP). Currently, a deep-water channel of up to 800 m in depth separates the island from the mainland (Pakenham, 1979), a separation thought to be tectonic in origin (Stockley, 1942). Most species of Molossidae bats occurring...
Population differentiation during the ice ages, followed by range expansions has significantly contributed to the geographic distribution patterns of the genetic diversity in Europe. In this regard, the Iberian, Italian, Balkan peninsulas and Anatolia comprise important glacial refugia. In different parts of Anatolia, suture zones, where lineages that diverged in the different glacial refugia met again, were observed for several species. In this study, we investigated the mitochondrial genetic differentiation of the greater horseshoe bat, *Rhinolophus ferrumequinum* in southeastern Europe and Anatolia. The mitochondrial DNA analyses indicated a suture zone in central Anatolia, similar to those recorded in other animal species, showing the presence of more than one refugium within the region. The time of the split of these lineages that diverged in allopatry was dated to the Pleistocene. However, the location of this suture zone did not coincide with the Sea of Marmara, not supporting a recent hypothesis, based on microsatellite data, which states that this water body might be an impediment to post glacial gene flow in this species.

**Key words:** Anatolia, Chiroptera, D-loop, ice age, mitochondrial DNA, phylogeography, *Rhinolophus*

**INTRODUCTION**

Ice ages, during the Pleistocene and Pliocene, are considered to be some of the most important natural events to have affected the present genetic variability of species in Europe (Benda and Horáček, 1998; Taberlet et al., 1998). During these ice ages, populations belonging to many taxa in central and northern Europe either went extinct or moved to southern refugia, depending on their mobility (Coope, 1994). Populations that were isolated in separate patches of glacial refugia differentiated in allopatry, and after the end of the glacial period, the subsequent range expansions of the surviving populations structured the roots of their present genomic distributions (Graham et al., 1996; Hewitt, 1999). The current intraspecific genetic diversity of many taxa in Europe is purportedly related with the diversification in different refugia. Such areas have been proposed to exist for Europe in the Iberian Peninsula, the Italian Peninsula, the Balkans, and Anatolia (Hewitt, 1999).

Anatolia is considered one of the major genetic sources during the post-glacial re-colonization of Europe (Rokas et al., 2003). Its geographical location in the Eurasian transition zone and relatively temperate climate during the glacial periods emphasized the significance of Anatolia as a refugium. However, some studies showed that Anatolia might comprise more than just one refugium. For instance, separate refugia have been proposed to exist in the southwest and the northeast of Turkey for the Anatolian mountain frog (Veith et al., 2003) and the Mediterranean oak gallwasp (Rokas et al., 2003). Current studies on the genetic differentiation of two bat species, the Mediterranean horseshoe bat, *Rhinolophus euryale* (Bilgin et al., 2008a), and the bent-winged bat, *Miniopterus schreibersii* (Bilgin et al., 2006, 2008b), showed that both of the species are composed of two distinctive mitochondrial clades in the Eurasian transition. The results of both of these studies indicated a sharp genetic break between the eastern Anatolian and the southeastern...
Alcathoe bat (Myotis alcathoe) in the Czech Republic: distributional status, roosting and feeding ecology

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Between 2001 and 2008, we recorded Myotis alcathoe at nine sites within three distant areas in the Czech Republic. The species identification was confirmed with cyt b sequences and four distinct haplotypes were identified. All the localities exhibit surprisingly uniform habitat characteristics: (1) old full-grown oak-hornbeam forests, with (2) numerous large trees in advanced stages of decay are present, and (3) a very small to large water bodies and/or patches of riparian vegetation surrounded by the forest. Using radiotracking techniques, we discovered 27 day roosts of M. alcathoe, located mostly in big oak, birch and lime trees inside extensive forest stands. All roosts were fissures or small cavities in a tree trunk and in branches in the canopies, some 16 m above the ground. Bats preferred trees that were higher, had higher canopy and canopy basement and had larger diameter at breast height than other available trees. Roost trees were surrounded by lower trees with lower canopy basements than available trees. Roost trees were in a poorer condition than other available trees. Roosts were occupied by up to 83 individuals in July but usually single individuals were found in the roosts in September. In contrast to syntopic M. mystacinus and M. brandtii, M. alcathoe has never been found in an anthropogenic roost (except for a fissure in concrete electricity pole). Preliminary analysis of the diet showed that nematoceran flies were the most important prey item along with spiders, caddis flies, small moths and neuropterans. In the observed ecological characteristics, M. alcathoe markedly differs from other European species of the genus Myotis. Its restricted habitat requirements are perhaps responsible for an islet-like pattern of its distribution and suggest an essential conservation value of the habitats of its occurrence.

Key words: radio tracking, diet analysis, tree roosts, forest bats, Myotis alcathoe

INTRODUCTION

The influx of the techniques of molecular taxonomy into domain of bat research by the end of the 20th Century revealed unexpected amount of cryptic variation. In Europe, at least seven new species not recognized before were distinguished (Ibáñez et al., 2006; Dietz et al., 2007; Mayer et al., 2007). The questions which are the biogeographical, ecological and behavioural specificities of particular species and which are the background factors responsible for sympathy of sibling species present a new challenge to current study of European bats. The results obtained subsequently for the common pipistrelle group, i.e. Pipistrellus pipistrellus (Schreber, 1774) and Pipistrellus pygmaeus (Leach, 1825), demonstrate significance of such studies and even enable to test various models of speciation dynamics (e.g.,
recent surveys of bats (Mammalia: Chiroptera) from China.
I. Rhinolophidae and Hipposideridae

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We conducted surveys of bats in China between 1999 and 2007, resulting in the identification of at least 62 species. In this paper we present data on 19 species, comprising 12 species from the family Rhinolophidae and seven from the Hipposideridae. Rhinolophids captured were Rhinolophus affinis, R. ferrumequinum, R. lepidus, R. luctus, R. macrotis, R. siamensis, R. marshalli, R. rex, R. pearsonii, R. pusillus, R. sinicus and R. stheno. Because of extensive morphological similarities we question the species distinctiveness of R. osgoodi (may be conspecific with R. lepidus), R. paradoxolophus (which may best be treated as a subspecies of R. rex), R. huananus (probably synonymous with R. siamensis), and we are skeptical as to whether R. sinicus is distinct from R. thomasi. Hipposiderids captured were Hipposideros armiger, H. cineraceus, H. larvatus, H. pomona, H. pratti, Aselliscus stoliczkanus and Coelops frithii. Of these species, two rhinolophids (Rhinolophus marshalli and R. stheno) and one hipposiderid (Hipposideros cineraceus) represent new species records for China. We present data on species’ ranges, morphology and echolocation call frequencies, as well as some notes on ecology and conservation status. China hosts a considerable diversity of rhinolophid and hipposiderid bats, yet threats to their habitats and populations are substantial.

