

A new species in the *Hipposideros bicolor* group (Chiroptera: Hipposideridae) from Peninsular Malaysia

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With 70 named species and multiple morphologically cryptic lineages, the genus *Hipposideros* is a diverse and taxonomically contentious group of insectivorous bats in the Old World tropics. Half of the named species and most of the cryptic diversity in *Hipposideros* are concentrated in the *bicolor* species group. Here we resolve the taxonomic status of *Hipposideros bicolor* (Temminck, 1834), the species group's namesake. Two morphologically cryptic but acoustically and genetically distinct lineages of *H. bicolor* co-occur in peninsular Malaysia and Thailand. Pending taxonomic revision, these lineages were named according to the average frequency of maximum energy of echolocation calls of populations in central peninsular Malaysia, *H. bicolor*-131 and *H. bicolor*-142. To determine the taxonomic status of the two lineages we measured cranial characters from all available type specimens in the *H. bicolor* species group, and collected morphometric, acoustic and mitochondrial DNA sequence data for *H. bicolor*-131, *H. bicolor*-142, and closely related lineages, from multiple localities on the Malay peninsula and Borneo. Consistent with prior studies, acoustic and genetic analyses strongly support species status for *H. bicolor*-131 and *H. bicolor*-142. We find subtle but significant differences in cranial characters, including a longer skull and longer upper and lower tooth rows in *H. bicolor*-131 relative to *H. bicolor*-142. Most importantly, inclusion of cranial measurements for type specimens in the *H. bicolor* species group indicates that *H. bicolor*-131 should retain the species name, while *H. bicolor*-142 is distinct from all previously named species. We therefore provide a complete description for this new species of bat from Southeast Asia, *Hipposideros kunzi* sp. nov.

Key words: cave roosting, Chiroptera, cryptic diversity, morphometrics, phonic type, Old World leaf-nosed bats, Sunda shelf, taxonomy

A new species of *Anoura* Gray, 1838 (Chiroptera: Phyllostomidae) from Peru, with taxonomic and biogeographic comments on species of the *Anoura caudifer* complex

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Anoura is a Neotropical genus of long-tongued bats containing at least 10 species, whose taxonomy has been revised substantially in recent years. Herein, we describe a new species of *Anoura* from the Cordillera Oriental of the Peruvian Andes, inhabiting montane forests (Yungas) at 1900–3450 m altitude, along the Río Cosñipata valley in Manu Biosphere Reserve, Cuzco; where it is sympatric with *A. peruana*, *A. cultrata*, and *A. caudifer*. This new species is most similar to *A. caudifer* and *A. aequatoris*, but it is distinguished from them by a unique combination of morphological characters: pelage dark; uropatagium narrow with margins densely furred; foot claws whitish; skull with a long and narrow rostrum; zygomatic arches complete and straight (in lateral view); posterolateral margins of palate without processes; braincase smoothly rounded; first upper premolar (P²) peg-like and separated from the upper canine by a wide gap; second upper premolar (P³) without anterobasal cusp; mandible long, straight, thin and delicate with a large symphysis. Principal Component Analysis separated well the new species from *A. aequatoris* and *A. caudifer*. In MANOVA analyses, followed by Bonferroni post-hoc test, the new species differed significantly from *A. aequatoris* and *A. caudifer* in six and 11 characters, respectively. The new species and *A. aequatoris* have montane distributions, whereas *A. caudifer* occurs at lower elevations. In Peru, the new species and *A. aequatoris* show disjunct distributions: the former in the central and southern regions, and the latter in the north-central region of the country. This suggests a vicariant effect probably related to the deep Río Apurímac. Finally, we comment on the taxonomy of the *A. caudifer* complex, discuss the biogeographical implications of the discovery of the new species, and suggest the recognition of a new region of endemism for small mammals in the southern Yungas, south of the Río Apurímac to Bolivia.

