Acta Chiropterologica, 21(2): 237–256, 2019 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/15081109ACC2019.21.2.001

### Systematics of West African Miniopterus with the description of a new species

ARA MONADJEM<sup>1, 2, 12</sup>, JULIE T. SHAPIRO<sup>3, 4, 5</sup>, LEIGH R. RICHARDS<sup>6</sup>, HATICE KARABULUT<sup>7</sup>, WING CRAWLEY<sup>8</sup>, IDA BROMAN NIELSEN<sup>9</sup>, ANDERS HANSEN<sup>9</sup>, KRISTINE BOHMANN<sup>10</sup>, and TOBIAS MOURIER<sup>11</sup>

<sup>1</sup>Department of Biological Sciences, University of Eswatini, Private Bag 4, Kwaluseni, Eswatini
<sup>2</sup>Mammal Research Institute, Department of Zoology & Entomology, University of Pretoria, Private Bag 20, Hatfield 0028, Pretoria, Republic of South Africa
<sup>3</sup>School of Natural Resources and Environment, University of Florida, 103 Black Hall, Gainesville FL, 32611, USA
<sup>4</sup>Department of Wildlife Ecology and Conservation, University of Florida, 110 Newins-Ziegler Hall, Gainesville FL, 32611, USA
<sup>5</sup>Centre International de Recherche en Infectiologie, Institut National de la Santé et de la Recherche Médicale, 46 Allée d'Italie, 69634, Lyon, France
<sup>6</sup>Durban Natural Science Museum, PO Box 4085, Durban, 4000, Republic of South Africa
<sup>7</sup>Department of Molecular Biology and Genetics, Middle East Technical University, Ankara 06800, Turkey
<sup>8</sup>53 Rosebank Crescent, Exeter, Devon EX4 6EH, United Kingdom
<sup>9</sup>Centre for GeoGenetics, GLOBE Institute, University of Copenhagen, 1350 Copenhagen, Denmark
<sup>10</sup>Section for EvoGenomics, GLOBE Institute, University of Copenhagen, 1350 Copenhagen, Denmark
<sup>11</sup>Pathogen Genomics Laboratory, Biological and Environmental Sciences and Engineering Division, King Abdullah University of Science and Technology, Thuwal, Saudi Arabia
<sup>12</sup>Corresponding author: E-mail: ara@uniswa.sz

The phylogenetic relationships and species limits within the chiropteran family Miniopteridae are poorly known in mainland Africa. Recent systematic studies in Madagascar have shown that this is a species-rich family, yet only eight species are currently recognized or hypothesized for continental Africa. Based on partial cytochrome *b* sequences and morphometric analysis, we describe a new species of *Miniopterus* that is endemic to a restricted, montane region of Liberia and Guinea. Furthermore, the taxonomic status of the West African *Miniopterus schreibersii villiersi* is resolved and shown to be a distinct species, *M. villiersi*, that is not closely related to *M. schreibersii*. Finally, the species *M. inflatus* is revealed to be paraphyletic, with the central African rainforest populations apparently not closely related to the savanna forms in eastern and southern Africa. Based on the results of this study, the number of *Miniopterus* species in Africa has increased from eight to 11, with more cryptic species likely to be discovered.

Key words: geometric morphometrics, cryptic species, West Africa, cytochrome b, taxonomy, Miniopteridae

Acta Chiropterologica, 21(2): 257–269, 2019 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/15081109ACC2019.21.2.002

# Cytogenetic investigations in Emballonuroidea. I. Taphozoinae and Emballonurinae karyotypes evolve at different rates and share no derived chromosomal characters

MARIANNE VOLLETH<sup>1, 9</sup>, STEFAN MÜLLER<sup>2</sup>, FAISAL A. ANWARALI KHAN<sup>3</sup>, HOI-SEN YONG<sup>4</sup>, KLAUS-GERHARD HELLER<sup>5</sup>, ROBERT J. BAKER<sup>6</sup>, DAVID A RAY<sup>6</sup>, and CIBELE G. SOTERO-CAIO<sup>6, 7, 8</sup>

<sup>1</sup>Department of Human Genetics, Otto-von-Guericke University, Leipziger Strasse 44, 39120 Magdeburg, Germany
 <sup>2</sup>Institute of Human Genetics, Munich University Hospital, Ludwig-Maximilians University, Goethestrasse 29, 80336 Munich, Germany
 <sup>3</sup>Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak, Malaysia
 <sup>4</sup>Institute of Biological Sciences, University of Malaya, 50603 Kuala Lumpur, Malaysia
 <sup>5</sup>Grillenstieg 18, 39120 Magdeburg, Germany
 <sup>6</sup>Department of Biological Sciences, Texas Tech University, 2901 Main Street, 79409-43131, Lubbock, Texas, USA
 <sup>7</sup>Department of Ecology, Faculty of Science, Charles University, Viničná 7, 12844, Prague, Czech Republic
 <sup>8</sup>The Wellcome Trust Sanger Institute, Genome Campus, Hinxton/Cambridge, CB10 1SA, United Kingdom
 <sup>9</sup>Corresponding author: E-mail: Marianne, Volleth@med.ovgu.de

We present a comparative molecular cytogenetic investigation of six emballonurid species using chromosome banding and crossspecies chromosome painting with probes from *Myotis myotis*, supplemented by selected probes from human, tree shrew, and lemur. The main differences between the 2n = 42 *Taphozous* karyotype and the 2n = 44 chromosomal complement of *Saccolaimus* can be explained by one Robertsonian fusion, one type-b, and one type-c whole arm reciprocal translocation. The 2n = 24 karyotype of *Emballonura* is highly derived by splitting of 11 of the 25 chiropteran evolutionarily conserved units resulting in a total number of 36 segments. In contrast to the presence of several autapomorphies in the karyotypes of studied species from both subfamilies, no cytogenetic synapomorphy uniting Taphozoinae and Emballonurinae was found.