Key words: Chiroptera, distribution, ecology, echolocation, morphology, China, new records

INTRODUCTION

The bat fauna of China is poorly documented. Allen (1938) listed 81 bat species in China and Mongolia, though this was recently increased to 120 species for China alone, following an extensive review of survey work and systematic research (Wang, 2003). However, the literature on bat species found in China is riddled with misidentifications and taxonomic confusion. For example, Wang’s (2003) list includes several species names that are now considered as synonyms in the most recent assessment of bat taxonomy (Simmons, 2005). Moreover, recent syntheses of the Chinese literature include isolated records of several species that are far from the known current centres of distribution, such as Pteropus giganteus and P. vampyrus in central China (Smith and Xie, 2008), and such records must be of a highly questionable nature.

To resolve some of these taxonomic and geographic anomalies, and to obtain data on current distribution patterns, a series of field surveys focusing on bat research was initiated in China between 1999 and 2007 by the Bat Research Group (BRG) at the Institute of Zoology, Chinese Academy of Sciences, Beijing, the Molecular Ecology and Evolution Group (MEEG) at East China Normal University, and the Wild Animal Research and Monitoring Group (WARMG) at Guangdong Entomological Institute. To date, more than 50 surveys have been conducted, involving researchers from the University of Bristol (UK), Queen Mary, University of London (UK), York University (Canada), University of California, Los Angeles (US) and University of Auckland (New Zealand). These surveys have resulted in the documentation of at least 62 species of bats captured in China, comprising five from the family Pteropodidae, two from the Megadermatidae,
The reproductive biology of the cave myotis (Myotis velifer)

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This study examines the anatomical structure, function and seasonal cyclicity of the male and female reproductive organs of the cave myotis (Myotis velifer) in Texas and southern Arizona. The data indicated that this is a monestrous, seasonally breeding species that stores spermatozoa in both sexes during extended winter torpor or hibernation. The male reproductive cycle was characterized by asynchronous function of the testes (spermatogenesis) and accessory sex organs. Structural factors in both sexes and fructose levels in male accessory organs were evaluated for their significance in prolonged spermatozoa storage. The reproductive anatomy and chronology were similar to other temperate-dwelling vespertilionid bats. Dextral dominance was a feature of the female reproductive tract.

Key words: Myotis velifer, testes, accessory sex glands, ovary, corpus luteum, spermatozoa storage, epididymis, fructose

INTRODUCTION

The cave myotis (Myotis velifer) is a small (7.5–10.0 g body mass), arid temperate to semi-tropical, monestrous, monotocous, insectivorous species which undergoes periodic winter torpor or hibernation. It occurs from parts of north-central and south-west Texas to south-central Kansas, extreme south-central Oklahoma, south-central and south-western Nevada, south-western New Mexico, southern Arizona, and extreme south-eastern California (along the Colorado River) southward in Mexico to Honduras. In this extensive range M. velifer is found primarily at lower altitudes in areas where desert, grassland and oak-pine vegetation predominate. Myotis velifer roosts colonially in a wide variety of man-made (bridges, buildings, mine tunnels) and natural (caves, cracks and crevices in rocks, cliff and barn swallow nests) sites, in populations varying in number from a few individuals to thousands (characteristic of maternity roosts) (Hayward, 1970; Kunz, 1973; Fitch et al., 1981).

Most vespertilionid bats occurring in the temperate zone of North America undergo periodic, deep torpor or prolonged hibernation during winter (Barbour and Davis, 1969). The resultant intermittent or continuous reduction in metabolism during these periods may delay, block or otherwise influence physiological functions, anatomical cycles, reproductive events, biochemical synthetic and elaborative processes or target organ responses. Details of the annual cyclic reproductive patterns of a number of North American temperate vespertilionid species have been reported (Myotis sodalis — Guthrie, 1933; M. lucifugus — Guthrie, 1933; Miller, 1939; Wimsatt, 1944a, 1944b; Gustafson and Damassa, 1985, 1987; Gustafson and Shemesh, 1987; M. grisescens — Guthrie, 1933; Miller, 1939; Corynorhinus rafinesquei = C. townsendii — Pearson et al., 1952; Pipistrellus subflavus — Guthrie, 1933; Krutzsch and Crichton, 1986; P. hesperus — Krutzsch, 1975). Bats enter torpor or hibernation in the autumn with involuted testes but with hypertrophied accessory sex glands which remain active throughout winter. This seemingly asynchronous pattern of accessory gland hypertrophy and secretory function, in the perceived absence of highly functional Leydig cells following testicular involution, is characteristic of temperate-dwelling vespertilionids (Gustafson, 1987; Krutzsch, 2000). Continued testicular androgen production apparently is sufficient to maintain ongoing libido throughout hibernation (Racey and Entwistle, 2000). Spermatozoa are delivered to the caudae epididymides during autumn where they are retained, though in gradually diminishing numbers, until bats arouse from hibernation or torpor in the spring (usually late-March to mid-April and, in some individuals, as late as May).
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The time in which a young mammal develops appropriate sensory and locomotors skills necessary to become independent from its mother is defined as the postnatal growth period (Bapitista et al., 2000; Sharifi, 2004). Since the rate of postnatal growth can directly reflect maternal investment in juveniles, it has been considered as an important trait for understanding the life history in mammals (Ricklefs, 1979; Kunz and Hood, 2000). Studies on postnatal growth are important for understanding various internal and external factors influencing the pattern of growth (Baptista et al., 2000). Moreover, studies on postnatal development would facilitate investigation on various aspects of early development such as initiation of flight and foraging, echolocation, feeding and breeding behavior (Rajan and Marimuthu, 1999), which can reveal key aspects of physiology, behavior, and ecology (Sears et al., 2006; Elangovan et al., 2007; Krochmal and Sparks, 2007; Raghuram and Marimuthu, 2007).

There are numerous studies on postnatal growth of bats both under natural (e.g., Case, 1978; Buchler, 1980; Kunz and Robson, 1995; Kunz and Stern, 1995) and captive conditions (e.g., Jones, 1967; Kleiman, 1969; Hughes et al., 1995). They have shown that measurement of body size, length of forearm and length of the gap of the fourth metacarpal-phalangeal joint can be used to estimate the age of bats during the early postnatal period. Field studies are of particular interest when one can actually capture newborn young and subsequently measure a spectrum of growth parameters starting from birth to the age of sexual maturity (Isaac and Marimuthu, 1996).

