A new genus and species of vespertilionid bat from West Africa, with notes on *Hypsugo*, *Neoromicia*, and *Pipistrellus* (Chiroptera: Vespertilionidae)

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We describe a new species of vespertilionid bat from Guinea and Liberia, West Africa. In this context we evaluate previously described taxa from West Africa assigned to *Pipistrellus*, *Neoromicia*, and *Hypsugo*. Based on genetics, morphology and ecology we conclude that the taxon *Pipistrellus eisentrauti bellieri* should be elevated to species level, and that the taxa *bellieri*, *crassulus*, *eisentrauti* plus the new species form a monophyletic clade for which a new genus name is proposed. The new genus occurs in forested regions south of the Sahara from Senegal to Ethiopia and Somalia, from where further taxa remain to be described.

*Key words*: Guinea, Liberia, morphology, molecular systematics, new genus, new species

**INTRODUCTION**

Vesper bats (Vespertilionidae) represent the largest and taxonomically most complex family of bats with recent estimates of species richness ranging from about 400 to almost 500 species (Simmons, 2005; Amador et al., 2018; Burgin et al., 2018). In Africa, species of *Neoromicia* Roberts, 1926, *Hypsugo* Kolenati, 1856 and *Pipistrellus* Kaup, 1829 can be easily confounded and were done so in the past. Hill and Harrison (1987) and Happold and Happold (2013) included all these proposed genera as subgenera of *Pipistrellus*, while Simmons (2005) and an increasing number of authors (Heller et al., 1994; Volleth et al., 2001; Kearney et al., 2002; Roehrs et al., 2010; Monadjem et al., 2013; Goodman et al., 2015, Decher et al., 2016) considered *Neoromicia*, *Hypsugo*, and *Pipistrellus* as distinct genera.

The genus *Hypsugo* comprises about 25 species of small brown bats with a mainly Palearctic distribution. Horáček and Hanák (1986) reviewed the genus, proposed new characters and compared it to *Pipistrellus* and *Eptesicus* Rafinesque, 1820. *Hypsugo* differed from these genera in the shape of the baculum, penis morphology, myotodont molars (shared with *Eptesicus*), and a moderately long free tail-tip. Mayer et al. (2007) provided genetic evidence for the *Hypsugo* group in Europe, northern Africa, and on the Canary Islands. Benda et al. (2011) named a new species from Yemen and reported new specimens of *H. ariel* (Thomas, 1904) from Socotra and Yemen.

In two recent studies of bats of the West African rainforest in Liberia and Guinea (Monadjem et al., 2013; Decher et al., 2016), new specimens referred to *Hypsugo* were reported. Some were allocated to *H. crassulus bellieri* (De Vree, 1972), but one was left unidentified. A taxon relevant in this context is *Pipistrellus eisentrauti bellieri*, which was described from Côte d’Ivoire. The species was then shifted from the genus *Pipistrellus* to *Hypsugo* by Heller et al. (1994). We demonstrate in this paper that all of these West African specimens previously referred to the genus *Hypsugo* actually represent a yet unrecognized genus. Furthermore, we describe a new species in this genus and discuss the taxonomy of the remaining African species.
Molecular phylogeny and systematics of the sheath-tailed bats from the Middle East (Emballonuridae: Taphozous and Coleura)

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The family of sheath-tailed bats (Emballonuridae) constitutes a considerable part of the bat fauna of the Middle East. This region on the crossroad of three biogeographical realms represents the sole significant extension of the family range into the Palaearctic, otherwise the family is distributed mostly in the tropics. Three emballonurid species occur in the Middle East, Coleura afra, Taphozous perforatus and T. nudiventris, each with a number of morphology-based subspecies reported from the region. For this study, we assembled a dataset of more than hundred samples that covers the Middle Eastern parts of the ranges of the respective species. We generated sequences of up to three mitochondrial and five nuclear markers and reconstructed a time-calibrated phylogeny of the family to infer the evolutionary history of emballonurids in the Middle East and to revise their intra- and interspecific taxonomy. The populations of Coleura from southern Arabia and the Red Sea coast of Africa show a low genetic structure, although as a lineage are well separated from other Coleura populations of Africa and the Indian Ocean islands. We suggest this Afro-Arabian lineage to represent a separate taxon which could be regarded as a species of its own, C. gallarum. Similarly, low genetic structure across the study area we revealed in T. perforatus; this indicates that only one taxon of this bat is present in the Middle East and adjacent areas that should be co-identified with the nominotypical form. On the contrary, T. nudiventris presents two clearly separated clades; one of them comprises the nominotypical form of north-eastern Africa and southern Arabia, as well as the eastern Arabian populations assigned to T. n. zayidi, which is thus unjustified, and the latter name to be considered a junior synonym of T. n. nudiventris. On the other hand, the analysis did not resolve satisfactorily the phylogenetic position of the large body-sized Mesopotamian populations of T. nudiventris, which thus remains to be regarded as a subspecies T. n. magnus. Finally, the position of Liponycteris as a separate subgenus of Taphozous was not found to be justified, while the traditional divisions of the family into the subfamilies Taphozoinae and Emballonurinae and the latter into the tribes Emballonurini and Diclidurini were supported by the analysis results.

Key words: Chiroptera, mitochondrial DNA, molecular genetics, nuclear DNA, southern Palaearctic

INTRODUCTION

The sheath-tailed bats (family Emballonuridae Gervais, 1855) have a circumtropical distribution with two core areas in the Old World part of their range, the Afrotropical and Oriental-Australasian regions (Simmons, 2005), which are biogeographically connected by the Middle East (including north-eastern Africa, the Arabian Peninsula and Iran). The family comprises two subfamilies: the circumtropical Emballonurinae, which is further divided into two tribes (the New World Diclidurini Gray, 1866 and the Old World Emballonurini; Robbins and Sarich, 1988; Griffiths and Smith, 1991; McKenna and Bell, 1997; Lim et al., 2008; Ruedi et al., 2012), and the Old World Taphozoinae Jerdon, 1867, which includes the genera Taphozous Geoffroy, 1818, and Saccolaimus Temminck, 1838 (Koopman, 1994; Simmons, 2005).