Key words: chromosomal evolution, centromere shift, FISH

Acta Chiropterologica, 21(2): 271–281, 2019 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/15081109ACC2019.21.2.003

# Cytogenetic investigations in Emballonuroidea. II. Chromosome painting in Nycteridae reveals cytogenetic signatures pointing to common ancestry of Nycteris and Emballonura

MARIANNE VOLLETH<sup>1, 6</sup>, STEFAN MÜLLER<sup>2</sup>, KLAUS-GERHARD HELLER<sup>3</sup>, and JAKOB FAHR<sup>4, 5</sup>

<sup>1</sup>Department of Human Genetics, Otto-von-Guericke University, Leipziger Strasse 44, 39120 Magdeburg, Germany <sup>2</sup>Institute of Human Genetics, Munich University Hospital, Ludwig-Maximilian University, Goethestr. 29, 80336 Munich, Germany <sup>3</sup>Grillenstieg 18, 39120 Magdeburg, Germany <sup>4</sup>Institute of Experimental Ecology, Ulm University, Albert Einstein Allee 11, 89069 Ulm, Germany <sup>5</sup>Zoological Institute, Braunschweig University of Technology, Spielmannstrasse 7, 38106 Braunschweig, Germany <sup>6</sup>Corresponding author: E-mail: marianne.volleth@med.ovgu.de

Two species of the monogeneric family Nycteridae were studied for the first time with chromosome banding techniques and chromosome painting. The diploid chromosome number of *Nycteris macrotis* and *N. tragata* is 40 and 38, respectively. Both karyotypes differ by a translocation, a telomeric fusion and a pericentric inversion. The genus *Nycteris* shows a highly derived karyotype where the 25 chiropteran evolutionarily conserved units (ECUs) are represented in 37 segments. Chromosome painting with *Myotis* probes revealed three common features of *Nycteris* and *Emballonura*, which are not present in *Taphozous*. From a cytogenetic point of view, *Nycteris* is therefore closer related to *Emballonura* than to *Taphozous*. Further, an additional synapomorphy for Vespertilioniformes is described, i.e. the synteny of a segment homologous to human chromosome 13 and ECU12a-22a in elements homologous to *Myotis* chromosome MMY6.

Key words: karyotypic evolution, FISH, phylogeny

Acta Chiropterologica, 21(2): 283–298, 2019 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/15081109ACC2019.21.2.004

### Genetic structure associated with the ecological traits of four species of phyllostomid bats inhabiting Selva El Ocote Biosphere Reserve, Chiapas, México

BÁRBARA CRUZ-SALAZAR<sup>1, 2</sup>, MARICELA GARCÍA-BAUTISTA<sup>1</sup>, and LORENA RUIZ-MONTOYA<sup>1</sup>

<sup>1</sup>Consejo Nacional de Ciencia y Tecnología, Universidad Autónoma de Tlaxcala, Carretera Federal Puebla-Tlaxcala Km 1.5, La Loma Xicohténcatl, CP 90062, Tlaxcala de Xicohténcatl, Tlaxcala, México <sup>2</sup>Corresponding author: E-mail: bcruz@ecosur.edu.mx

Phyllostomid bats display a variety of social structures and mating systems; the influence of these features on the distribution of genetic diversity within and between bat populations is currently unknown. Based on the mitochondrial DNA D-loop region, we investigated the relationship between genetic structure and social characteristics in four species of phyllostomid bats (Sturnira hondurensis, Artibeus jamaicensis, Carollia sowelli, and Dermanura tolteca) inhabiting Selva El Ocote Biosphere Reserve (REBISO). According to their ecological characteristics, we expected a relatively high genetic diversity and stable populations, as well as a weak genetic structure in S. hondurensis and C. sowelli, and a moderate one in A. jamaicensis and D. tolteca. The demographic history and mismatch distribution were inferred. Besides, we estimated the time elapsed from demographic change (in number of generations). Finally, we calculated standard genetic diversity indicators and determined the genetic structure, haplotype networks, and conducted spatial autocorrelation analyses. Genetic diversity was higher in S. hondurensis, intermediate in C. sowelli, and low in A. jamaicensis and D. tolteca. The neutrality tests indicated population expansion in A. jamaicensis, C. sowelli, and D. tolteca; S. hondurensis showed differentiation between populations with no apparent demographic changes. The extent of genetic differentiation was high in S. hondurensis, intermediate in C. sowelli, weak in A. jamaicensis, and nil in D. tolteca. The spatial autocorrelation revealed genetic structure at certain geographic distances in A. jamaicensis, C. sowelli, and S. hondurensis, while D. tolteca displayed a low structure at the greatest geographic distances. No clear relationship was evident between ecological attributes and genetic structure in the bat species studied, probably due to the slight differences in the ecological characteristics of these species. Further studies should include ecological factors such as resource availability and habitat selection, as well as nuclear markers, to obtain a biparental genetic estimation. This study highlights the need of conduct further research about the relationship of ecological and genetic traits of tropical bats in high-biodiversity reserves.

Key words: conservation, D-loop, population genetic structure, REBISO, social structure, tropical bats

Acta Chiropterologica, 21(2): 299–308, 2019 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/15081109ACC2019.21.2.005

# The past occurrence of the Guadeloupe big-eyed bat *Chiroderma improvisum* Baker and Genoways, 1976 on Marie-Galante (French West Indies) with comments on bat remains from pre-Columbian sites in the Eastern Caribbean

#### ARNAUD LENOBLE<sup>1, 2</sup>

<sup>1</sup>UMR CNRS 5199 PACEA, University of Bordeaux, B2 – Allée Geoffroy Saint-Hilaire, CS 50023, 33615 PESSAC, CEDEX, France <sup>2</sup>Corresponding author: E-mail: arnaud.lenoble@u-bordeaux.fr

The present work reports the first Quaternary specimen of the Guadeloupe big-eyed bat *Chiroderma improvisum* represented by a left mandible fragment collected from a pre-Columbian midden on Marie-Galante in the Lesser Antilles. The subfossil material was identified based on the description of the morphology of the mandible and lower molar of modern *C. improvisum* specimens and a comparison with other previously described *Chiroderma* species. In addition to being the first documented occurrence of *C. improvisum* on Marie-Galante, it extends the known geographic distribution of this species further south and increases the number of bat species extirpated from the island. A series of associated radiocarbon dates reliably places the last occurrence of this species to between the 11th and 13th centuries, suggesting that some local bat extinctions occurred during the historical period. In addition, a review of bat remains from archaeological contexts in the Eastern Caribbean allows to discuss the possible consumption of bats by indigenous peoples, as well as to stress the potential limitations of the archaeological record for reconstructing past bat communities in this region.