Postnatal growth and age estimation in big-footed myotis, Myotis macrodactylus

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We quantified the length of the forearm, the body mass and the length of the total gap of the fourth metacarpal-phalangeal joint of marked individuals of big-footed myotis bats (Myotis macrodactylus) from birth to flight in Dalazi Cave in Ji’an, Jilin Province, China. By using these data, we develop empirical growth curves, derive growth rates, establish age-predictive equations, and compare growth parameters based on three nonlinear growth models. Neonates of M. macrodactylus were born within a half-month period, with length of forearm averaging ca. 38.4% of the size of adult females and body mass averaging ca. 39.6% of their mother’s body mass. Length of forearm increased linearly until 14 days after birth (growth rate = 1.20 mm/day), as did body mass until 11 days after birth (growth rate = 0.32 g/day). The length of the total gap of the fourth metacarpal-phalangeal joint decreased linearly from 13 days to 45 days of birth. Two most appropriate linear regression equations predicting the age of young bats were derived from forearm length ($x \pm SE$) from 15.35 ± 0.96 mm to 33.24 ± 1.87 mm and the length of the epiphyseal gap from 13 to 45 days. These two equations make it possible to estimate the age of pups from 1 to 45 days of age in M. macrodactylus. Of the three nonlinear growth models (logistic, Gompertz, and von Bertalanffy), the logistic equation provides the best fit to the empirical curves for length of forearm and body mass.

Key words: Myotis macrodactylus, postnatal growth, age equations, nonlinear growth models
Skull morphology of two cryptic bat species: *Pipistrellus pipistrellus* and *P. pygmaeus* — a 3D geometric morphometrics approach with landmark reconstruction

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Differences in skull morphology between two cryptic species of bat, *Pipistrellus pipistrellus* (n = 14) and *P. pygmaeus* (n = 15), originating from Great Britain, were investigated. Four different data sets were analysed: (1) 23 landmarks and (2) 26 landmarks on the dorsal and ventral sides of the cranium, respectively, (3) 49 landmarks on the upper jaw, and (4) 34 landmarks on the labial side of the mandible. For almost all data sets, when compared within sex groups, *P. pipistrellus* were significantly larger than *P. pygmaeus*; the biggest difference being observed in the mandible size. Interspecific differences in shape, analysed by Principal Component Analysis and Discriminant Function Analysis (DFA) of the Procrustes superimposed landmarks, were also mostly visible in the mandible, and were related to dietary differences between the species. For example, the longer and more upright canines of *P. pipistrellus* allow them to pierce harder prey, the bigger molars ease its processing, and the shortened body of the mandible and the more developed coronoid process presumably generate a stronger bite. The shape and size of the mandible proved to be a good characteristic for distinguishing both cryptic taxa. A procedure for estimating missing landmarks for 3D geometric morphometric purposes was created. Our procedure of finding the missing landmarks had no effect on the within-group loss of variation. DFA of data sets with reconstructed versus original (but reduced) landmarks yielded similar results (three versus two misclassified specimens in leave-one-out cross-validation).

Key words: geometric morphometrics, skull morphology, diet, cryptic species, *Pipistrellus* spp., landmark reconstruction

**INTRODUCTION**

For more than 200 years *Pipistrellus pipistrellus* (Schreber, 1774) and *P. pygmaeus* (Leach, 1885) had been regarded as a single species — the common pipistrelle *P. pipistrellus* (Schreber, 1774). However, in the early 1980’s Ahlén (1981) recorded a Scandinavian form of *Pipistrellus* emitting calls on higher frequencies than a ‘standard’ common pipistrelle. Then this high-frequency form of *Pipistrellus* was discovered in Switzerland, Spain and Greece (Weid and von Helversen, 1987; Zingg, 1990). Zingg (1990) described the occurrence of both phonic types from the same location. Up to this point authors thought that the two phonic types represented one species that changed its echolocation calls in different habitats. However, Jones and van Parijs (1993) noted that both phonic types (calling with maximum energy at the frequencies of 55 kHz and 45 kHz, respectively) did not form mixed maternity colonies, and they showed that bats from the same maternity colony emitted consistent echolocation behaviour in a fixed habitat type, suggesting that cryptic species were present. Subsequently assortative mating was confirmed since individuals found in a given mating group always belonged to one phonic type (Park et al., 1996). Then, studies on the genetic differentiation presented a convincing evidence for the existence of two cryptic species; particularly sequence divergences in the mitochondrial cytochrome b gene proved to be more than 10 times larger between two phonic types than within one phonic type (Barratt et al., 1997). Moreover, clear differences between the two species were obtained from the nuclear genome (Mayer and von Helversen, 2001; Racey et al., 2007; Bryja et al., 2009). The cryptic species were named the common pipistrelle *P. pipistrellus* sensu stricio (so-called 45 kHz form) and the soprano pipistrelle *P. pygmaeus* (55 kHz form) by Jones and Barratt (1999; see ICZN, 2003).

Subsequent studies on these two cryptic species showed important differences in some external characters (Häussler et al., 2000), songflight and social
INTRODUCTION

The quantification of habitat associations for different taxa is a common goal in ecology, and can be useful to inform land management decisions (Guisan and Zimmermann, 2000). A vital first step in the development of robust habitat models is the collection of appropriate field data (Austin, 2002). Invariably, ecologists face a trade-off between collecting highly precise data from relatively few locations, or collecting less precise data from a larger number of locations. This trade-off may be resolved in part by an understanding of different sources of variability in field data, and how substantial within-site variability is relative to between-site variability. If temporal and spatial within-site variability are negligible, between-site differences can be quantified accurately with relatively little survey effort per site. In contrast, if temporal or spatial within-site variability is large, significant differences between sites may be masked by excessively imprecise site-level data, even if the total number of sites is large.

Several bat ecologists have attempted to quantify how changes in survey methodology can lead to increasingly precise estimates of bat activity (Hayes, 1997; Moreno and Halffter, 2000; Duchamp et al., 2006). Although we appreciate the value of using multiple survey techniques in combination (O’Farrell and Gannon, 1999; Duffy et al., 2000; Milne et al., 2005), in this paper we are concerned with studies that rely solely on the use of ultrasound bat detectors. In contrast to trapping studies, acoustic monitoring is often the only logistically feasible way of obtaining bat data over a large study area. For acoustic monitoring, key sources of variability in measured bat activity include: (i) Differences in...
Insectivorous bat activity at cenotes in the Yucatan Peninsula, Mexico

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The behaviour and habitat associations of aerial insectivorous bats are poorly understood despite constituting up to 65% of bat species in the Neotropics. In 2003, 2004 and 2005 we quantified the activity of insectivorous bats and their insect prey at pastureland and forest sites with and without cenotes (water-filled sinkholes) in the Yucatan Peninsula, Mexico. We used a time-expansion bat detector to survey each habitat for 24 nights and analysed 2,880 one-minute recorded sequences to determine bat activity. We identified 14 species and five phonic types belonging to four families. Bat activity and the average number of bat species acoustically sampled each night were significantly greater in habitats with cenotes than in those without. Pteronotus personatus and an unidentified molossid were recorded exclusively at cenotes. Peropteryx macrotis showed the highest activity of all bat species. In all habitats insects were more abundant during the rainy season but only in pastureland was bat activity significantly greater during the rainy season. Insect abundance was correlated with bat activity only at cenotes in pastureland. Cenotes are important foraging habitats for insectivorous bats as 16 species, 84% of those revealed by this study, were recorded feeding in these habitats and the number of feeding buzzes was higher in comparison to habitats without cenotes. Protection of cenotes and their surrounding vegetation should be a management priority in order to conserve the high diversity of insectivorous bats associated with these distinctive habitats.