Key words: Andes, bats, biogeography, Cusco, new species, Peru, taxonomy, Yungas

Intraspecific evolutionary relationships and diversification patterns of the Wagner's mustached bat, *Pteronotus personatus* (Chiroptera: Mormoopidae)

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Wagner's mustached bat (*Pteronotus personatus*) is an insectivorous bat distributed throughout America from Mexico to Brazil, which inhabits a range of habitats from rain forests to dry deciduous forests. There are two currently recognized species within the *P. personatus* complex, for which we examined 235 cytochrome oxidase I (COI) sequences and 138 cytochrome *b* (*Cytb*) sequences in order to explore its genetic variation in Mexico as well as in Central and South America. Our results reveal considerable differences in the genetic structure inside this species complex, indicating five genetic lineages: 1) Gulf of Mexico and the Mexican Pacific coastal plain to the Isthmus of Tehuantepec, 2) Southeastern Mexico, 3) Guatemala, 4) Guyana and Suriname-COI/Guyana and Venezuela-Cytb, and 5) Guyana, Suriname, French Guiana and Brazil. In addition, we used the isolation-with-migration coalescent method to estimate divergence times. The results indicate that vicariant events occurred roughly 1,624,000–2,450,000 years ago during the Early Pleistocene, wherein Central America was the center of two separate diversification processes, one toward Mexico and the other South America. The intraspecific lineages obtained for *P. personatus* demonstrate the need to reevaluate the species complex limits of this taxon.

Key words: cytochrome oxidase I, cytochrome *b*, mitochondrial lineage, isolation with migration, Mormoopidae

Low levels of population structure among geographically distant populations of *Pteropus vampyrus* (Chiroptera: Pteropodidae)

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Pteropus vampyrus, the largest bat in the world, has a broad geographic range covering much of Southeast Asia. The wide distribution of *P. vampyrus* and its ability to cross oceanic expanses makes management of this threatened species an international concern. *Pteropus vampyrus* is an essential seed disperser and pollinator of rain forest trees, many of which are ecologically and economically important. Understanding population dynamics of *P. vampyrus* is thus critical to addressing conservation issues and global health concerns. We used phylogenetic inference and population genetic indices to infer past gene flow between populations of *P. vampyrus* throughout most of the species' range. Population genetic parameters indicate low levels of nucleotide variability with high haplotype diversity across its range, implying a demographic scenario of recent population expansion after a bottleneck. Subspecies were not found to be monophyletic from the genetic data, which may reflect some level of genetic variation on even shallower time scales. The low level of population genetic structure throughout the species range is not necessarily surprising given its high vagility and seasonal migratory behavior. However, it cannot be entirely excluded that these results may reflect historical connectivity or lineage sorting issues rather than more recent persistent gene flow. These findings highlight the need for international cooperation and monitoring to ensure persistence of populations and to create a species management plan that can protect the species throughout its range. Increased genetic sampling is needed to ascertain *P. vampyrus*' commonly used dispersal routes and to assess the possibility of asymmetric gene flow among populations.

Key words: Southeast Asia, population genetics, Indonesia, flying fox, Philippines, *Pteropus vampyrus*

Mitochondrial phylogeny and morphological variation of the African sheath-tailed bat (*Coleura afra*, Emballonuridae)

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The African sheath-tailed bat (*Coleura afra*, Emballonuridae) occurs patchily throughout sub-Saharan Africa and in southern Arabia. While the populations in southeastern Africa have been studied, those from the other parts of its distribution range have not been known well. We assessed genetic and morphological variation among some African and Arabian populations including those previously not studied. The recovered phylogenetic pattern suggests the existence of three major evolutionary lineages in this species. One lineage comprising populations from Kenya and Tanzania could be attributed to the nominotypical subspecies, although it surprisingly included also the population from Ghana. The respective populations from Yemen and Gabon were represented by the other two lineages. The recently discovered population of *C. afra* from Gabon shows considerable external morphological variation and a certain degree of sexual size dimorphism. Two morphogroups, based mainly on overall skull size, could be identified among populations from West Africa, East Africa, and Arabia. The larger-sized group corresponded to the nominotypical form. The smaller-sized group could be split into two subgroups defined by the skull shape, comprising populations from northeast Africa and Arabia, and West Africa, respectively. Although these two morphological subgroups seemed to correspond to forms *gallarum/nilosa* and *kummeri*, these allocations were not corroborated by the molecular analyses. Given the comparatively large genetic distances in *C. afra*, taxonomic revisions of the southern Arabian and Central African forms are anticipated.