Key words: Chiroderma improvisum, dental morphology, fossil, bat fauna turnover, West Indies, pre-Columbian subsistance, zooarchaeological epistemology

Acta Chiropterologica, 21(2): 309–319, 2019 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/15081109ACC2019.21.2.006

# Embryonic development of the Egyptian fruit bat *Rousettus aegyptiacus* (Mammalia: Chiroptera: Pteropodidae)

ERAQI R. KHANNOON<sup>1, 2†</sup>, KAORU USUI<sup>3†</sup>, and MASAYOSHI TOKITA<sup>3, 4</sup>

<sup>1</sup>Biology Department, College of Science, Taibah University, Al Madinah Al Munawwarah, PO Box 30002, Saudi Arabia
 <sup>2</sup>Zoology Department, Faculty of Science, Fayoum University, Fayoum, 63514, Egypt
 <sup>3</sup>Department of Biology, Faculty of Science, Toho University, 2-2-1 Miyama, Funabashi, Chiba, 274-8510, Japan
 <sup>4</sup>Corresponding author: E-mail: masayoshi.tokita@sci.toho-u.ac.jp

Bats have evolved several unique morphological traits related to powered flight, such as wings, patagia, minute hindlimbs, large pinna, and a larynx specialised for echolocation. Studies of embryonic development in bats provide important insights into the mechanisms underlying the evolution of flight-related structures in vertebrates. Although embryonic development has been described in some bats species, only one species of Old World fruit bats (family Pteropodidae) has previously had its embryonic development examined. In this paper, we describe the embryonic development of the Egyptian fruit bat, *Rousettus aegyptiacus*, ranging from middle pharyngula to just before birth. We compared the growth patterns during embryogenesis among nine bat species for which data on embryonic development have been obtained. We discovered that i) the crown-rump length (CRL) is almost equivalent among the bat species until stage 22, and ii) compared to other bat species examined, the growth rate rapidly and substantially increases in two pteropodid species (*R. aegyptiacus* and *R. amplexicaudatus*) after stage 22. In placental mammals, larger body size at birth is advantageous for postnatal survival. To obtain large adult body size, some pteropodid bats may accelerate their postnatal growth and take advantage of larger body size at birth.

Key words: crown-rump length, embryogenesis, external morphology, growth rate, Old World fruit bat

Acta Chiropterologica, 21(2): 321–329, 2019 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/15081109ACC2019.21.2.007

# More traffic, less bat activity: the relationship between overnight traffic volumes and *Chalinolobus tuberculatus* activity along New Zealand highways

KERRY M. BORKIN<sup>1, 2, 3</sup>, DES H. V. SMITH<sup>1</sup>, WILLIAM B. SHAW<sup>1</sup>, and JOANNA C. MCQUEEN<sup>1</sup>

<sup>1</sup>Wildland Consultants Ltd, PO Box 7137, Te Ngae, Rotorua 3042, New Zealand <sup>2</sup>Present address: Department of Conservation, PO Box 1146, Rotorua 3040, New Zealand <sup>3</sup>Corresponding author: E-mail: kborkin@doc.govt.nz

Despite a growing body of evidence worldwide that bats are affected by roads, there has been little research into the effects of traffic volume on bat activity. In New Zealand, there is considerable uncertainty over whether, or to what extent, roads affect New Zealand's endemic bat populations, and this has resulted in uncertainty during the planning and consent phases of road development projects. This research investigated whether *Chalinolobus tuberculatus* (long-tailed bat) activity correlates with night-time traffic volume on New Zealand's highways. Bat activity was monitored at 57 traffic monitoring sites throughout New Zealand using pairs of bat detectors, with one placed beside the highway (highway) and one placed  $\geq 200$  metres from the highway (distant). Generalised linear mixed effects models were used to investigate the relationship between bat detections, position in relation to the highway, and various measures of traffic volume. The model that best explained the variation in bat detections was the interaction effect between bat detector position (highway, distant) and night-time traffic volume (volume). Outputs from this model show a negative relationship between bat activity and night-time traffic volume. These results indicate that night-time traffic volume affects the use of roads by bats, i.e. when overnight traffic increased, the probability of detecting bats decreased. Whether or to what extent this will affect the long-term viability of New Zealand's *C. tuberculatus* populations is a high priority for further investigation.

Key words: acoustic monitoring, detection rates, Chalinolobus tuberculatus, long-tailed bat, traffic volume, roads

Acta Chiropterologica, 21(2): 331–339, 2019 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/15081109ACC2019.21.2.008

# Skyrocketing flights as a previously unrecognized behaviour of open-space foraging bats

CHRISTIAN C. VOIGT<sup>1,4</sup>, KSENIIA KRAVCHENKO<sup>1</sup>, FELIX LIECHTI<sup>2</sup>, and SARA BUMRUNGSRI<sup>3</sup>

<sup>1</sup>Department Evolutionary Ecology Leibniz Institute for Zoo and Wildlife Research Alfred-Kowalke-Strasse 17, 10315 Berlin, Germany <sup>2</sup>Swiss Ornithological Institute, Seerose 1, CH-6204 Sempach, Switzerland <sup>3</sup>Department of Biology, Faculty of Science, Prince of Songkla University, Hat Yai, Songkhla, Thailand <sup>4</sup>Corresponding author: E-mail: voigt@izw-berlin.de

The airspace of the lower troposphere is an important habitat for many animals, including open-space foraging bats. Yet, we are missing a detailed understanding of how bats forage in the seemingly unstructured open space. As part of an exploratory study, we present data on flight activity for *Taphozous theobaldi* (Dobson 1872), an aerial insectivore known to hunt in the open space close to mountain ridges in central Thailand. Using logger data from five individuals, covering a total period of 26 observation days, we show that *T. theobaldi* remained airborne for  $4.8 \pm 3.1$  h per night (mean  $\pm$  SD). We confirmed that *T. theobaldi* performed altitudinal flights with quick ascents, short horizontal flights followed by descents. Each night, *T. theobaldi* engaged on average in  $2.9 \pm 1.4$  altitudinal flights during which they reached an average peak altitude of  $306 \pm 53$  m above cave elevation. On average, bats spent about 14% of the total foraging time in altitudinal flights. We conclude that *T. theobaldi* is a regular, but most likely not an obligatory exploiter of high altitudes. We speculate that *T. theobaldi* may ascend to higher altitudies in search for insects, for example migrating or dispersing insects at higher air layers or swarms of hill-topping insects. Short altitudinal flights with fast ascents and descents (a slender bell-shaped flight trajectory over several 100 m altitude) may present a so far unrecognized flight behaviour of bats that may be more widespread among other aerial insectivores.