Key words: Chiroptera, echolocation, insects, pastureland, time-expansion, water resources, Mexico

INTRODUCTION

Although insectivorous bats represent nearly 65% of the bat fauna of the Neotropics (Simmons, 2005), information on their abundance, distribution, behaviour and habitat associations is scarce in comparison to species within other ensembles. The majority of insectivorous species are difficult to capture and most free-flying bats cannot easily be identified visually when in flight (Preatoni et al., 2005), particularly in the tropics where there are many sympatric congeners. All microchiropteran insectivorous bats emit ultrasonic signals and process the returning echoes to detect, characterize and localize reflecting objects (Schnitzler and Henson, 1980). Bat detectors allow investigators to hear and record the ultrasonic calls of bats (Fenton, 1988), and therefore represent an important tool in their study. The analysis of echolocation calls can be used to identify species and to determine bat activity acoustically (e.g., Vaughan et al., 1997), although, the accuracy and reliability of this method have sometimes been controversial (Barclay, 1999; O’Farrell et al., 1999).

Bat detectors have been used in the Neotropics to describe species’ calls (O’Farrell and Miller, 1997, 1999; Rydell et al., 2002; Vaughan et al., 2004), produce more complete species inventories (Ochoa et al., 2000; Barnett et al., 2006), investigate foraging behaviour (Barclay et al., 1981; Schnitzler et al., 1994; Kalko and Condon, 1998; Thies et al., 1998; Jung et al., 2007) and examine the role of vocalisations in reproduction (Behr and von Helversen, 2004). Fewer studies have used bat detectors to investigate habitat use by insectivorous bats, which depends not only on the wing morphology and echolocation characteristics of each species (Norberg and Rayner, 1987; Kalko and Schnitzler, 1998), but also on factors such as distance to clutter (i.e., foliage, water), weather...
INTRODUCTION

Migration is defined as a seasonal, two-way movement from one habitat to another whose objective is to either avoid unfavorable or seek more favorable energetic conditions (Fleming and Eby, 2003). In light of the large-scale landscape changes that occur as a result of human activity, many migratory species face problems due to their specific habitat requirements and their tendency to congregate in certain areas. The fact that migration routes often cross international boundaries implies that large-scale integrated conservation programs are needed to effectively protect migratory species (Myers et al., 1987; Eby et al., 1999).

Data on bird migration based on 100 years of bird banding (Davidson et al., 1999) have successfully identified the migration routes of many bird species (e.g., Isakov, 1970; Davidson and Stroud, 2006) and encouraged the implementation of an international conservation framework for wetlands and waterbirds (Ramsar Convention Secretariat, 2007). Transnational movement patterns of bats, nevertheless, have received far less attention (Findley, 1993; Altringham, 1996). The absence of large-scale networks of observers is the major reason why the migratory movements of many bat species can only be inferred, often only at an anecdotal level. However, in recent years efforts aimed at conserving bats have focused on the importance of wetlands for sustaining migrant bats (Ramsar Convention Secretariat, 2007).

Habitat selection in Nathusius’ pipistrelle (Pipistrellus nathusii): the importance of wetlands

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Wetlands are internationally recognized as a crucial habitat type for the conservation of many migratory birds. Despite the fact that many bats are also long-distance migrants, the importance of foraging habitats for sustaining migrant bats has to date received little attention. We analyzed habitat selection patterns in the migrant bat, Nathusius’ pipistrelle Pipistrellus nathusii, in the southernmost part of its range (Iberian Peninsula), an area in which both mating and hibernation occur. We found that natural wetlands and riparian habitats (Phragmites reed beds) were positively selected, whereas human-transformed aquatic habitats (rice paddies) were avoided. Although semi-natural human-managed wetlands are perceived as being valuable for many species, our data emphasizes the importance of preserving natural wetlands (including riparian forests) as appropriate habitats for sustaining crucial phases of the life cycle of this bat. Agricultural transformation of the land is likely to be detrimental to this species since it reduces the availability of its preferred foraging habitat.

Key words: Pipistrellus nathusii, habitat selection, wetlands, conservation, migrant, mating
Host-parasite interactions of tropical bats in Puerto Rico

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Bats are receiving increasing attention in the parasitological world due to their potential role as reservoir hosts for zoonotic pathogens. However, details of the macroparasitic fauna (helminths and ectoparasites) are currently recorded and studied. Here, we start to address this paucity of data by detailing a study where we have documented the macroparasite fauna of a sample of tropical bats (Mormoops blainvillei, Pteronotus quadridens, and Monophyllus redmani) from Puerto Rico. Additionally, we investigated the possible host characteristics influencing the prevalence and intensity of macroparasite infection. Macroparasites were collected and identified from three species of bat, which were thoroughly washed and dissected. The overall parasite community of all three bat species consisted of a range of ectoparasites as well as the cestode Vampirolepis christensoni and the nematode Capillaria pusilla, although there was considerable variation in the parasite community of each individual species. We discovered bat flies of a previously undescribed species of the Nycterophila genus as well as new parasite records for all three species of bats. All parasites had an aggregated distribution within the host population. Differences were observed in the intensity of the helminths between bat species, but not for ectoparasite prevalence. As the helminth intensity increased so the ectoparasite intensity decreased. Overall, the helminth intensity was female-biased and increased, for both sexes with increasing body mass; no sex-bias or body mass effects were associated with ectoparasite prevalence.

Key words: Mormoops blainvillei, Pteronotus quadridens, Monophyllus redmani, macroparasites, parasite infection, tropical bats, Puerto Rico, Caribbean

INTRODUCTION

Despite having nearly one thousand known extant species in the order of Chiroptera (Wilson and Reeder, 2005), bats remain little studied in terms of the parasites and pathogens they harbor, particularly those from tropical regions. This lack of documentation of the parasite fauna of bats is of some concern since tropical bats have been implicated in the emergence of several important zoonotic infections, such as Nipah and Hendra virus as well as a possible sylvatic reservoir for Ebola (Calisher et al., 2006). As a consequence, recent studies have focused on documenting microparasitic infections of bats, while at times overlooking the macroparasitic infections (but see Gannon and Willig, 1995). Macroparasites are a group of parasites which typically live in or on the host body and include ectoparasites and intestinal helminths. This group of macroparasites has been shown to be important in regulating host populations and may interact with other parasites within the host to alter pathogen dynamics (Christensen et al., 1987; Bentwich et al., 1999, 2000; Cox, 2001). As such, an investigation into the macroparasitic fauna of bats is undeniably important.