The Middle East and areas adjoining to it are inhabited by both subfamilies. The Emballonurinae is represented by Coleura afra (Peters, 1852), Taphozous by Taphozous perforatus Geoffroy, 1818 and T. nudiventris Cretzschmar, 1830 (Ellerman and Morrison-Scott, 1951; Harrison and Bates, 1991; Horáček et al., 2000). The two Taphozous species have been recognized to belong to two different subgenera, the former to Taphozous s.str., and the latter to Liponycteris Thomas, 1922 (Simmons, 2005). Liponycteris differs from Taphozous in having an
Distinct patterns of genetic connectivity found for two frugivorous bat species in Mesoamerica

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Sturnira parvidens and Sturnira hondurensis are two frugivorous bat species distributed throughout the Mesoamerican region. Sturnira parvidens inhabits tropical lowland forests and S. hondurensis montane cloud forests. Their populations are respectively separated by the intervening highlands or lowlands. We used mitochondrial DNA control region sequences to compare genetic structure among the populations of these two species in the region of the Gulf of Mexico. We also measured genetic connectivity among their populations and assessed the distribution model for each species. We found high genetic diversity in both species: the $F_{ST}$ comparisons values were low to high in S. hondurensis and low in S. parvidens. For S. hondurensis, we found isolation by landscape resistance (IBR) where the highland habitat heterogeneity may have restricted gene flow among the populations of the Sierra Madre Oriental, Sierra de Los Tuxtla, Chiapas and Guatemala. For S. parvidens, the isolation is explained by geographic distance rather than by landscape heterogeneity.

Key words: habitat heterogeneity, refuge, humid forest, Sturnira hondurensis, S. parvidens

INTRODUCTION

Studying the distribution of genetic variation among populations can improve our understanding of population dynamics and connectivity, particularly for smaller organisms for which it is not generally feasible to use mark-recapture techniques (Burland and Wilmer, 2001). Studies of landscape genetics bring together genetic data and complex aspects of the composition and configuration of the landscape, allowing researchers to describe spatial genetic patterns, to explore the processes that gave rise to the observed patterns and to determine the effect of territorial heterogeneity on ecological or functional connectivity (i.e. gene flow — Manel et al., 2003; Storfer et al., 2007; Holderegger and Wagner, 2008). Frugivorous phyllostomid bats disperse critically important early pioneer plant species that are among the most abundant during primary and secondary succession (Muscarella and Fleming, 2007). They also play an important role in forest regeneration. In addition, the frugivorous bats facilitate the connectivity of forest communities (Fleming, 1988; Medellín and Gaona, 1999), particularly in fragmented landscapes, and may prove increasingly important as worldwide habitat loss threatens ecosystems with increasingly higher degrees of fragmentation (Hubbell et al., 2008).

Mexican cloud forests or montane forests are characterized by a high diversity of epiphytic and climbing plants and by the mixture of trees of both temperate (North America) and tropical (South America) origin (Rzedowski, 1996). Cloud forests have a wide geographic distribution in the Gulf of Mexico, along the Sierra Madre Oriental (SMOr) mountain range from northeastern Mexico to Chiapas and the Guatemala highlands in the south. Wide patches remain in the highlands of the coastal mountain range Sierra de Los Tuxtla (SLTX) in Veracruz. The lowlands of the Isthmus of Tehuantepec (IT) separate the cloud forests of the SMOr from those in Chiapas, and the lowlands of the Gulf of Mexico separate the coastal SLTX from other cloud forest areas (Ornelas et al., 2013). The Mexican cloud forest is one of the most threatened types of vegetation in Mesoamerica, with less than 1% of its total...
INTRODUCTION

Molossidae is the fourth most speciose family of bats and has a cosmopolitan distribution (Solari and Martínez-Arias, 2014; Gregorin and Cirranello, 2015). In recent years, reconstruction of the phylogenetic relationships among genera of molossids have been hypothesized from both morphological (Gregorin and Cirranello, 2015) and molecular data (Ammerman et al., 2012). Phylogeny and systematics within some New World genera such as Promops (Gregorin and Chiquito, 2010), Eumops (Timm and Genoways, 2004; McDonough et al, 2008; Baker et al., 2009; Gregorin et al., 2016), and Cynomops (Moras et al., 2015, 2018) have also been examined. However, other highly diverse genera, such as Molossus, lack a multilocus molecular approach to re-solving patterns of genetic variance and testing evolutionary relationships that are based on traditional morphology.

Molossus is one of the most diverse and common genera of Molossidae. It is mainly Neotropical in distribution, occurring from the southeastern United States to southern Argentina and the Caribbean islands (Dolan, 1989; López-González and Presley, 2001; Eger, 2007; Lindsey and Ammerman, 2016). Molossus is morphologically conservative and although many species and subspecies have been described, most of the morphological differences are slight and the resulting taxonomy is confusing and unstable (Dolan, 1989; Simmons, 2005; Eger, 2008; Loureiro et al., 2018). In addition, the level of genetic divergence among many species, which has masked the actual species diversity in the genus. We analyzed the evolutionary relationships among species within Molossus using three mitochondrial (COI, Cytb, and 16S RNA), and two nuclear genes (RAG2 and β-fib) from more than 400 specimens across the Neotropics. We also investigated the genetic integrity of currently recognized species, especially those with broad geographic distributions and controversial taxonomic arrangements. Maximum likelihood and Bayesian phylogenetic reconstructions show that some recognized species are not monophyletic. The use of combined mitochondrial and nuclear genes as well as the use of only mitochondrial markers revealed more robust phylogenies than those for individual data sets and those restricted to the two nuclear genes. We recovered the recently described M. fentoni and M. alvarezi, validated M. milleri and M. verrilli as distinct species relative to M. molossus, and confirmed that the name M. barnesi should be considered as a junior synonym of M. coibensis. Additionally, M. rufus appears to be a complex of cryptic species, showing that the broadly distributed genus Molossus is more diverse than previously reported.

Key words: molecular systematics, genetic diversity, phylogeny, Molossus

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Not all Molossus are created equal: genetic variation in the mastiff bat reveals diversity masked by conservative morphology

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The genus Molossus of the free-tailed bat family Molossidae is morphologically conservative and the level of genetic divergence is also low among many species, which has masked the actual species diversity in the genus. We analyzed the evolutionary relationships among species within Molossus using three mitochondrial (COI, Cytb, and 16S RNA), and two nuclear genes (RAG2 and β-fib) from more than 400 specimens across the Neotropics. We also investigated the genetic integrity of currently recognized species, especially those with broad geographic distributions and controversial taxonomic arrangements. Maximum likelihood and Bayesian phylogenetic reconstructions show that some recognized species are not monophyletic. The use of combined mitochondrial and nuclear genes as well as the use of only mitochondrial markers revealed more robust phylogenies than those for individual data sets and those restricted to the two nuclear genes. We recovered the recently described M. fentoni and M. alvarezi, validated M. milleri and M. verrilli as distinct species relative to M. molossus, and confirmed that the name M. barnesi should be considered as a junior synonym of M. coibensis. Additionally, M. rufus appears to be a complex of cryptic species, showing that the broadly distributed genus Molossus is more diverse than previously reported.