Key words: movement ecology, aeroecology, thermal winds, troposphere, aerosphere

Acta Chiropterologica, 21(2): 341–348, 2019

PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/15081109ACC2019.21.2.009

# Activity and behaviour of Nathusius' pipistrelle *Pipistrellus nathusii* at low and high altitude in a North Sea offshore wind farm

ROBIN BRABANT<sup>1,3</sup>, YVES LAURENT<sup>1</sup>, BOB JONGE POERINK<sup>2</sup>, and STEVEN DEGRAER<sup>1</sup>

<sup>1</sup>Royal Belgian Institute of Natural Sciences, Operational Directorate Natural Environment (OD Nature), Aquatic and Terrestrial Ecology (ATECO), Marine Ecology and Management (MARECO), Vautierstraat 29, 1000 Brussels, Belgium <sup>2</sup>Ecosensys, Hoofdweg 46, 9966 VC Zuurdijk, Groningen, the Netherlands <sup>3</sup>Corresponding author: E-mail: rbrabant@naturalsciences.be

Several bat species are known to migrate long distances between summer and winter roosts. During migration, many bats even cross the North Sea. The developments of offshore wind farms in the North Sea could therefore pose a collision risk for migrating bats. While bats have been observed inside offshore wind farms, their activity at turbine rotor height yet remains unknown. We therefore installed acoustic bat detectors at wind turbines in the Belgian part of the North Sea. Seven detectors were installed on the service platform of the transition piece (16 m above mean sea level) and four were installed on the nacelle of the turbines, in the centre of the rotor swept area (93 m above mean sea level). A total of 151 recordings of call sequences of *Pipistrellus nathusii* (Nathusius' pipistrelle) were made during 20 nights over an entire autumn migration season (8 August – 30 November 2017). 45 recordings contained more than 10 calls. These were further investigated for behavioural clues. We identified 32 recordings of animals in transit and 10 sequences of animals passing by while simultaneously exploring. Only three detections contained feeding buzzes and/or intense exploratory behaviour. The number of recordings at 93 m were around 10% of the number of recordings made at 16 m. This indicates that the activity of *P. nathusii* at our study site, measured at that particular altitude is low. Our observations therefore suggest that the collision risk might be lower than what could be expected from low altitude observations. However, a low number of recordings at nacelle height does not necessarily mean that only a low number of bats will collide with the turbines. The activity in the outer parts of the rotor swept zone, outside the detection range of our acoustic detectors, remains unknown and should be further investigated.

Key words: bats, bat activity, Nathusius' pipistrelle, Pipistrellus nathusii, offshore wind turbines, nacelle height, collision risk

Acta Chiropterologica, 21(2): 349–358, 2019 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/15081109ACC2019.21.2.010

### Bat fatalities at wind-farms in the lowland Mediterranean of southern Spain

SONIA SÁNCHEZ-NAVARRO<sup>1</sup>, JENS RYDELL<sup>2</sup>, and CARLOS IBÁÑEZ<sup>1</sup>

<sup>1</sup>Department of Evolutionary Ecology, Estación Biológica de Doñana (CSIC), Av. Américo Vespucio 26, 41092 Sevilla, Spain <sup>2</sup>Department of Biology, Lund University, S-223 62 Lund, Sweden <sup>3</sup>Corresponding author: E-mail: sonia.sanchez@ebd.csic.es

Wind energy is an important source of bat mortality worldwide. Extensive mortality data were gathered by a provincial surveillance program carried out at wind farms in lowland Mediterranean areas of the province of Cadiz, Andalusia (South Spain) between 2005 and 2016. As many as 2,371 bat fatalities were found. We determined the patterns of fatality in this sample and tested the quality of the surveillance program used. The data generally support previous observations regarding the seasonal timing, the species affected and the sex and age of fatalities. However, contrary to studies made at higher latitudes, fatalities mostly (95%) affected sedentary species and occurred on wind farms in flat landscape used for farming and livestock rearing. The current operational surveillance programme did not focus on bats initially, and, consequently, we urge that an improvement should consider a standardized search methodology including bats, verification of species identity, precise data collection, and mandatory and regular scavenger-removal and search-efficiency trials, in order to obtain correctly adjusted fatality estimates that can be used for efficient mitigation or compensatory measures.

Key words: Andalusia, bat conservation, bat migration, Cadiz, mortality, Nyctalus lasiopterus, wind energy

Acta Chiropterologica, 21(2): 359–373, 2019 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/15081109ACC2019.21.2.011

# Elucidating the consequences of a warming climate for common bat species in north-western Europe

NIAMH ROCHE<sup>1,4</sup>, STEVE LANGTON<sup>2</sup>, TINA AUGHNEY<sup>1</sup>, DEIRDRE LYNN<sup>3</sup>, and FERDIA MARNELL<sup>3</sup>

<sup>1</sup>Bat Conservation Ireland, Carmichael House, 4-7 North Brunswick Street, Dublin 7, D07 RHA8 Ireland
 <sup>2</sup>Hallgarth, Leavening, Malton, N Yorkshire, YO17 9SA, United Kingdom
 <sup>3</sup>National Parks and Wildlife Service, 90 North King Street, Dublin 7, D07 N7CV, Ireland
 <sup>4</sup>Corresponding author: E-mail: niamhr@batconservationireland.org