We provide here a documentation of the macroparasitic infections of three different species of tropical bat from Puerto Rico. The bats species studied include Mormoops blainvillei (Antillean ghost faced bat), Pteronotus quadridens (sooty mustached bat), and Monophyllus redmani (Greater Antillean long tongued bat). Puerto Rico is the smallest and most eastern of the Greater Antillean islands. As such it stands as an island fulcrum between the Greater and Lesser Antilles and contains flora and fauna of both. The bat fauna and distribution on the island have been previously well documented (Gannon et al., 2005).

We investigated which host characteristics may be associated with macroparasitic infection. For example, increasing body mass has been associated with increasing parasite intensity (Arneberg et al.,
Group-specific signatures in the echolocation calls of female little brown bats (Myotis lucifugus) are not an artefact of clutter at the roost entrance

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In species where conspecifics form discrete social groups, the production of signals advertising group membership may promote cohesion among group members. Female little brown bats (Myotis lucifugus) show high fidelity to maternity roost sites where they aggregate in large numbers every spring to rear young. While the presence of group-specific signatures has been demonstrated in the echolocation calls of this species, differential clutter at recording sites may account for the observed differences. Bats optimize their ability to maneuver and detect prey within a given environment by tailoring their echolocation calls to physical attributes of that environment. Therefore, if clutter is responsible for the apparent group specificity in the calls of little brown bats, groups of bats experiencing similar levels of clutter at roost entrances should emit similar calls. We examined the effect of differential clutter on the emergence calls of M. lucifugus by comparing recorded echolocation calls of bats emerging from three maternity roosts in Georgian Bay, Ontario. The roosts varied in distance from each other and in their proximity to surrounding clutter. The more distant group emerged in an environment with clutter deemed intermediate to the two more proximate roost entrances and yet was the most acoustically distinct. The finding that similarity among emergence calls correlated better with spatial proximity than with the level of clutter around roost entrances is consistent with the development of true group-specific signatures in the emergence calls of M. lucifugus.

Key words: Myotis lucifugus, echolocation, group signature, clutter, emergence call

INTRODUCTION

Signals emitted by animals may encode information about the identity of the signaler. Within those signals, signature elements may communicate species, kinship, social status, group membership and/or individual identity (Hare, 1994; Dapporto et al., 2006). While cues in any sensory modality can allow discrimination, many birds, mammals, and insects employ chemical and/or auditory cues to convey and discriminate group membership among conspecifics (Price, 1999; Safi and Kerth, 2003; Dapporto et al., 2006).

Group-member recognition imparts many benefits. In certain species, group-specific signal(s) facilitate the detection of intruders and promote the defense of resources (e.g., calls of territorial birds — Boughman, 1997; chimpanzees — Crockford, 2004; and some bats — Boughman and Wilkinson, 1998). Group-recognition may also strengthen social bonds within a group and promote philopatry (Hare, 1994; Bull et al., 2000), which may facilitate the acquisition of thermal and reproductive benefits (Pearl and Fenton, 1996), diminish individual predation risk (Sweeney and Vannote, 1982), and facilitate the transfer of information regarding resources (Ward and Zahavi, 1973; Boughman and Wilkinson, 1998).

Multiple mechanisms may account for the appearance of group recognition signatures, including convergence through intraspecific interactions (Crozier and Dix, 1979), genetic inheritance (Dapporto et al., 2006), and/or the acquisition of cues from a common environment (Crozier and Dix, 1979; Gamboa, 2004; van Wilgenburg et al., 2006). These three mechanisms of signature development imply that there should be greater similarity among the signatures of groups living in close spatial proximity, where there is greater opportunity for intergroup interaction.

Most North American bat species depend on echolocation to avoid obstacles and detect prey in flight (Griffin, 1958). Echolocation signals thus
INTRODUCTION

This study examines social calls produced by Pipistrellus pipistrellus in flight. Bats produce social calls in a variety of interactions like mother-young recognition, as isolation signals, in a warning or aggressive context, as sexual calls to attract females to males, or to coordinate foraging (Fenton, 1985, 1986; Barlow and Jones 1996; Wilkinson and Boughman, 1998; Altringham and Fenton, 2003). Social calls can be produced by resting bats, especially at roost sites, but also during flight. They have a high variability and structural differences among calls from different individuals allow individual recognition (Gelfand and McCracken, 1986; Balcombe, 1990; Jones, Hughes and Rayner, 1991; Pfalzer and Kusch, 2003; Jahelková, 2008). Besides individual specificity of some types of social calls, at least some social calls are species specific (Pfalzer and Kusch, 2003). Social calls are emitted during specific situations, and different types of social calls correspond to specific situations. A study of Pfalzer and Kusch (2003) reviewed the different types of social calls which showed similar functions among different species. Discriminant function analysis of call variability was used in this study to test for discrimination of social call types into interspecific and intraspecific groups. The social calls were classified into four groups: A, B, C, and D. Social calls of ‘type A’ are ‘squawk-like’ calls of constant frequency and a broad bandwidth. They are loud, unspecific and with longer duration (63–198 ms). These calls are emitted during aggressive or scaring situations. They are usually emitted in roosts, and it has been suggested that bats find the entrance of a roost by listening to these calls. Social calls of ‘type B’ (distress calls) consist of high numbers of short pulses (< 10 ms) that begin at high frequencies and end at lower frequencies.
INTRODUCTION

Islands are characterized by lower species richness, but this poverty is often associated to a high percentage of endemic and relict species (Carlquist, 1974). Geographical isolation is an important barrier to gene flow, allowing genetic differentiation of populations, promoting the evolution of locally unique taxa. On the other hand, small and geographically isolated populations have a higher probability of extinction due to stochastic fluctuations of population size, or to other events (see Frankham, 1997; Frankham et al., 2004). Islands may play an important role in differentiation phenomena both in invertebrate and vertebrate populations, including vocal features. Acoustic studies on insects, birds and bats showed that insular forms can exhibit marked differences from mainland populations (Pinto-Juma et al., 2005; Baker, 2006; Armstrong and Coles, 2007; Russo et al., 2007), emphasising that data from mainland studies should not be passively applied to island populations.

The bat fauna of Madeira Archipelago is poorly known. When historical and recent records are taken into account, the following taxa are known in this island group: the grey-long-eared bat, Plecotus austriacus (Fischer, 1829), the European free-tailed bat, Tadarida teniotis (Rafinesque, 1814), Savi’s pipistrelle, Hypsugo savii (Bonaparte, 1837), Madeira pipistrelle, Pipistrellus maderensis (Dobson, 1878) and Madeira Leisler’s bats, Nyctalus leisleri verrucosus (Kuhl, 1817) (Sarmento, 1948; Pereira, 1956; Mathias, 1988; Báez, 1993).