Key words: molecular systematics, genetic diversity, phylogeny, Molossus
INTRODUCTION

The hypophysis (pituitary gland) plays an important role at the life history of vertebrates; this endocrine complex formed by a glandular (adenohypophysis) and a neural component (neurohypophysis) influences via hormones various biological functions at physiological, developmental, reproductive and social levels (Wingfield, 1994; and citations therein). Although there are numerous works on the neurobiology of various species of bats, including volumetric data of the brain and its components in relation to the ecology and evolution (e.g., Barton et al., 1995, 1996a, 1996b, 1996c; Pitnick et al., 2006; Lemaitre et al., 2009), the available information for endocrine glandular structures such as the hypophysis, is primarily focused on gross morphology, histology and histochemistry over a few species (e.g. Patil, 1974; Richardson, 1979; Widmaier et al., 1994; Anthony, 2000; Krishna and Bhatnagar, 2011). The volumetric database of bats hypophysis recently published by Bhatnagar et al. (2016) has been determinant in our knowledge on the hypophysis size variation in at least 15 families of bats. However, such study did not address the information in an evolutionary framework. A great advantage for the evolutionary study of structures strongly committed in biological functions in bats is the existence of certain databases on ecological variables for this group (e.g., McCracken and Wilkinson, 2000; Hodgkinson et al., 2003; Wilkinson and McCracken, 2003; Jones and MacLarnon, 2004). On the other hand, recent phylogenetic hypotheses including a comprehensive diversity of bat species provide robust and well-resolved topologies (e.g., Shi and Rabosky, 2015; Amador et al., 2018), which constitute a crucial step for an evolutionary approach in any study of character variation in the group. The diversity of habits, reproductive patterns, and social behavior observed in Chiroptera (see...
Conventional monitoring tools are seldom effective for studying the ecology of rare and elusive mammals. In the present study, we use automated ultrasound detectors to provide information about seasonal activity of the greater noctule bat \textit{(Nyctalus lasiopterus)}, the largest and one of least known European bats. We selected localities within Central Europe with diverse geomorphological contexts, including rivers of different sizes and mountain passes. The study demonstrates the capability of the automatic recording approach to achieve bioacoustic discrimination of this species, but also pointed to the persistent need of integrating results from automatic classification software applications with the feedback from manual approaches. The high throughput capacity of the assay proved to be efficient, and the regular occurrence of the species was identified at two localities. These locations are associated with two known and intensely used migratory corridors of winged animals going through Vltava River valley and Červenohorské Saddle in Jeseníky mountains, as illustrated also by the activity patterns of other migratory species. Together with the occurrence of spring and autumn peaks in activity, these findings are in concordance with the plesiomorphic condition in pipistrelloid bats, showing also migratory behavior, and represent further indirect evidence of migration of the greater noctule. This pattern could be facilitated by the trophic niche of the species, involving predation of migrating songbirds. Differences in phenomenology of migratory species observed at particular sites likely mirror position of the locality in relation to migration flyways, seasonal and geographic variation in prey availability and energy demands etc. Further application of bioacoustic monitoring and other tools is necessary to obtain detailed information about the range and movement ecology of the species in higher latitudes.

\textit{Key words:} migration, automated detectors, central Europe, greater noctule, \textit{Nyctalus lasiopterus}, SonoChiro, Vltava River valley, Červenohorské Saddle

\section*{Introduction}

The phylogenetic position of the vespertilionid bat genus \textit{Nyctalus} was surprisingly ascertained as an inner lineage of the \textit{Pipistrellus} radiation (Hoofer and Van den Bussche, 2003; Koubinová \textit{et al.}, 2013). Striking apomorphies in these groups are related to body size — species belonging to the pipistrelloid bats, with lower weight limits reaching 3 grams, rank among the smallest representatives of the order Chiroptera, while the largest member of the genus \textit{Nyctalus}, the greater noctule bat, \textit{Nyctalus lasiopterus} (Schreber, 1780) may reach 80 grams and is among the largest bats of the family Vespertilionidae. The macroevolutionary transition of the genus \textit{Nyctalus} was apparently related to a shift in the trophic niche of this lineage. Plesiomorphic states within the tribe Pipistrellini encompass ecomorphological types characterized by a high variety of wing parameters usually related to slow, short-range hawking, while \textit{Nyctalus} is typified by average aspect ratios, short or rather short wing-spans, small wing areas, high wing loading and long or pointed wingtips typical for fast, long-range hawking (Norberg and Rayner, 1987). In largest members of the genus \textit{Nyctalus}, as the greater noctule bat (\textit{N. lasiopterus}) or the birdlike noctule (\textit{N. aviator}), further shift in trophic niche occurred, which enabled these bats to prey on migrating songbirds on the wing, as corroborated by several studies (Dondini and Vergari, 2000; Ibáñez \textit{et al.} 2001, 2016; Popa-Lisseanu \textit{et al.}, 2007). Such a strategy is rare among bats and was reported additionally only for the great evening bat (\textit{Ia io}). However, insects represent a regular (Dondini and Vergari, 2000) and, in some cases, prevailing part of the diet (Uhrin \textit{et al.}, 2006).
Long-term monitoring of the effects of weather and marking techniques on body condition in the Kuhl’s pipistrelle bat, *Pipistrellus kuhlii*

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Bats are one of the most widespread and speciose orders of mammals. Despite their huge biodiversity, little is known about the natural behaviour and ecology of many species given the difficulty in monitoring and studying them. *Pipistrellus kuhlii* is one of the most common bats of the Mediterranean biome but its ecology remains ambiguous given the scarcity of longitudinal studies. Such basic information is urgently needed to predict the shift of species distribution range under climate change scenarios. Here, we analysed the effects of weather variables (namely temperature, precipitation, wind speed and air humidity) on the body conditions of *P. kuhlii* monitored in five maternity roosts in Southern Europe over more than a decade (17 years). Using linear mixed-effect models, we disentangled the impact of weather predictors on body condition variations in 347 individuals. Our results revealed species-specific sensitivity to variations in the monitored four main weather parameters. Through the modelling analysis, we show how weather seasonal variables recorded prior to the capture period had a substantial role in driving bat body condition. A combination of warmer spring-summers and cooler winters was found associated with optimal body condition in *P. kuhlii*. Our analysis also showed that *P. kuhlii* bats were favoured by higher spring humidity combined with intermediate precipitation and humidity levels recorded during the summers prior to the capture. The latter parameters (precipitation and humidity) were arguably linked with the proliferation of entomofauna on which bats feed. Additionally, we assessed the body condition of 45 bats that were previously captured and tagged either with bands or PIT-tags, two of the most widespread marking techniques for bats. We showed that bats carrying a ring (band) or a PIT-tag had a body condition that did not differ to that expected for untagged bats. This suggests that transponding bats has no significant effect on body condition, enabling new opportunities for passive monitoring and large-scale long-term longitudinal studies for these animals.