Climate change presents a serious threat to global biodiversity. In the extreme north of Europe, for example, some boreal bat species have been predicted to become extinct by the end of the century. We have used bat activity data derived from car-based surveys across Ireland to examine the effects of weather and climate using an approach that teases apart their spatial and temporal effects. This allows more accurate modelling of the impacts of weather than has heretofore been possible. Our results also support previous work that suggests the standard approach for combining the spatio-temporal variation in weather covariates is unsound. We used the results of this modelling exercise to forecast the effects of predicted climate change on three widespread Irish species for the years 2046–2059. *Nyctalus leisleri*, in its international stronghold, is predicted to undergo a decline in the north-west with increases likely in the south-east. *Pipistrellus pipistrellus* is predicted declines in the north of Ireland run somewhat contrary to expectations since increased ambient temperature there may have been anticipated to favour bat population growth. This work is a promising step towards disentangling the spatial and temporal impacts of weather and, from there, assessing the effects of climate change on bats in Europe. Pipistrelle species, in particular, are likely to be north-western Europe's most abundant consumers of aerial nocturnal insects and future conservation plans must consider potential losses of these species from agricultural areas and how any resulting reduction in ecosystem services can be mitigated.

Key words: spatio-temporal variability, weather, Chiroptera, climate change model, conservation, bat population

Acta Chiropterologica, 21(2): 375–383, 2019 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/15081109ACC2019.21.2.012

# Mango orchards and their importance in maintaining phyllostomid bat assemblages in a heterogeneous landscape

SERGIO M. MADRID-LÓPEZ<sup>1</sup>, JORGE GALINDO-GONZÁLEZ<sup>1</sup>, and ALEJANDRO A. CASTRO-LUNA<sup>1, 2</sup>

<sup>1</sup>Instituto de Biotecnología y Ecología Aplicada (INBIOTECA), Universidad Veracruzana, Av. De las Culturas Veracruzanas #101, Col. Emiliano Zapata, CP 91090, Xalapa, Veracruz, México <sup>2</sup>Corresponding author: E-mail: castrolun@hotmail.com

A large part of the natural vegetation in the tropics has been replaced by pastures and crop fields. To evaluate the value of mango orchards in the conservation of phyllostomid bats in a fragmented, heterogeneous landscape in Veracruz, Mexico we compared species richness, total abundance, dominance, evenness and abundance per feeding guild of bats in mango polycultures, mango monocultures and in semi-deciduous seasonal forest. Using mist nets at ground level, we captured 882 phyllostomid bats belonging to 17 species. Bat species richness was similar between the mango orchards and the forest, but the number of bats was significantly higher in mango polycultures, followed by mango monocultures and the forest. The frugivore guild was the most numerous in the mango orchards. Sanguivores were notably more numerous in the forest. Our results suggest that both types of mango orchards are different from the forest, since they are characterized by differences in bat species composition and feeding guild. We conclude that mango agroecosystems, when small in size and close to the forest, are important in the conservation of bats; it is there where bats are abundant and maintain a level of species richness similar to that of the original vegetation.

Key words: agroecosystem, composition, diversity, Phyllostomidae, perennial crops, Mexico

Acta Chiropterologica, 21(2): 385–393, 2019 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/15081109ACC2019.21.2.013

### Diet segregation between sexes by a gregarious Greater Antillean bat, *Phyllonycteris poeyi* (Chiroptera: Phyllostomidae)

MARGARITA SÁNCHEZ-LOSADA<sup>1</sup> and CARLOS A. MANCINA<sup>2, 3</sup>

<sup>1</sup>Centro Oriental de Ecosistemas y Biodiversida jambos, José A. Saco, No. 601, esquina a Barnada. Santiago de Cuba, Cuba <sup>2</sup>Instituto de Ecología y Sistemática, Carretera Varona # 11835, Reparto Parajón, La Habana, Cuba <sup>3</sup>Corresponding author: E-mail: mancina@ecologia.cu

Phyllonycteris poeyi is endemic to Cuba and Hispaniola in the Greater Antilles, and it is among the most common and widespread bats of the Cuban archipelago. This species is an obligate cave dweller and forms the largest aggregations of bats found in Cuban caves; and could be considered a hot cave specialist. This high gregariousness could increase intraspecific competition of food resources. In this study, we examined the diet of P. poevi at Cueva de los Majáes located in Baconao Biosphere Reserve in the southeastern region of Cuba. We hypothesized sexual diet variation as a way to reduce intraspecific competition. We estimated the percentage volume and frequency of occurrence of different food categories consumed by both sexes, using faecal analysis. Throughout the year, the diet of P. poeyi is a combination of fruits, pollen and insects; fruits of at least 17 plant species and flowers of five species are used by P. poeyi and the most frequent items were pollen of Roystonea regia and fruits of Piper aduncum and Piper umbellata. Insects occurred in the faeces of both sexes and their frequency and volume were low and did not differ between sexes. Although both sexes fed on similar food categories, we found significant variation in diet composition between sexes. Throughout the year, the majority of females mainly consumed fruits while males had preference for floral resources. We did not find differences in the sexes-reproductive season interaction, therefore the differences could not be attributed to changes associated to reproduction energetics. The average volume of fruits and pollen consumed by females were independent of the reproductive season, only significant differences were found in the consumption of insects, being the highest during the reproductive season. We conclude that this dietary partitioning behaviour between sexes of P. poeyi may be a strategy to maintain a high year-round gregariousness that could be critical to the viability of their large colonies in Cuban caves.