However, we recently conducted extensive bat surveys on the Madeiran archipelago, comprising 1,431 hours of field work, using three different techniques (captures, roost search and acoustic monitoring) and confirmed the presence of three species: Plecotus austriacus and the two endemics, Pipistrellus maderensis and N. l. verrucosus. Although the echolocation calls of T. teniotis are conspicuous and even audible to the unaided ear (Russo and Jones, 2002), this species was not documented by our field...
Detecting bat calls: an analysis of automated methods

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Long-term and large-scale acoustic surveys of bats have become possible with the increased availability of recording hardware and advances in battery and memory storage technologies. The volume of data generated in surveys necessitates automated call detection, either in real time via a triggering function or offline, yet researchers are hesitant to replace traditional hand analysis without a thorough understanding of the accuracy and costs of automated detection. We compared detection accuracy and computational cost of the underlying algorithms used in commercial detectors (a zero-crossing detector, a spectral peak detector, and a high-band energy detector) with a model-based analysis method called the links detector. We predicted that the links detector would be more accurate than the other detectors, producing a larger effective detection range, because the links detector uses more information to make detection decisions. We also predicted that the links detector would be the most computationally expensive algorithm because of the processing needed for the extra information. We quantified the performance of the detectors using a synthetic recording environment, which provided an absolute ground truth for the experiments and allowed us to measure the effective detection range of each algorithm. The zero-crossing and high-band energy detectors, the fastest, were about 40 times faster than the links detector. Most of the computational cost was attributed to the filter used to remove low-frequency noise. The links detector, the most accurate, increased effective detection range by 6–12 m compared to the other detectors depending on species. The results will allow bat researchers to better understand the costs and benefits of automated detection methods.

Key words: Chiroptera, automated detection, synthetic recording environment, links detector

INTRODUCTION

The study of echolocation behavior of bats has progressed in the wake of developments in technology, reflecting the pattern that in technological evolution hardware advances lead those in software. Griffin (1958) used a custom-built microphone connected to an oscilloscope to make the first recordings of bat echolocation signals. He analyzed calls and passes by photographing the oscilloscope display triggered by the microphone signal amplitude and measuring call characteristics from the photographs by hand. Hooper (1969) introduced a portable heterodyne bat detector for recording the calls of echolocating bats in the field. Call duration and zero-crossing periods were measured by hand from the signal in the time domain and used to differentiate species.

Widespread field research on echolocation calls began with the introduction of commercial bat detectors from companies such as QMC Instruments (later Ultrasound Advice, London, UK), Avisoft Bioacoustics (Berlin, Germany), Pettersson Elektronik AB (Uppsala, Sweden), and Titley Electronics (Ballina, Australia). New recording hardware allowed researchers to listen to frequency-shifted and time-expanded calls, view real-time displays of the data in the time domain and time-frequency domain, and store recordings on magnetic tape and later on digital memory devices.

Commercial detectors allow us to collect vast amounts of data (e.g., one night of recording at a swarming site may generate 15 GB of data per microphone), expanding the scope of field research and making long-term monitoring experiments feasible (Lausen and Barclay, 2006). However, manual analysis, including call detection and measurement of call characteristics, remains a bottleneck in this research. To cope with the detection problem, commercial systems include triggering functions to reduce the amount of data collected by recording only detected calls. Avisoft and Pettersson use a triggering function that records the full-bandwidth signal only when the amplitude exceeds a user-defined threshold. The trigger assumes that calls are defined as having larger amplitudes than the...
Selection of timber mortises in a church roof by *Pipistrellus* sp. at 52°N

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Key words: roost selection, hibernation, synanthropy

INTRODUCTION

Pipistrelles (*Pipistrellus pipistrellus* and *P. pygmaeus*) are among the commonest and most synanthropic bats in the UK and form maternity colonies during summer in domestic dwelling houses and churches (Jones and Racey, 2008). During winter, houses are often too warm for use as hibernacula, and most pipistrelles are found in churches, particularly unheated mediaeval country churches (Racey, 1973; Jones and Racey, 2008). Here they are found in small groups, often in mortise joints between wooden beams, which, because they were handmade and because timbers have shrunk as they dried out after the roof was constructed, seldom fit tightly and thus contain crevices. This contrasts with the situation in Central Europe where large aggregations of pipistrelles may be found during winter in caves and tunnels (Nagy and Szanto, 2003; Taake and Vierhaus, 2004). The aim of the present study was to determine whether bats selected such roosts in mortise joints at random.

MATERIALS AND METHODS

The study was conducted at Dore Abbey, a large mediaeval church in Herefordshire, England, UK (latitude 51.96°N, longitude 2.89°W at 80 m elevation). The main roof space is used by two species of pipistrelle in both summer and winter: *Pipistrellus pipistrellus* and *P. pygmaeus* and by two additional species in summer: the brown long-eared bat *Plecotus auritus*, and Natterer’s bat *Myotis nattereri*, although individuals of the latter species occasionally occur in the winter. Other roof spaces in the same building are used by two further species in the summer: lesser horseshoe bat *Rhinolophus hipposideros*, barbastelle *Barbastella barbastellus*. The main roof is supported by 15 timber trusses, each of which is held together with 31 mortise joints, many of which have gaps at the sides large enough to admit bats (Fig. 1). These potential roosts are between 1.2 m and, at the apex 5.5 m, above the floor of the roof space.

Of 282 open mortise crevices in timber roof trusses in Dore Abbey attic, 248 openings were at least 9 mm wide, sufficiently wide to admit pipistrelles and some are regularly occupied during winter. These were censused for the presence and number of bats on 29 occasions from 1995 to 1999, once in January, February and April over the survey period. They were censused twice in July, but both occasions were in the same year. The census for all other months was carried out in at least two different years. For welfare reasons, and to avoid external influence on roost selection, the bats using such roosts were not disturbed, and consequently pipistrelles were identified only to genus.

The temperature of an unoccupied mortice joint on the north side of the church was recorded using a Grant Instruments Squirrel data logger (Grants Instruments Cambridge, UK) with a thermistor probe on a lead. The thermistor had a quoted accuracy of ± 0.2°C. Temperatures were recorded every half-hour during 24 hours each day over a 12 month period commencing December 1996. Gaps in recording were caused by battery failure.