**Key words:** bats, bat ringing, linear mixed-effect models, passive integrated transponder PIT, principal component analysis, scaled mass index, bat banding

**INTRODUCTION**

Bats are unique mammals capable of active powered flight, echolocation-driven orientation and prey detection for most species, and have surprisingly long lifespans given their relatively small body size (Podlutsky *et al.*, 2005; Munshi-South and Wilkinson, 2010; Healy *et al.*, 2014; Teeling *et al.*, 2017). Despite that there are more than 1,300 bat species, many of which are under strict protection and of conservation concern (e.g., for Europe see the Habitat Directive 92/43/EEC, Berne and Bonn agreements), little is known about several aspects of their biology and ecology, which make challenging their conservation strategies (Kunz and Fenton, 2005).

Several long-term monitoring studies have been conducted on vertebrates to gather key information regarding their population dynamics (e.g., population age and sex composition, demographic growth, etc.) and ecology (Cody and Smallwood, 1996; Shenbrot *et al.*, 2010). This is, however, challenging for evasive and nocturnal species such as bats. Most European bat species hibernate from October until March–April. After hibernation, females gather in their natal maternity roost, where they typically give
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Population size and survival of the Malagasy fruit bat *Rousettus madagascariensis* (Pteropodidae) in Ankarana, northern Madagascar

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Population size and survival are crucial factors to understand population dynamics of a given species, especially those that have long life spans and delayed sexual maturity, such as Pteropodidae bats. We studied the population size and apparent survival of individuals at a day roost site of an endemic cave-dwelling Malagasy fruit bat, *Rousettus madagascariensis*, in relation with age and sex. 1,801 individuals were captured and tagged over the course of four years in the Grotte des Chauves-souris, Réserve Spéciale d’Ankarana, northern Madagascar. The Cormack-Jolly-Seber model and the POPAN model in the program MARK were used to analyze mark-recapture data and to estimate apparent individual survival and population size. The apparent survival of individuals ranged from 0.46 to 0.60, but exhibited significant variability associated with age, sex, and time. Apparent survival is lower in adults compared to sub-adults ($\Phi_{adult} = 0.49$; $\Phi_{sub-adult} = 0.63$). For adults, the apparent survival of males was higher ($\Phi_{male} = 0.50$; $\Phi_{female} = 0.47$), and conversely for sub-adults, it was in favor of females ($\Phi_{male} = 0.55$; $\Phi_{female} = 0.70$). Population size ranged from 1,245 (CI: 268–3,050) to 5,868 (CI: 3,520–10,601) and was significantly higher during the wet season as compared to the dry season. The survival rate in this population is strongly influenced by mortality and secondarily by dispersal. We found that the apparent survival of individuals has a positive impact on population growth but less than birth rate. Thus, the health and sustainability of the population relies heavily on individual survival.

Key words: dispersal, *Rousettus madagascariensis*, population size, fruit bat, apparent survival

INTRODUCTION

For a given species, studying population dynamics can help to understand the spatial and temporal evolution of population size and their related causes (Barbault, 1981). These data can be used as indicators of population stability and be informative for conservation programs (Balmford et al., 2005; Kloepfer et al., 2016). There are several parameters that influence population size, such as natality, individual survival, mortality, and migratory movements (immigration and emigration). Among these parameters, individual survival contributes in an important manner to the determination of population dynamics and species demography (Lebreton et al., 1992; Monadjem et al., 2015), yet this parameter is often disregarded. Given the importance of all these factors, data on population size and individual survival are essential to pilot the conservation activities (Sripathi et al., 2004; Pryde et al., 2005; Kunz et al., 2009; Frick et al., 2010; Papadatou et al., 2011).

Among the multitude methods used to estimate population size, direct observation counting is the one that gives notably reliable results. However, for bats, which are flying and nocturnal (Banfield, 1977; Barclay and Bell, 1988; Webb and Tideman, 1996; O’Shea and Bogan, 2003), this method proves to be difficult (Ransome, 1989; Frick et al., 2007). Another drawback of counting is that it does not allow estimation of individual survival. Therefore, use of other methods, based on population samples, is more appropriate (Lincoln, 1930; Otis et al., 1978; Seber, 1986). Among these methods, the most common used is mark-recapture. Mark-recapture data can be used to estimate both apparent survival
INTRODUCTION

The majority of bat species roost in groups (McCracken and Wilkinson, 2000; Kerth, 2008) and benefit from the physiological advantages of this type of social living, with clustered individuals maintaining body temperature at a more constant value and reducing individual expenditure of energy (Tuttle, 1975; Baudinette et al., 1994). Energetic challenges are not the same for bats with frugivorous and insectivorous diets, since insects have notably higher protein content than fruits (Thomas, 1984). Further, some insectivorous bat species are able to enter torpor (e.g., Dwyer, 1971; Speakman and Rowland, 1999) and certain living in temperate areas can hibernate (e.g., Thomas et al., 1990; Humphries et al., 2006). The fact that frugivorous bats are unknown to hibernate is related to their geographical distribution, as they occur largely in tropical or sub-tropical zones (Mickleburgh et al., 1992; Benda et al., 2011; Stevens, 2011; Fenton and Simmons, 2014), where minimal temperatures are less pronounced than in temperate zones. However, frugivorous bats need to adapt their physiology to cope with the relatively low nutritional content of fruit. Previous studies have shown that frugivorous bats can vary their diets and consume a variety of fruits (Heithaus et al., 1975; Fleming, 1986; Mello et al., 2005; Nelson et al., 2005; Andrianaivoarivelolo et al., 2012; Sánchez et al., 2012). However, this food source can show considerable variation in quality and seasonal availability, specifically the ratio...
Roost composition and sexual segregation in a lowland population of Daubenton’s bats (Myotis daubentonii)

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Using data from 1100 day roosts containing a minimum of 9424 Myotis daubentonii bats, we compare the distribution of adult males, adult females, and juveniles, within Schwegler™ box roosts distributed across 394 ha of woodland adjacent to a river corridor in lowland England. Five social groups, containing both males and females (each comprising 55–230 adult bats per annum, using 37–127 known roosts per colony), occupy discrete roosting areas to which individuals show high inter-annual fidelity. Natal philopatry is also high, compared to between colony movements, for both sexes in our study population. Despite considerable spatial overlap and variability in roost composition over the summer (April to October), related to temporal changes in reproductive status, there is sexual segregation within day roosts. Bachelor (adult male dominated) roosts are situated significantly further from water than maternity (adult female or juvenile dominated) roosts on average. This spatial partitioning between maternity and bachelor roosts operates within rather than between colony home roost ranges, however, with adult males from some social groups found roosting closer to water than are adult females from adjacent colonies. The co-occurrence of maternity and bachelor groups roosting in close proximity, including extensive spatial overlap in roosts occupied, and temporal overlap during roost sharing between the sexes, provides novel insights into social organisation and potential drivers of sexual segregation and mating strategies for this widespread and common species within lowland habitats.