Key words: morphometry, phenotype, mitochondrial DNA, cytochrome *b*, Chiroptera

Comparative population structure in species of bats differing in ecology and morphology in the Andaman Islands, India

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Gene flow results from movement between populations, homogenising gene pools and impacting genetic variation and evolution. Growing evidence suggests that movement of individuals among populations may be more strongly determined by ecological traits. We compared genetic and morphometric differentiation in four species of bats — *Eonycteris spelaea*, *Cynopterus sphinx*, *Rhinolophus affinis* and *Hipposideros pomona* — which differ in their flight capability and roosting requirement to understand their effects in shaping genetic structure. Hypervariable region I of the mitochondrial control region was amplified from 40 *E. spelaea*, 28 *C. sphinx*, 44 *R. affinis* and 57 *H. pomona* sampled from locations spread across the Andaman archipelago. Populations of *E. spelaea* were nearly panmictic; *R. affinis* were differentiated into two clusters, and *H. pomona* were differentiated into three clusters. Consistent genetic and morphometric clusters were obtained for *C. sphinx* and the genetic break for *C. sphinx* occurs between Middle and South Andaman Islands, coincided with the Jarawa Tribal Reserve. In conclusion, poorly-dispersing, cave-roosting species show high population structure, but when flight capability is very well-developed, the effect of disjunct roost availability is offset. The genetic structure of *C. sphinx* where we expected panmixia, is possibly confounded by the colonization history of its two genetic lineages and its habitat use which may prevent significant gene flow between the two lineages.

Key words: population genetic structure, cave roosting, tree-roosting, flight capability, morphology, Andaman and Nicobar Islands

Taxonomy of the genus *Gardnerycteris* (Chiroptera: Phyllostomidae)

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The Neotropical genus *Gardnerycteris* has been recently erected and described as a result of a morphologically-based phylogenetic analysis of Phyllostominae with emphasis on representatives of *Mimon* sensu lato. As currently understood *Gardnerycteris* is formed by two species, *G. crenulatum* and *G. koepckeae*. However, it has been hypothesized that *G. crenulatum* might be a complex of species, from which the form *G. c. keenani* exhibits the clearest morphological differences from other populations of 'crenulatum'. Species limits and relationships among forms of *Gardnerycteris* have been only partially explored on the basis of morphological variation. Herein, we obtained partial sequences of two mitochondrial genes (*cytb* and *COXI*) and one nuclear gene (*RAG2*) from representatives of *G. koepckeae* and *G. c. keenani* in order to clarify the relationships within the genus. Furthermore, we performed qualitative and quantitative morphological comparisons among *G. crenulatum* sensu stricto, *G. c. keenani*, and *G. koepckeae* to limit species. Our results support the monophyly of *Gardnerycteris*, as well as the molecular and morphological differentiation of *G. c. keenani* from other congeners. In the light of the results, we propose changes in the taxonomy of the genus, raising 'keenani' to the species level.

Key words: species delimitation, *keenani*, morphology, species tree

Bat community and roost site selection of tree-dwelling bats in a well-preserved European lowland forest

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Worldwide species density of bats is highest in forests ecosystems. European primeval forests are now reduced to a few small and isolated patches because almost all forests are subject to management. Therefore, knowledge about bats in ancient and near-natural forests in Europe is scarce. In the well-preserved forest stands of the Belovezhskaya Pushcha National Park in Belarus we studied the bat community (1), the presence of maternity colonies and their preference in tree roost selection (2) and parameters of roosts used by forest dwelling bats (3). By mist-netting surveys, we identified 13 bat species and acoustic data suggested the presence of another three species. We detected 15 maternity colonies of seven bat species by radio-tracking reproductive females and 40 tree roosts within the forest. Roosts of *Barbastella barbastellus*, *Pipistrellus pygmaeus* and *Plecotus auritus* were almost exclusively behind the loose tree bark of decaying trees, or within narrow crevices. *Myotis nattereri* and *Nyctalus leisleri* showed a preference towards hollows (e.g., woodpecker-made cavities) within oak trees (*Quercus robur*). Our study shows that all tree-dwelling bat species are highly dependent on natural processes within forests that allow the formation of roost sites. Therefore, we strongly support that the natural aging process of trees, as well as the consequences of natural disturbance (e.g. through weather), should be permitted. This should extend beyond the protected zones of National Parks. In contrast, sanitary cuttings decrease the habitat's suitability for forest-dwelling bats. Finally, our results indicate that the forest complex of Belovezhskaya Pushcha and Białowieża is one of the most important bat areas in Europe.