Occupation of crevices was tested for difference from random using a variance to mean ratio test (Elliot, 1977). Subsequently the subject of occupied crevices was tested for random use against expected values derived from the zero-
Remaining cryptic during motion — behavioral synchrony in the proboscis bat  
(Rhynchonycteris naso)

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Key words: Rhynchonycteris naso, cryptic roosting, behavioral adaptation, synchronous rocking, grooming, urinating

INTRODUCTION

Most bat species inhabit roosting sites in which they are well concealed during the day, such as caves or tree holes, whereas others roost in exposed locations on tree trunks or branches (Kunz and Lumsden, 2003). For the latter, it is essential to appear cryptic in order to avoid predation or disturbance at the day-roost. Several traits have evolved to enhance the bats’ cryptic appearance, including cryptic coloration (e.g., the greenish wings of the foliage-roosting bat Paranyctimene raptor — Bonaccorso, 1998) or disruptive markings (e.g., the contrasting metacarpals and phalanges of the tent-roosting flying fox Cynopterus brachyotis — Kunz and Lumsden, 2003). Behavioral habits may also aid in camouflaging roosting bats. One remarkable example is the ‘leaf wrapping behavior’ exhibited by the Australian flute-nosed bat Murina florium, which conceals these foliage-roosting bats effectively from visually oriented predators (Schulz, 1999). In general, there are many more known examples of morphological adaptations for cryptic roosting than there are of behavioral adaptations (Kunz, 1982; Kunz and Lumsden, 2003). Remaining completely motionless during the day is a behavioral habit that obviously assists in camouflage, but it conflicts with the bats’ need for comfort behavior, such as grooming or stretching.

We studied the cryptic roosting habits of the proboscis bat, Rhynchonycteris naso. This neo-tropical member of the emballonurid family roosts in very exposed areas on tree trunks, branches, vines or man-made structures which are in close proximity to running water (Bradbury and Emmons, 1974). Group size is intermediate, and ranges from 5 to 50 individuals of both sexes (Bradbury and Vehrencamp, 1976). Individuals of small groups normally roost in a vertical line, whereas larger groups tend to form ovals (Bradbury and Emmons, 1974). Independent of group size, a vertical line is always formed when individuals roost on structures with a small diameter, such as thin trunks, branches and vines (authors’ personal observation). Despite its exposed day-roosts, R. naso is physically very cryptic due to the woolly and mottled pelage with two wavy pale lines on the back and tufts of pale hair on the forearms (Dalquest, 1957; Bradbury and Vehrencamp, 1976). This protective camouflage allows the roosting bats to resemble a patch of lichen or moss (Hill and Smith, 1984). Bradbury and Emmons (1974) first reported a ‘synchrony in grooming periods by group members’ and ‘frequent periods of gentle rocking’, a stereotypic behavior in which the bats sway rapidly from side to side while both feet and wrists remain attached to the surface of the roost. This peculiar behavior occurs frequently during the day and is often exhibited synchronously by many or all group members, but it is not triggered by disturbance. When startled or approached, the bats do not rock, but instead remain motionless before they fly off together. Therefore, the functional significance of rocking has remained unclear (Bradbury and Emmons, 1974), but a somewhat related behavior in arachnids, termed whirling or bobbing, is proposed to provide a camouflage defense against predators (Jackson, 1990; Heuts et al., 2001; Grether and Donaldson, 2007). Group members of R. naso not only synchronize rocking and grooming but also urinating (authors’ personal observation), but the benefit, if any, of this behavioral synchrony is unknown.
A strange tale of taillessness in a vespertilionid bat

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Key words: taillessness, Vespertilionidae, individual foraging strategy, fitness, evolution, Phyllostomidae

INTRODUCTION

Having a well-developed tail and uropatagium is a key adaptation to aerial insectivory in bats (Lawlor, 1973; Bullen and McKenzie, 2001), with the exception of rhinopomatids (Schnitzler and Kalko, 2001), which have long tails, but reduced uropatagia (Nowak, 1994). I report on a little brown bat (Myotis lucifugus; Vespertilionidae) with an unusual morphology: the absence of a tail and a greatly reduced uropatagium. To my knowledge, this is the first record of taillessness in Vespertilionidae or in any aerial insectivores (M. B. Fenton, personal communication). I place my finding in two contexts: the defect’s apparent effect on fitness and the potential evolutionary implications to the loss of the tail in certain phyllostomid lineages.

MATERIALS AND METHODS

I caught a tailless bat in the course of a three-year study of Prairie bats in southwestern Alberta, Canada, during which I captured a total of 2,125 bats, including 1,629 M. lucifugus, in mist nets erected in riparian sites on 160 nights. I took photos with a 35 mm digital camera (Canon PowerShot A560). I backlit bats’ wings, and classified bats with fused phalangeal epiphyses as adults and bats with visible cartilaginous gaps as juveniles (Anthony, 1988). I estimated the relative age of each adult by scoring canine tooth wear (Anthony, 1988), assigning it to one of seven classes (2 = youngest; canines no longer pinpoint sharp, 7 = oldest; well-worn canines). I scored bats with asymmetrical wear halfway between classes (e.g., 3.5 for a bat with right canine 3, left canine 4), and bats with one broken or missing canine according to wear on the intact tooth. I weighed each bat to the nearest 0.1 g on a digital balance, after holding it for at least an hour to allow it to void its digestive tract and provide an accurate mass. I measured forearm length to the nearest 0.1 mm with calipers. I estimated relative body condition following Entwistle et al. (1998) and Schulte-Hostede et al. (2005) as the residual difference of individual mass from the expected value based on the within-group effect of forearm and date on mass ($r^2 = 0.20, F = 7.56, n = 65, P = 0.01$).

I visually examined males, classifying them as reproductive if they exhibited swelling of the caudae epididymides, where sperm are stored once spermatogenesis is complete (Entwistle et al., 1998). Using calipers, I measured the linear extent of swelling to the nearest 0.1 mm along the craniocaudal axis, to assess the relative extent of spermatogenesis in reproductive males (P. A. Racey, personal communication). I calculated relative caudal swelling as the residual difference of individual caudal swelling from the expected value based on the within-group effect of body condition (the only significant predictor) on caudal swelling, excluding bats captured before the date on which I captured the first reproductive male ($r^2 = 0.09, F = 5.29, n = 55, P = 0.03$). To find information on vertebral formulae in various species of Phyllostomidae and on their primary modes of nutrition (Table 1), I conducted a literature search and consulted the National Science Foundation’s Digital Morphology library, at www.DigiMorph.Org, which provides 3D digital images of the skeletons of certain bat species, taken by X-ray CT scan.

RESULTS

On 5.08.2008, at Fish Creek Provincial Park (50°55’38.14”N, 114°7’5.06”W), in Calgary, Alberta, Canada, I captured an adult male M. lucifugus. Although this bat had a severely reduced, symmetrically cleft-shaped uropatagium and no obvious caudal vertebrae, it had normal-looking calcars, a fringe of hairs on the trailing edge of the rudimentary membrane, no apparent scar tissue and showed no evidence of a past injury resulting in tail loss (Fig. 1).