Key words: landscape, philopatry, occupancy, colony, fidelity, maternity, male, social

INTRODUCTION

Daubenton’s bat, Myotis daubentonii (Kuhl, 1817) (Chiroptera: Vespertilionidae) is common and widespread across the Palearctic where it specialises in hunting low over calm water surfaces by aerial hawking or trawling (Todd and Waters, 2017), feeding predominantly on Chironomids (Diptera, Nematocera) (Swift and Racey, 1983; Vesterinen et al., 2016). Male sociality, where bachelor groups containing multiple males have been reported sharing day roosts during the active season, is known to occur in this species (Encarnação et al., 2005; Nardone et al., 2015), possibly due to their foraging strategy, which is dependent on the location of patchily distributed prey, and may therefore involve some level of group cooperation or information sharing (Safi and Kerth, 2007).

Previous studies have demonstrated that sexual segregation occurs during the maternity period in M. daubentonii, with females and their dependent offspring occupying roosts closer to optimal foraging habitat compared to bachelor roosts, and males typically travelling further during foraging bouts than females, especially lactating females which return to their offspring in the maternity roost several times per night (Encarnação et al., 2005; Senior et al., 2005).

Landscape topography and local microclimate can influence the distribution and quality of foraging sites, i.e. size of waterbodies, water surface characteristics, and prey availability, along an elevational gradient (Warren et al., 2000). Male M. daubentonii are typically more widely distributed, occurring at higher altitude within sub-optimal habitat, compared to females which, due to their higher energy demands during pregnancy and lactation, are restricted to lower elevation roosts and foraging sites where climatic conditions are more favourable and prey availability is higher (Russo, 2002; Dietz et al., 2006; Angell et al., 2013). It has been suggested that competitive exclusion exists where females, and
INTRODUCTION

Coexisting species with similar requirements may often be limited according to the degree of overlap in one or more dimensions of their niche (Schoener, 1974; Griffin and Silliman, 2011). Animals have therefore developed different strategies that reduce competition for resources and its negative effects (Briffa and Sneddon, 2010; Griffin and Silliman, 2011), such as modifications in foraging space, time and diet (Tschapka, 2004; Clare et al., 2013). Niche partitioning is one of the most important strategies that enable species coexistence (Schoener, 1974) through the exploitation of resources in different ways (Tavizon, 1998; Griffin and Silliman, 2011; Denzinger and Schnitzler, 2013; Salinas-Ramos et al., 2015).

Niche segregation in bat species has been found to be driven by a combination of bat traits such as skull morphology, wing design and body size (Bonaccorso and Gush, 1987; Norberg and Rayner, 1987; Fleming, 1993; Freeman, 1995; Lou and Yurrita, 2005; Bloch et al., 2010; Denzinger and Schnitzler, 2013). In addition to these specializations, physiological limitations, food characteristics, resource availability and biotic interactions may also determine feeding behavior in bat species (Heithaus et al., 1975; Nicolson and Thornburg, 2007; Ayala-Berdon et al., 2011; González-Terrazas et al., 2012; Salinas-Ramos et al., 2015). Among bats, nectarivores are highly specialized and dependent on food characteristics due to the elevated cost of flight (Hainsworth and Wolf, 1972; Winter and von Helversen, 1998). Diet may thus be considered one of the main constraints during competition and species may therefore need to develop strategies that enable coexistence (Schoener, 1974; Griffin and Silliman, 2011).

Some of the dimensions in which niche partitioning can usually occur are activity patterns...
Activity of aerial insectivorous bats in two rice fields in the northwestern Llanos of Venezuela

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Even though agricultural lands provide abundant food to aerial insectivorous bats (AIB), our understanding of how spatio-temporal factors affect their foraging behavior in these habitats is limited and mostly restricted to temperate regions. In this study, we examined species richness, composition and patterns of activity of AIB in rice fields in the northwestern Llanos of Venezuela. Between 2013 and 2014, we conducted acoustic monitoring of AIB in two rice fields with contrasting forest cover, throughout three phases of the life cycle of this crop (vegetative, reproductive, and ripening), during the dry and rainy season. Out of 108 h recorded, we processed 12,630 files and identified 15 species and 10 sonotypes of AIB from families Molossidae, Mormoopidae, Vespertilionidae, Emballonuridae and Noctilionidae. Molossus molossus and Myotis nigricans showed the highest levels of feeding and general activity across species. The index of general activity (IGA) of AIB was higher above rice fields with more surrounding forest cover, during the dry season and throughout the entire life cycle of the plant. Relative feeding activity (RFA) did not change with respect to forest cover, season or crop phase, but a significant effect of the interaction of these factors was observed on this variable. The response of IGA and RFA to forest cover, season or crop phase was different between M. molossus and M. nigricans and among functional groups. Our results indicate that rice fields in the Venezuelan Llanos can be active feeding grounds for open space and edge-habitat foraging species of insect-feeding bats. Forest patches can promote AIB activity by favoring foraging of ‘edge’ species above rice fields. Higher general activity of most AIB species during the dry season suggests that rice fields are used more intensively when insect populations decrease in semi-deciduous forest patches around them. Overall, our results suggest that availability of abundant feeding areas to AIB, provided by the rice fields, together with presence of artificial and natural roosts to these bats, could ensure year-round permanence of a rich ensemble of AIB in the rice field-forest landscape in the northwestern Llanos of Venezuela. Some of these species could be the subject of field experiments to test their value in the control of rice’s insect pest populations.

Key words: echolocation, rice, Venezuelan Llanos, insectivorous bats, Molossus molossus, Myotis nigricans, Neotropics

INTRODUCTION

Aerial insectivorous bats (AIB) are one of the most important guilds of wildlife in agricultural landscapes, not only because they are resilient to habitat fragmentation, but because they can provide valuable ecosystem services to farmers (Kunz et al., 2011; Williams-Guillén et al., 2016). Aerial insectivorous bats can frequent a variety of crops across agricultural landscapes, where they seek insects that depend on plants to complete their life cycle, and can help farmers by reducing the costs of food production (Wanger et al., 2014; Maine and Boyles, 2015; Puig-Montserrat et al., 2015). Crops such as rice, corn, cotton, sugar cane, coffee, and cocoa can function as habitats for AIB, and produce insect aggregations that bats can exploit (Leelapaibul et al., 2005; McCracken et al., 2012; Noer et al., 2012; Heer et al., 2015; Ongole et al., 2018).
Activity records of the endangered Paraguaná moustached bat, *Pteronotus paraguanensis*, in the main vegetation types of the Paraguaná Peninsula, Venezuela

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The Paraguaná moustached bat, *Pteronotus paraguanensis* (Mormoopidae), is one of the four species of bats endemic to Venezuela. Besides having a geographic distribution restricted to the Paraguaná Peninsula, it is currently classified as Endangered in the IUCN Red List of Threatened Species. Changes in land use, frequent human disturbance at diurnal roosts and poisoning with agro-pesticides from farming operations are some of the main threats that affect this species. Despite its conservation status and the pressing need to protect its feeding areas, habitat use of this species has not been well documented. The aim of this study was to record this bat’s activity using acoustic monitoring to identify the vegetation types most frequently used throughout the year.