Key words: mate competition, dietary sex difference, dietary breadth, sexual behaviour, sexual segregation, resource partitioning

Acta Chiropterologica, 21(2): 395–402, 2019 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/15081109ACC2019.21.2.014

#### The antioxidant status of three Neotropical bat species with different feeding habits

#### RENATA M. PEREIRA FREITAS<sup>1</sup>, JERUSA M. OLIVEIRA<sup>1</sup>, DAVID L. JUSTINICO CASTRO<sup>1</sup>, MARIAUREA MATIAS SARANDY<sup>1</sup>, REGGIANI VILELA GONÇALVES<sup>1</sup>, and MARIELLA BONTEMPO FREITAS<sup>1, 2</sup>

<sup>1</sup>Department of Animal Biology, Federal University of Vicosa, Av. PH Rolfs, Campus UFV, Viçosa — MG, Brazil 36570-900 <sup>2</sup>Corresponding author: E-mail: mariellafreitas@gmail.com

Among mammals, bats represent the most diverse order regarding feeding habits, with such variety of diets influencing the antioxidant capacity of tissues. While frugivory provides an intake of natural antioxidants, such as carotenoids and vitamins, which support non-enzymatic antioxidant defense, a blood meal, as consumed by vampire bats, is rich in protein and iron, which are assumed to induce reactive oxygen species (ROS) accumulation. Nectar is another food item shared by a few bat species, and also possesses the potential to generate ROS through glucose auto-oxidation. The aim of this study was to investigate differences in the antioxidant capacities of tissues (liver, muscles, heart and kidneys) in the adult male blood-feeding bat *Desmodus rotundus* (n = 11), fruit-feeding bat *Sturnira lilium* (n = 8) and nectar-feeding bat *Anoura caudifer* (n = 6). Superoxide dismutase and catalase activities were higher in the liver and muscles of blood-feeding and nectar-feeding bats, respectively. Superoxide dismutase was also higher in the kidneys of blood-feeding bats when compared to frugivorous *S. lilium*. Glutathione S-transferase showed its highest activity in the liver and muscles of frugivorous *A. caudifer* and in the kidneys of sanguivorous *D. rotundus*. Lipid peroxidation, measured through malondialdehyde levels, was lower in the liver and heart of frugivorous bats and in the kidneys of nectarivorous bats. The results showed that feeding habit influences the antioxidant capacity of tissues involved in metabolism, and all three bat species showed different adaptations to their diets. In general, even facing high oxygen consumption and dietary challenges, *D. rotundus* and *A. caudifer* showed a higher capacity to combat oxidative damage, which might contribute to their longevity compared to similar sized mammals.

Key words: diet, frugivorous, hematophagous, nectarivorous, oxidative stress

#### Acta Chiropterologica, 21(2): 403-409, 2019

PL ISSN 1508-1109  $\ensuremath{\mathbb{C}}$  Museum and Institute of Zoology PAS doi: 10.3161/15081109ACC2019.21.2.015

# Detection of antimicrobial resistance in faecal *Escherichia coli* from European free-tailed bats (*Tadarida teniotis*) in Portugal

ANDREIA GARCÊS<sup>1</sup>, SUSANA CORREIA<sup>2, 3, 4</sup>, VANESSA SILVA<sup>5, 6</sup>, JOSÉ EDUARDO PEREIRA<sup>5</sup>, FRANCISCO AMORIM<sup>7, 8</sup>, GILBERTO IGREJAS<sup>2, 3, 4</sup>, and PATRICIA POETA<sup>5, 9, 10</sup>

<sup>1</sup>Centre for the Research and Technology of Agro-Environment and Biological Sciences, University of Trás-os-Montes and Alto Douro, Vila Real, Portugal

 <sup>2</sup>Functional Genomics and Proteomics Unit, University of Trás-os-Montes and Alto Douro, Vila Real, Portugal
 <sup>3</sup>Departament of Genetics and Biotechnology, University of Trás-os-Montes and Alto Douro, Vila Real, Portugal
 <sup>4</sup>Associated Laboratory for Green Chemistry (LAQV-REQUIMTE), University NOVA of Lisboa, Lisboa, Caparica, Portugal
 <sup>5</sup>Microbiology and Antibiotic Resistance Team (MicroART), Department of Veterinary Sciences, University of Trás-os-Montes and Alto Douro, Vila Real, Portugal
 <sup>6</sup>Functional Genomics and Proteomics Unit, University of Trás-os-Montes and Alto Douro, Vila Real, Portugal
 <sup>7</sup>CIBIO-InBIO – Research Center in Biodiversity and Genetic Resources, University of Porto, Agrarian Campus of Vairão, Portugal
 <sup>8</sup>CEABN-InBIO, Center for Applied Ecology 'Professor Baeta Neves', Instituto Superior de Agronomia, University of Lisbon, Portugal
 <sup>9</sup>Associated Laboratory for Green Chemistry (LAQV-REQUIMTE), University NOVA of Lisboa, Lisboa, Caparica, Portugal

In the last decades, the increase of antimicrobial resistance bacteria has become a concern of public health, already affecting unintentional hosts as isolated wild populations. In the present study, we evaluated the incidence of antimicrobial resistance, molecular mechanisms of resistance and virulence genes among 42 strains of *Escherichia coli* isolated from faecal samples from wild colonies of European free-tailed bats (*Tadarida teniotis*) in Portugal. High antimicrobial resistance rates for ampicillin (57.14%) and streptomycin (52.38%) were observed. Genes encoding resistance to antimicrobial agents were detected in most of the resistant isolates. The *E. coli* isolates were ascribed to phylogroups A (44.24%), B1 (16.67%), B2 (2.38%) and D (35.71%). The virulence gene *fimA* (alone or in association) was detected in 21 samples. This study shows the presence of antimicrobial resistance in commensal bacteria from wild European free-tailed bats populations. Future studies are necessary in order to investigate the main source of contamination (through the environment or the food chain) and identify how they can be contributing to the spread of those bacteria throughout the environment.