Key words: tree-dwelling bats, primeval forests, dead wood, radio tracking, Belovezhskaya Pushcha, conservation

Species richness, abundance and functional diversity of a bat community along an elevational gradient in the Espinhaço mountain range, southeastern Brazil

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Bats are an excellent taxonomic group for research on elevational gradients and functional diversity, as they present a large number of species and functional traits. In general, elevation has a negative influence on bat diversity, but the effect is not necessarily linear. Often the effect of elevation on diversity may have a hump-shaped pattern, in which diversity metrics peak in intermediate elevations before decreasing at the highest parts of the elevational gradient. In this study, we investigated the effect of elevation on bat species richness, abundance, and functional diversity in Rio Preto State Park (RPSP), a protected area located in the Espinhaço mountain range, a region globally recognized for its high rates of biodiversity. We found that RPSP harbours 22 bat species, which represent 69% of the species occurring in the Espinhaço range and include species of conservation concern. Bat species richness and abundance was linearly and inversely correlated to elevation, whereas functional diversity had a hump-shaped pattern, with higher values found in the intermediate portion of the elevational gradient. Our findings agree with other studies showing the overall negative effect of elevation on bat diversity and contribute to the still sparse knowledge about the effect of elevation on bats in Brazil and in the Espinhaço range. Furthermore, our results suggest that natural environments in lower and intermediate elevations (< 1,100 m a.s.l.) in this mountain range may have high biodiversity value for bats, and actions aiming at their protection would complement the conservation efforts focusing on endemic species associated with higher habitats in the Espinhaço.

Key words: Chiroptera, Cerrado, environmental gradient, mountain ecosystems

Ecological networks between tent-roosting bats (Phyllostomidae: Stenodermatinae) and the plants used in a Neotropical rainforest

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Roost ecology in bats is a complex interaction of behavioral, morphological and physiological adaptations, thus, there are many factors involved in roost selection by bat species. Approximately 22 species of bats are able to modify leaves to establish their roost, 17 of which are in the Neotropics. Although there are many studies of tent-roosting bats, this is the first describing the structure of the interaction between bats and the plants they are using as roosts. We describe a potential antagonistic network between these bats and the plants used for tent construction in La Selva Biological Station in Costa Rica. We calculated descriptors of the network such as the number of bats and plants interacting, as well as the number of pairwise interactions based on published records or direct observations. We also tested for connectance and nestedness in the network structure. We propose a name for this non-trophic antagonistic interaction, which is a structural antagonism, where bats damage the leaves, reducing their lifespan and the plant fitness. In La Selva the network is composed of eight bats and 45 plant species reported by 60 pairwise interactions. Only 2.16% of vascular plant species in La Selva are being modified as tents. The network had low connectance (0.167) and no significant nestedness or modularity. Considering the species richness of plants in La Selva, there are few links between tent-roosting bats and plants species, which shows the specialization of these interactions and the high dependence of most of these bats on a few plant species, even if they are very specific and temporary resources.

Key words: animal-plant interactions, antagonistic networks, Costa Rica, La Selva Biological Station, structural antagonism, tent-roosting bats

Disassembly of fragmented bat communities in Orange Walk District, Belize

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The assembly, or disassembly, of ecological communities is thought to be driven by competition, environmental filtering, and dispersal limitation. These processes leave patterns in the functional, phylogenetic, and taxonomic diversity of communities. Bat communities in the tropics tend to have many species that are niche specialists with varying dispersal propensities. We investigated the effects of fragmentation on bat communities in an isolated forest fragment and a nearby larger forest preserve in Belize. Over four field seasons (2014–2017), we captured over 1,480 individuals from 32 species using mist nets and harp traps. The community in the fragment was a nested subset of species (20) compared to the preserve (30), and species richness was relatively stable over time. Functional richness was higher in the preserve than in the fragment, and species in the preserve were more closely related phylogenetically than expected by chance. Closely related species and species with different diet guilds co-occurred at both sites more often than distant relatives and those with the same diet guild. Bat species with flexible roost use had higher abundance in the fragment than the preserve, while closely related roost-specialist species had higher abundance in the preserve. Local extirpation and decreased dispersal are the most likely mechanisms of community disassembly in this system, and variation in roosting habits results in nonrandom community composition. These results have significant implications for the effects of ongoing deforestation and habitat fragmentation in Belize and adjacent dry forest areas.