We recorded echolocation calls over the course of eight months between 2015 and 2016, using walking transects distributed along the vegetation types most representative of the peninsula. Activity of *P. paraguanensis* differed significantly among vegetation types, reaching highest relative activity in thorn woodlands (45%), followed by premontane woodlands (20%), disturbed habitats (19%), thorn scrubs (11%), and columnar cactus forests (4%). Activity (mean number of bat passes/h) was comparatively higher in premontane woodlands (78.17 ± 49.82 SD) than in the other vegetation units (range: 4.39 ± 5.71 SD – 15.51 ± 16.11 SD) where this species was detected. This result is indicative that this species is mainly associated with forest habitats; however, it can also be present at lower frequency in disturbed lands. Our bat call recordings also help confirm that the Paraguaná Peninsula’s isthmus represents an ecological barrier that precludes dispersion of *P. paraguanensis* to the mainland. Based on our findings, we highlight the need to focus conservation actions for this species on protection of the remnant patches of forest vegetation still present in the peninsula.

**Key words**: echolocation calls, endangered species, habitat degradation, Mormoopidae, *Pteronotus paraguanensis*

**INTRODUCTION**

Arid lands in the Caribbean region are under permanent threat whether by land conversion, desertification, introduction of exotic species, and effects of global climate change (Dinerstein *et al.*, 1995; Herrera *et al.*, 2016; Medina *et al.*, 2016). The Paraguaná Peninsula, located in the northwestern coast of Venezuela, contains a mosaic of plant communities mostly dominated by xerophilous vegetation, including thorn scrubs, cactus forests, and very dry tropical forest (Huber and Alarcón, 1988). The peninsula is connected with the mainland through an isthmus 30 km long and 5 km width. With the exception of five protected areas (‘Cerro de Santa Ana’ Natural Monument, ‘Montecano’ Biological Reserve, Santuario de Fauna ‘Cuevas de Paraguaná’ and ‘Medanos de Coro’ National Park, Refugio de Fauna y Reserva de Pesca ‘Laguna Boca de Caño’ — Romero, 1989; Bisbal, 1990; Delfin *et al.*, 2011), which represent 17% of the total peninsula’s surface, the rest of the peninsula has been exposed to intensive land conversion, which has led to the loss of pristine habitats (Rodríguez *et al.*, 2010).

The Paraguaná moustached bat, *Pteronotus paraguanensis* Linares & Ojasti 1974 (Mormoopidae), is one of four species of endemic bats present in Venezuela (Sánchez and Lew, 2012) and is listed as Endangered by the IUCN Red List of Threatened Species (IUCN, 2018) and the Venezuelan Fauna Red List (Rodríguez and Rojas-Suárez, 2008). This medium-size mormoopid (Gutiérrez and Molinari, 2008) was originally described as a subspecies of *P. parnelli* (*P. p. paraguanensis* — Linares and
Microclimate of developing tubular leaves used as roost sites by bats

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Roosts are critical for the reproduction and survival of bats and many species spend a significant portion of their lives in them; thus, individuals should carefully select sites that reduce predation risk while providing ideal microclimatic conditions. Many studies have determined that bats select warmer and more humid roosts in temperate regions, but few studies have determined if roosts selected by tropical species also provide suitable conditions. In this study we compare temperature and humidity within and outside furled tubular leaves of plants in the order Zingiberales, which are used by several tropical species as roost-sites, to determine if these structures provide microclimatic advantages to bats. We found very small differences between the internal and external temperatures of tubular leaves, and the difference further decreased as leaves developed. However, we found large differences in humidity within the tubular leaf compared to external conditions, which were strongly dependent on a leaf’s diameter and genus. The internal humidity was often 20% above the external, particularly when leaves were narrower, and tubular leaves in the genus Heliconia were more humid than those in the genus Calathea. Our findings suggest that, despite being fairly exposed structures, furled tubular leaves provide suitable microclimatic conditions for tropical species.

Key words: disc-winged bats, evaporative water loss, humidity, temperature, thermoregulation

INTRODUCTION

Bats use a diversity of roost sites that provide ideal conditions for resting, feeding, and for engaging in many social interactions that include rearing young, copulation, allogrooming, and information transfer. Roosts are also critical for bats’ survival as they protect them from predators and harsh environmental conditions (Kunz, 1982; Kunz and Lumsden, 2003; Altringham, 2011). In fact, as bats leave their roosts, they become significantly more vulnerable to predation (Speakman, 1991; Fenton et al., 1994; Rodríguez-Durán et al., 2010), and thus many species spend a significant portion of their lives in them. By selecting adequate roosts, bats may additionally increase their fitness by spending less energy in thermoregulation and by reducing the rates of evaporative water loss (Webb et al., 1995; Speakman and Thomas, 2003). The latter advantages are known as major driving forces of roost-site selection, primarily in temperate regions (Kerth et al., 2001; Sedgeley, 2001).

In tropical regions, bats use some of the same roost types available in temperate regions, such as caves and tree cavities. These sites are ideal as they provide stable temperatures and high humidity compared to more exposed conditions (Rodríguez-Durán, 1995; Lundberg and McFarlane, 2015; Maziarz et al., 2017). However, in the tropics a large proportion of species also roost in more exposed sites, such as under modified leaves or inside the
Bat folivory in numbers: how many, how much, and how long?

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Folivory in bats has been described as chewing bits of leaves to extract the liquids, and then discarding the remaining fibers in form of oral pellets. At least eight species of Neotropical fruit-eating bats have been reported to use folivory as a strategy potentially to provide bats with vitamins, micronutrients and proteins usually scarce in fruits, as well as secondary metabolites that stimulate or inhibit reproductive processes, or even as a supply of water. All reported cases of folivory in bats consist of short, descriptive natural history notes with few supporting details. In depth understanding of leaf consumption by bats is lacking. To bridge this gap, we studied two colonies of Artibeus living under different conditions in the Venezuelan Andes: an urban colony (A. lituratus) and a forest colony (A. amplus) whose individuals exhibited folivorous habits. We hypothesized that bats: (1) feed on leaves from many plant species, and more frequently eat certain plant species over others, (2) show monthly variation in leaf consumption, (3) eat specific parts of each leaf and discard the rest, and (4) within a plant species, eat the same part of each leaf. We collected leaves found below the roosting site of the colonies of both species and analyzed digital images of each leaf to quantify the consumed area. All leaves (n = 1,188) were classified and quantified in terms of the pattern of observed consumption (apical, basal, other). We found that both species of bats fed on leaves from certain plant species over others, showed monthly variation in leaf consumption, and on average consumed less than 50% of the leaf, equivalent to an area of 5–7 cm² (n = 655). Maximum consumption of leaves was observed in both species in the weeks immediately prior to males exhibiting scrotal testes and females becoming palpably pregnant. Results from our study provide the first systematic and detailed assessment of folivory in bats, showing the use of leaves all year long by two bat species. Future research should investigate whether males and females consume leaves to the same extent, and on the chemical properties of consumed plant species.