Key words: antimicrobial resistance, Tadarida teniotis, Escherichia coli, one health

Acta Chiropterologica, 21(2): 411–423, 2019 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/15081109ACC2019.21.2.016

# Thermally-assisted monitoring of bat abundance in an exceptional cave in Brazil's Caatinga drylands

AÍDA OTÁLORA-ARDILA<sup>1, 3</sup>, JAIRE MARINHO TORRES<sup>1, 2</sup>, EDER BARBIER<sup>1, 2</sup>, NARJARA TÉRCIA PIMENTEL<sup>1, 2</sup>, EDSON S. BARBOSA LEAL<sup>1, 2</sup>, and ENRICO BERNARD<sup>1</sup>

<sup>1</sup>Laboratório de Ciência Aplicada à Conservação da Biodiversidade, Departamento de Zoologia, Universidade Federal de Pernambuco, Recife, Pernambuco, Brazil 50670-901
<sup>2</sup>Programa de Pós-graduação em Biologia Animal, Centro de Biociências, Universidade Federal de Pernambuco, Recife, Pernambuco, Brazil 50670-420
<sup>3</sup>Corresponding author: E-mail: aotalora@gmail.com

Caves are very important roosts for bats. Neotropical countries, like Brazil, harbor both high bat species richness and abundance of underground cavities. The Caatinga drylands in northeastern Brazil are a good example with potentially 100 bat species and a high number of caves. Among those caves, some harbor exceptionally large bat populations, but, even thus, they still remain poorly known and studied. Here we present a 48-months monitoring based on a non-invasive thermal detection system to estimate the abundance changes of a large colony in a bat cave in the Caatinga drylands of Brazil. That cave harbors ten bat species — two nationally endangered — and 70% of them are main cave users. We found a marked inter-month fluctuation in the total bat abundance, with no consistent pattern. Total bat abundance was neither related to precipitation nor to the reproductive seasonality. During certain moments, the bat population can reach up to 120,000 individuals, making this cave a priority site for bat conservation in Brazil.

Key words: bat abundance, cave-dwelling bats, Caatinga, cave conservation

#### Acta Chiropterologica, 21(2): 425-442, 2019

PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/15081109ACC2019.21.2.017

### Bats in three protected areas of the Central Amazon Ecological Corridor in Brazil

TAMILY C. M. SANTOS<sup>1, 2, 6</sup>, GERSON P. LOPES<sup>2, 3</sup>, RAFAEL M. RABELO<sup>2, 4</sup>, and TEREZA C. GIANNINI<sup>1, 5</sup>

<sup>1</sup>Instituto Tecnológico Vale, 66055-090, Belém, Pará, Brazil

<sup>2</sup>Grupo de Pesquisa em Ecologia de Vertebrados Terrestres, Instituto de Desenvolvimento Sustentável Mamirauá, 69553-225, Tefé, Amazonas, Brazil

<sup>3</sup>Laboratório de Evolução e Genética Animal, Programa de Pós-Graduação em Zoologia, Universidade Federal do Amazonas, 69080-900, Manaus, Amazonas, Brazil

<sup>4</sup>Programa de Pós-Graduação em Ecologia, Instituto Nacional de Pesquisas da Amazônia, 69080-971, Manaus, Amazonas, Brazil <sup>5</sup>Programa de Pós-Graduação em Zoologia, Universidade Federal do Pará, 66077-830, Belém, Pará, Brazil <sup>6</sup>Corresponding author: E-mail: tamily-lfy@hotmail.com

Bats have the second highest mammalian species richness globally, and account for about half of the mammal species diversity in tropical forests. In the Neotropical region, Brazil is the second most bat species-rich country, and the Brazilian Amazonia harbours most of the Brazilian bat diversity. However, many areas of the Amazon have sampling gaps in biodiversity inventories, and this is the situation of most Protected Areas (PAs) of the Central Amazon Ecological Corridor (CAEC) of Brazil. In the CAEC, there are PAs that are relatively intact, globally relevant for biodiversity, having high priority for conservation at the regional scale, but are greatly deficient in faunal inventories. In this sense, species inventories are the first step to consolidate management plans for PAs, as well as the conservation of the species occurring there. Thus, in this study we survey the bat assemblages in three PAs in the CAEC of Brazil: Jutai River Extractive Reserve (JRER), Jutai-Solimoes Ecological Station (JSES) and Auati-Parana Extractive Reserve (APER). In addition, we compared the bat diversity of these three areas with a compilation of data from 44 localities in the Amazon biome in two different biogeographic contexts. The first involves three geographic regions separated by large Amazonian rivers (Eastern Amazonia, Western Amazonia and the Guiana Shield) and the second based on three biogeographic dominions (Boreal Brazilian, Southeastern Amazonia and South Brazilian). We recorded 36 species at JRER in ten nights of sampling, 33 species at JSES in nine nights, and 55 species at APER in 17 nights. Of the total number of species, 20 were captured exclusively at APER, seven at JSES and only four at JRER, with 21 species being common to the three PAs. One species (Artibeus bogotensis) was recorded for the first time in Brazil. In a biogeographic context, species composition differed among biogeographic regions. This suggests that when designing strategies of conservation to protect the rich diversity of the large-scale bat fauna of the Amazon, considering the location of PAs, as well as the biogeographic regions is key. Although there have been major efforts in Brazil to identify priority conservation areas, for most priority areas of Amazon, bat surveys have not been performed, highlighting the urgent need for further studies.

Key words: Chiroptera, tropical forest, biodiversity, conservation, biogeographic regions

#### Acta Chiropterologica, 21(2): 443-452, 2019

PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/15081109ACC2019.21.2.018

# High specificity and aggregation, but low prevalence in bat-fly interactions in an environmental protection area in Brazil

EDER BARBIER<sup>1, 4</sup>, GUSTAVO LIMA URBIETA<sup>2</sup>, HANNAH NUNES<sup>2</sup>, SAULO SANTOS BOMFIM<sup>3</sup>, and Patrício A. da Rocha<sup>2</sup>

<sup>1</sup>Programa de Pós-graduação em Biologia Animal, Centro de Biociências, Departamento de Zoologia, Universidade Federal de Pernambuco, Avenida Prof. Moraes Rego, 1235, Cidade Universitária — Recife, PE, 50670-901, Brazil
 <sup>2</sup>Programa de Pós-graduação em Ciências Biológicas, Centro de Ciências Exatas e da Natureza, Departamento de Sistemática e Ecologia, Laboratório de Mamíferos, Universidade Federal da Paraíba, Cidade Jardim Universitário, s/n, Castelo Branco — João Pessoa, PB, 58051-900, Brazil
 <sup>3</sup>Departamento de Ecologia, Universidade Federal de Sergipe, Avenida Marechal Rondon, s/n, Jardim Rosa Elze — São Cristóvão, SE, 49100-000, Brazil