The bat had a body mass of 6.7 g ($\bar{x} \pm SE = 8.0 \pm 0.23$ g, range 6.7–11.1 g; $n = 20$ adult male M. lucifugus captured on the same night), a forearm length of 37.4 mm ($\bar{x} = 38.0 \pm 0.06$ mm, range 35.0–40.6 mm; $n = 262$ adult male M. lucifugus over entire study), and exhibited slightly greater tooth wear (class 4) than the average adult male M. lucifugus over all three years of my study (class 3.7; $n = 248$). This bat was in below average body condition (Studentized residual -0.81; 95% LCI -0.25; UCI 0.25), with caudal swelling (5.1 mm) that was
Negative consequences of forearm bands that are too small for bats

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INTRODUCTION

Marking of animals so that they are individually identifiable is essential to the study of population biology (e.g., population structure and dynamics, home range use and habitat selection, dispersion and migration — McCallum, 2000). Adverse effects of the marking method should not bias such investigations and avoiding negative effects of marking is usually a tacit assumption (Godfrey et al., 2003). However, possible negative effects of marking are manifold including, in the short term, disturbances which may change the natural behaviour or activity, and in the long term, disturbances which may lead to a reduced fitness and an enhanced mortality.

Thousands of bats have been individually marked for decades to unravel the elusive ecology of these nocturnal mammals (e.g., Allen, 1921; Steffens et al., 2004). Recent literature points at negative effects of marking methods on the animals and on the results derived from the investigations (Baker et al., 2001; Dietz et al., 2006). We believe recognising problems in marking bats is important for sound science. Results derived from individuals that are not representative of the population are of limited scientific value for generalization.

In this short note we contribute to the knowledge on marking problems by reporting observed injury rates by forearm bands in an endangered, medium sized insectivorous bat, the Leisler’s bat Nyctalus leisleri. We derive recommendations for choosing a suitable forearm band size for a relevant species.

MATERIALS AND METHODS

Between 2000 and 2004, we marked Leisler’s bats N. leisleri with forearm bands (Zambelli et al., 2008) to assess the effect of the restoration of traditionally managed chestnut orchards in Southern Switzerland, which are the winter sites from where the species migrates to the reproduction roosts in Northeastern Europe (Hoch et al., 2005; Spada et al., 2008). Nyctalus leisleri is IUCN red listed as lower risk/near threatened (IUCN, 2007) but it is considered endangered or vulnerable in several European countries (Hutson et al., 2001).

We used forearm bands (split metal rings) of two different diameters (alloy 2.9 mm and 2.4 mm, measured as the longest inner diameter when nearly closed, type narrow, produced by Porzana Ltd, Icklesham, East Sussex, UK). These ring sizes were delivered by the Natural History Museum in Geneva, the official authority in Switzerland for the distribution of forearm bands. The marking technique was in accordance with the national regulations (BVET and BAFU 2004) and marking was licensed by the responsible department (Ufficio della natura e del paesaggio, Bellinzona). The bats were examined, weighed, and marked by one experienced person. It was ensured that the bands still could move loosely on the forearm and the ring gap did not allow the radius bone to slip through it. After the first injured bats were found, the forearm bands were removed from all individuals displaying evidence of band-related injuries. Difference in injury rates were analysed by randomised χ2-tests by Actus (Estabrook and Estabrook, 1989). No evidence was found that the gender of bats has an influence on injury rate and gender is therefore not reported in the results. In November 2004 we ceased marking but we continued controlling the bats until December 2006.

RESULTS

Frequency of Problems

We ringed 377 N. leisleri, of which 349 were ringed with 2.9 mm forearm bands and 28 with
Healing rates of wing punch wounds in free-ranging little brown myotis (Myotis lucifugus)

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Key words: Chiroptera, energy balance, immune function, Myotis lucifugus, wing biopsy, wing damage, wound healing

INTRODUCTION

Defects in the wing membranes of bats are commonly observed as a natural consequence of a membrane-wing method of flight (Davis and Doster, 1972). This type of flight remains successful not only because bats can tolerate asymmetries resulting from these injuries, but also because they can rapidly heal rips and fill in missing membranes and even sometimes fractures of the wing bones (Davis, 1968; Bogdanowicz and Urbańczyk, 1986). The wound healing process can generally be classified into three overlapping stages: an inflammatory stage, a proliferative stage, and a protracted remodeling stage. The initial inflammatory stage typically lasts up to four days, while the proliferative stage predominates from days 4–21. Only after the wound has closed upon itself can the wound healing process advance to the final, protracted remodeling stage, which can last up to two years (Kinsey et al., 2003; Christian et al., 2006). Because this process is energy-dependent, healing rates may vary by life history stage, sex, and season, and may be especially slow in immune compromised animals (Nelson and Demas, 1996; Worthington-Wilmer and Barratt, 1996; Kinsey et al., 2003; Martin et al., 2008).

While much is known about the basic ecology and physiology of Myotis lucifugus (the little brown myotis), little baseline information is available regarding immune function in this or any other bat species. The primary objective of our study was to assess wound healing rates in this species. Wound healing rates can be viewed as an indicator of both immune competence and of variations in energy allocation. Additionally, because the use of sterile biopsy punches to collect tissue for DNA analysis (as originally described by Worthington-Wilmer and Barratt, 1996) has become quite common, it is important to understand how quickly the resulting wounds heal. While the rate of wound healing has not been closely monitored in M. lucifugus, previous studies in free ranging M. bechsteinii have indicated that 3 mm wounds heal in 3–4 weeks (Kerth et al., 2000, 2002). Church and Warren (1968) reported that 2 cm × 2 cm holes took approximately 24 days to heal in captive Eidolon helvum while Davis and Doster (1972), working with captive Antrozous pallidus, reported that 14 mm holes in the wings required up to 33 days to heal. Davis and Doster (1972) noted that the regenerated region often remains pale, which they and others have suggested explains the pale splotches often found on the wings of free-ranging bats.

We created 3.0 mm circular wounds in the wing membranes of free-ranging M. lucifugus and monitored the healing process. Based on previous research on bats and on the general timeline of the wound healing process described from other mammals, we hypothesized that little healing would occur during the first week, but that wounds would close completely within two to three weeks. Wound healing rates in the field were assessed using calipers and digital photographs for later analysis with ImageJ software. A secondary objective of our study was to evaluate the reliability of these two methods. We hypothesized that the use of digital photographs would yield more accurate and precise measurements of wound area.

MATERIALS AND METHODS

Harp traps were used to capture 150 female (140 lactating and 10 non-reproductive) M. lucifugus from a summer maternity colony at dusk from a farm outbuilding in Lycoming County in Central Pennsylvinia, USA. Bats were captured in July 2008, banded, weighed, and had their forearms measured. Both wing membranes were punctured with a sterile 3.0 mm biopsy punch (Miltex, Inc., USA) (Worthington-Wilmer and Barratt, 1996; Kerth et al., 2000). Although multiple sizes of biopsy punches