Key words: Chiroptera, forest, Phyllostomidae, behavior, feeding habits, Venezuela, leaves, Stenodermatinae

INTRODUCTION

Folivory has been reported in eight species of bats, all of them phyllostomids from the genera Artibeus, Platyrrhinus (Greenhall, 1957; Van der Pijl, 1957; Zortéa and Mendes, 1993; Kunz and Ingalls, 1994; Kunz and Díaz, 1995; Zortéa, 1996; Bernard, 1997; Esberard et al., 1998; Muñoz-Romo, 2003; Aguiar, 2005; Acosta and Aguanta, 2006; Novaes and Nobre, 2009; Bobrowiec and Cunha, 2010; Ruiz-Ramoni et al., 2011; Cordero-Schmidt et al., 2016), and more recently, Carollia (Pereira et al., 2017). Most observations of leaf consumption document bats chewing small portions of the leaf, extracting the leaf liquids, and discarding the remaining fibers (Kunz and Díaz, 1995), with the exception of one case of young leaves which were consumed whole, presumably because they were less fibrous and more easily digested (e.g., C. perspicillata — Pereira et al., 2017). Although first considered an anomaly (Van der Pijl, 1957), this behavior, reported for the first time more than sixty years ago (Greenhall, 1957), is now seen as a strategy that might provide vitamins and micronutrients not always available in fruits, proteins that are particularly important during pregnancy and lactation but usually scarce in fruits, or secondary metabolites (hormonal precursors) that stimulate or inhibit
Vocal development of Horsfield’s leaf-nosed bat pups (*Hipposideros larvatus*)

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Bats are an appealing animal for investigating the biological basis and evolution of speech-related traits in wild mammal systems. We investigated vocal development in Horsfield’s leaf-nosed bat pups, *Hipposideros larvatus*. We found that newborn bats emit many types of isolation calls, including downward frequency modulation (DFM), arched frequency modulation (AFM), upward frequency modulation (UFM), and others. The gradual decrease of Euclidean distance measurements revealed that pup isolation calls (DFM, AFM, UFM) gradually change into adult social calls. Furthermore, one of the isolation call types (UFM type) encoded an individual signature. By contrast, we report that early echolocation calls and isolation calls develop in parallel. As pups develop, early echolocation calls gradually mature and transform into adult-like echolocation calls. The interval and duration of echolocation calls decreases, while the peak frequency and bandwidth of frequency modulation increases.

**Key words**: bats, isolation calls, individual signature, echolocation calls, vocal development

**INTRODUCTION**

As young mammals grow, they gradually develop the appropriate sensory and locomotor skills that enable them to become independent of their parents (Baptista *et al*., 2000; Sharifi, 2004). During this period, vocalizing mammals usually undergo a vocal development process (Oller *et al*., 1976; Kent and Murray, 1982; Tchernichovski and Marcus, 2014). As speech acquisition is mostly driven by a maturation effect, with some additions to the repertoire being influenced by vocal learning, studies of mammalian vocal development might offer an insight into human speech evolution (Fitch *et al*., 2010; Vernes, 2016; Fitch, 2017).

Bats, as mammals, share brain structures with humans, such as the six-layered cortex and the hippocampus regions involved in cognition and memory of language-related tasks (Vernes, 2016; Rodenas-Cuadrado *et al*., 2018). Bat echolocation calls and social calls are used to facilitate navigation, hunting, recognition, and other social interactions (Kunz and Fenton, 2003; Arnold and Wilkinson, 2011; Smotherman *et al*., 2016), which require auditory systems and neurobiology to be finely tuned to acoustic information (Vernes, 2016). Therefore, bats are an appealing animal for investigating the biological basis and evolution of speech-related traits in wild mammal systems (Knörnschild, 2014; Morell, 2014; Nowicki and Searcy, 2014; Lattenskamp and Vernes, 2018).

Studies on vocal development in bats have focused primarily on isolation calls, which are used to solicit maternal care, and early echolocation calls, which develop into mature calls similar to adult echolocation calls. In some bat species, isolation calls are precursors that gradually develop into echolocation calls (Konstantinov *et al*., 1990; Fanis and Jones, 1995; Moss *et al*., 1997; Sterbing, 2002; Andrews *et al*., 2011, 2017; Wang *et al*., 2014), but in others, isolation calls and echolocation calls can develop in parallel (Brown *et al*., 1983; Vater *et al*., 2003; Liu *et al*., 2007; Jin *et al*., 2011; Monroy *et al*., 2011; Carter *et al*., 2014), or are even mixed (Rübsamen, 1987; Mayberry and Faure, 2015).

Isolation calls are composed of various syllable types, thus, isolation calls can be either monosyllabic or composed of several syllable types (multisyllable). The acoustic features of isolation calls can change as pups mature and their larynx, vocal tract, and lungs all change shape (Matsumura *et al*., 1979, 1981; Vater *et al*., 1997; Monroy *et al*., 2011).
INTRODUCTION

Techniques for monitoring bats have changed rapidly over the past few decades as technology has evolved. In early bat studies, capture methods such as mist netting and harp trapping were heavily relied upon to collect basic community data (Baker and Ward, 1967; Fleming et al., 1972; Kunz, 1973; Bell, 1980; Barclay, 1991; Kuenzi et al., 1999). As acoustic sampling technologies were developed and improved, biologists began to study bats in locations that were otherwise difficult to sample using capture methods (e.g., Hayes, 1997, 2000). By contrast, passive sampling can yield lower quality calls, but procedures are easily repeatable and data can be used to measure temporal variation in activity throughout the night and detect individuals and species that are missed during active sampling. Researchers are increasingly attempting to monitor and compare bat communities over time, including sites where both active and passive sampling have occurred. However, these two techniques can yield different detection probabilities and the extent to which data collected using these two techniques can be compared is unclear. Thus, in July 2017 we simultaneously collected acoustic data actively and passively to compare detection probabilities of bats at the Savannah River Site, South Carolina, USA. Using Anabat Express detectors, we detected five species or species groups (Eptesicus fuscus/Lasiurus cinereus, L. borealis/L. seminolus, Perimyotis subflavus, Myotis austroriparius, and Nycticeius humeralis) using each method. Using single season occupancy modeling, we found that method (passive vs. active sampling) had a significant effect on detection probabilities of all species, and that passively sampling throughout the night yielded the highest detection probability for all species. As a result, if differences in detection probability are not taken into account, comparison of historical active datasets with current passive datasets could lead to different insights into habitat use by similar bat communities. Based on our findings, we recommend that researchers use passive sampling throughout the night when studying and monitoring bat communities.