Nycteribiids and streblids are obligate hematophagous flies restricted to bats. These flies are widely distributed throughout the Neotropical region, although little is known about their spatial distribution and patterns in parasitic associations in different environments. Studies assessing bat-fly interactions are mostly qualitative, but quantitative studies that allow testing and/or establishing more specific patterns for these interactions are still scarce. Here, we qualitatively and quantitatively assessed the bat-fly interactions in an environmental protection area in northeastern Brazil using prevalence, mean intensity of infestation, aggregation, and abundance indices. We captured 654 bats of 21 species and five families. Only 157 bats (24%) were parasitized by 351 flies of 19 species and eight genera. Among the most representative bat species ( $n \ge 15$ ), the host-parasite relationship between the white-lined broad-nosed bat (*Platyrrhinus lineatus*) and a streblid fly *Trichobius angulatus* had the highest prevalence (33.3%). The highest mean intensity of infestation recorded was for *Trichobius joblingi* on the Seba's short-tailed bat (*Carollia perspicillata*) (2.05 flies per host). The fly with higher values of aggregation was *Strebla guajiro* (D = 0.98) on *C. perspicillata*. Ninety-five percent of the fly species were highly host-specific (monoxenous). Regarding the mean abundance of flies, we found no differences between dry and rainy periods. No noticeable pattern for northeastern Brazil was observed when comparing our results with previous studies, except for specificity that was consistently high throughout the region. Our study raises questions about the pattern of fly parasitism on bats and may guide future research on this subject.

Key words: Atlantic forest, Chiroptera, host-parasite relationships, northeastern Brazil, Nycteribiidae, parasitological indices, Streblidae

Acta Chiropterologica, 21(2): 453–464, 2019 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/15081109ACC2019.21.2.019

# Effects of omnidirectional microphone placement and survey period on bat echolocation call quality and detection probabilities

SUSAN C. LOEB<sup>1, 4</sup>, BROOKE A. HINES<sup>2</sup>, MICHAEL P. ARMSTRONG<sup>3</sup>, and STANLEY J. ZARNOCH<sup>1</sup>

<sup>1</sup>U.S. Forest Service, Southern Research Station, Clemson, SC 29634, USA <sup>2</sup>HDR, Engineering Inc., Denver, Colorado 80202, USA <sup>3</sup>U.S. Fish and Wildlife Service, Kentucky Ecological Services Field Office, Frankfort, Kentucky 40601, USA <sup>4</sup>Corresponding author: E-mail: susan.loeb@usda.gov

Many factors, including microphone type, affect the quality of acoustic calls recorded by bat detectors and detection probabilities of individual species. Because omnidirectional microphones tend to have a shorter range and record more noise than directional microphones, it has been suggested that these microphones be set farther from reflecting surfaces. Our objective was to determine the effects of microphone height (1.5, 5, and 9 m), distance from forest edge (1, 3, and 5 m), and survey timing on the number of bat files recorded, quality of recorded files, the proportion of identifiable files, and the probability of detecting individual species. We deployed 3×3 arrays of two types of bat detectors with omnidirectional microphones at two sites in Kentucky during two survey periods. We found little evidence for effects of microphone height or distance from forest edge on call quality or detection probabilities of any species. In contrast, survey period significantly affected the number of files recorded, the proportion of identifiable files, and the probability of detecting individual species; the length of the recording session also significantly affected the probability of detecting some species. Thus, it appears that biologists have some latitude when placing detectors with omnidirectional microphones on the landscape but timing of surveys should be considered when designing and analyzing bat acoustic survey and monitoring studies.

Key words: Indiana bat, Myotis sodalis, detection probabilities, omnidirectional microphones, acoustic surveys, clutter, survey timing

Acta Chiropterologica, 21(2): 465–471, 2019 PL ISSN 1508-1109 © Museum and Institute of Zoology PAS doi: 10.3161/15081109ACC2019.21.2.020

#### Bee markers: a novel method for non-invasive short term marking of bats

#### Lucinda Kirkpatrick<sup>1</sup>, Grzegorz Apoznański<sup>2</sup>, Luc de Bruyn<sup>3</sup>, Ralf Gyselings<sup>3</sup>, and Tomasz Kokurewicz<sup>2</sup>

<sup>1</sup>EVECO, Department of Biology, Universiteit Antwerpen, Universiteitsplein 1, Antwerp, 2610, Belgium
<sup>2</sup>Department of Vertebrate Ecology and Paleontology, Institute of Biology, Wrocław University of Environmental and Life Sciences, Kożuchowska 5b, 51-631 Wrocław, Poland
<sup>3</sup>Species Diversity, Research Institute for Nature and Forest (INBO), Havenlaan 88 Bus 73, 1000, Brussels, Belgium
<sup>4</sup>Corresponding author: E-mail: Lucinda.Kirkpatrick@uantwerpen.be

The ability to accurately identify individuals is essential for both management and research of wild or captive animals. Marks need to be clear enough to be recovered, long-lived enough to provide useful information and not have health implications for the tagged animal which may affect survival. Substantial evidence suggests that more invasive, permanent marking techniques such as wing banding can cause injuries to bats, limiting the species with which such procedures can be used. Furthermore, low recovery rates can mean that the long term impacts of permanent marking on survival cannot be assessed. Here we present a new non-invasive, low cost approach to tag bats which can be carried out with the minimum of handling. Recovery of marks is simple and does not require handling. Our approach repurposes 'queen bee markers', small, coloured and numbered plastic disks which are commonly used to mark queen bees; instead they are affixed with superglue directly onto the fur of the bat. We carried out a pilot study at a large hibernaculum in West Poland, home to ca. 35,000 bats, the majority of which are *Myotis myotis*, the target species for this study. In November 2017 we marked 203 bats during a census of the underground fortification system. We recovered 30% of the originally marked bats over a time period of five months; 27% of the originally marked bats were identified to individual when resighted. Fifteen individuals were recovered in March that were not recovered in January, suggesting that they were either missed by recorders or were not present in the system during the census. Using the colour marking system allowed us to derive information about changes in bat behaviour when identification to individual was not possible, and individual identification revealed differences in hibernation strategies. We conclude that bee markers are an effective, cheap and less invasive approach for short term monitoring of bat populations and will also be useful to monitor whether recovery rates warrant the use of more invasive marking techniques.

Key words: Chiroptera, non-invasive marking, hibernation