Key words: acoustics, active sampling, clutter, passive sampling, occupancy probability

Detection probability of bats using active versus passive monitoring

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As technology has evolved, bat researchers have relied more heavily on using acoustic techniques to collect data on bat communities. Acoustic data can be collected actively, where the researcher is present at the sampling point and follows the bat with the detector, or passively, where the researcher is not present and the detector is set out by itself. Active sampling can yield longer, clearer calls, and is only conducted during part of the night (usually from sunset to about 02:00 hours) for short bouts (20 minutes). By contrast, passive sampling can yield lower quality calls, but procedures are easily repeatable and data can be used to measure temporal variation in activity throughout the night and detect individuals and species that are missed during active sampling. Researchers are increasingly attempting to monitor and compare bat communities over time, including sites where both active and passive sampling have occurred. However, these two techniques can yield different detection probabilities and the extent to which data collected using these two techniques can be compared is unclear. Thus, in July 2017 we simultaneously collected acoustic data actively and passively to compare detection probabilities of bats at the Savannah River Site, South Carolina, USA. Using Anabat Express detectors, we detected five species or species groups (Eptesicus fuscus/Lasiurus cinereus, L. borealis/L. seminolus, Perimyotis subflavus, Myotis austroriparius, and Nycticeius humeralis) using each method. Using single season occupancy modeling, we found that method (passive vs. active sampling) had a significant effect on detection probabilities of all species, and that passively sampling throughout the night yielded the highest detection probability for all species. As a result, if differences in detection probability are not taken into account, comparison of historical active datasets with current passive datasets could lead to different insights into habitat use by similar bat communities. Based on our findings, we recommend that researchers use passive sampling throughout the night when studying and monitoring bat communities.

Key words: acoustics, active sampling, clutter, passive sampling, occupancy probability
INTRODUCTION

At its most simple expression, monitoring is a set of repeated assessments within a defined area over a specified time period and can be a tool to assess and achieve management objectives (Thompson et al., 1998). MacDonald et al. (1991) define seven types of monitoring, some of which include types which aim to establish baselines or follow temporal trends in the measured variables (later defined as surveillance monitoring by Nichols and Williams, 2006) and types that aim to assess and evaluate the impact of a change, often made in a before-after basis (named target monitoring by Nichols and Williams (2006). Pereira et al. (2017) give a list of essential variables in monitoring, which includes among others species abundance and distribution, species interactions, and taxonomic diversity. A rapid decline in populations like the one found in bat species affected by White-Nose Syndrome (WNS — Frick et al., 2010) is an example of a case may induce jurisdiction to rapidly implement a target type of monitoring at a large scale. Furthermore, Pereira et al. (2017) discuss the possible reuse of existing data, which conservation biologists may use to gather a baseline of what stimulated population variations prior to the decline and identify variables that would either influence future monitoring or impact mitigation methods.

The challenges of collecting valuable data for monitoring is well exemplified by the North American Bat Monitoring Program (NABat — Loeb et al., 2015). They developed a monitoring program which combines multiple monitoring protocols, such as colony counts, hibernacula counts, and acoustic recordings to assess and inform stakeholders of the current threats to bats, but also to detect unanticipated threats in the future (Loeb et al.,...
Isolation and characterization of hyper-xylanase producing *Bacillus* spp. from faeces of the Indian flying fox (*Pteropus giganteus*)

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In the present study, hyper-xylanase producing novel bacterial strains were isolated from faeces of the Indian flying fox (*Pteropus giganteus*). Considering the qualitative assay, off 27 bacterial isolates, three strains were observed to be the hyper producers of xylanase. The potent isolates were identified using biochemical as well as molecular characterization tools, and were categorized under *Bacillus* spp. Further, the production of extracellular xylanase was quantified up to 72 h using standard methodology. The hyper production of xylanase was observed in the order of *Bacillus amyloilefaciens* strain LAA64 (998.32 ± 17.6 U/mL) > *B. methylotrophicus* strain DLA64 (937.89 ± 16.1 U/mL) and > *B. velezensis* strain DLLA28 (910.46 ± 14.5 U/mL) at 48 h of incubation period. Evidently, these novel strains were identified as promising source for xylanase yield. Xylanase represents one of the most important groups of industrial enzymes and thus xylanases obtained from *Bacillus* spp. suggest their wide applications in diversified industries.

Key words: xylanase, molecular characterization, faeces, *Pteropus giganteus*

INTRODUCTION

Bats (Order Chiroptera), after rodents comprise the most diverse group of mammals with more than 1,360 species (Kingston, 2016). The family Pteropodidae with 43 genera and 174 species of bats are confined to the old world tropics and sub-tropics. Among the pteropodid bats, flying foxes (*Pteropus giganteus*) occur mainly in tropical regions of South Central Asia from Pakistan to China (Nowak, 1999). They eat a wide range of flowers, fruits, and leaves (Fleming and Kress, 2011) to meet their nutritional energy demand.

Bats supply their high energy demands through their ability in executing a fast combustion of ingested carbohydrates. In fact, they must burn diet nutrients instantly to sustain immediate energy and high requirements for flight (Voigt et al., 2010). In fruit bats, the protein requirements are met by digestion of pollen and leaves (Kunz and Ingalls, 1994; Long and Racey, 2007).

The phyllostomid bats show diversity in feeding habits and are unique among all the mammals. This taxon includes species that are highly specialized on insects, blood, small vertebrates, fruits, nectar, and pollen. Feeding specialization is accompanied by morphological, physiological, and behavioural adaptations (Datzmann et al., 2010; Phillips et al., 2012).

Phyllostomids are also known because of their folivory. This phenomenon has been reported in eight species of them (genera Artibeus, Carollia and Platyrrhinus — reviewed by Duque-Márquez et al., 2019). Cellulose and xylan are the major component of leaves. Surprisingly, although animals commonly consume cellulose and xylan, most species do not produce cellulases and xylanases by themselves. They live in symbiotic relationship with cellulolytic and xylanolytic microorganisms (Anand et al., 2012). It is reported that the digestive tract must contain cellulolytic and xylanolytic bacteria which help in the digestion of cellulose and xylan found in the diet of *P. giganteus*. In contrast, an insectivorous bat, *Hipposideros fulvus* does not possess cellulolytic and xylanolytic bacteria (Anand and Sripathi, 2004).

Xylanases are of increasing commercial interest because they allow the utilization of xylan, abundant in wastes from agriculture and the food industry. Xylan is a major skeletal component of the plant cell wall in primary and secondary cells. It is an abundant organic compound found in storage and