Key words: Chiroptera, phylogenetic community structure, harp trap

Bats and their bat flies: community composition and host specificity on a Pacific island archipelago

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Bats and their ectoparasites are excellent model organisms to assess the conservation status of protected areas because both groups are speciose, and bats can be particularly affected by land use changes. The majority of bat studies conducted in Panama are clustered in protected areas around the Isthmus of Panama, while protected areas outside the Isthmus have not been studied in depth or remain largely unexplored. Coiba National Park is located on the Pacific coast of the country and is the fourth largest national park in Panama. Despite its distinct isolation from the mainland and the periodic dry spells it has undergone during the last 25,000 years, Coiba National Park has highly preserved forests. We provide the first study that assesses the structure of the bat assemblage of Coiba National Park, describe echolocation calls of some of its aerial insectivorous species, and contribute the first species list of ectoparasitic bat flies (Diptera: Streblidae). Using mist nets and acoustic monitoring techniques, we identified 30 bat species from 904 captures and 751 recordings. *Artibeus jamaicensis* and *Carollia perspicillata* were the most abundant species captured, while *Myotis nigricans*, *Saccopteryx leptura* and *Molossus bondae* were the most frequently recorded aerial insectivores. Associated with the bats we also identified 22 species of streblid flies, all representing new records for Coiba National Park. The host specificity was 98.2%, a high value compared to studies in other areas of Latin America. In total, we found eight new bat species for Coiba National Park, increasing the species list to 39, making it, with a rather limited study effort, the National Park with the fourth highest bat species richness recorded in Panama. We reckon that such levels of richness are correlated with the highly preserved forests of Coiba National Park.

Key words: biodiversity monitoring, national parks, Central America, protected areas

Parasitism by bat flies on an urban population of *Cynopterus brachyotis* in Singapore

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This study characterizes the patterns of bat fly parasitism on *Cynopterus brachyotis*, the most common fruit bat in the tropical urban environment of Singapore. Mist netting was conducted over a period of five months in two secondary forest sites, where 211 unique individuals were captured and examined for ectoparasites. The relative density, prevalence and mean intensity of parasitism by the wingless nycteriid *Leptocyclopodia ferrarii ferrarii* were compared with respect to sex, age and reproductive status of captured bats. The overall prevalence of parasitism was 40.3% and analyses revealed no significant differences in the three parameters when comparisons were made between demographic subgroups. However, adults, females and pregnant females had a higher prevalence of infestation, while juveniles, males and non-pregnant females had higher mean intensity of bat flies. Roosting behavior is likely to be the driving factor for parasite transmission, as bat flies are more likely to encounter females because of *C. brachyotis*' harem-based social structure. No correlation was found between bat body condition and parasite load, even when the relationship was examined for juveniles and adults separately. The observation of a re-infestation within 46 days suggests that there is high intra-individual and intra-roost parasite transmission. Research into roost group size, distribution, site fidelity, and connectivity is needed to better understand the patterns and dynamics of parasitism on bats living in the urban environment.

Key words: Nycteribiidae, Chiroptera, tropics, ectoparasite, host-parasite systems, Southeast Asia

Postnatal variation in ectoparasite (*Spinturnix emarginata*) load in neonates of Geoffroy's bat (*Myotis emarginatus*): how fast do young bats become infested with ectoparasites?

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We studied, simultaneously, postnatal variation in ectoparasite load in neonates, lactating, pregnant and non-pregnant females — in a free-ranging nursing colony of Geoffroy's bat (*Myotis emarginatus*) in Kerend Cave, western Iran. During this survey we monitored 120 (78 ♂♂, 42 ♀♀) neonate bats, as well as 21 pregnant, 42 lactating and 15 non-pregnant females. These individuals yielded a total of 1857 wing mites of the species *Spinturnix emarginata*. The first 14 days following the birth of pups was found to be associated with a rapid increase in numbers of *S. emarginata* on the neonates — up to an average (\pm SE) 21.3 ± 5.34 ectoparasites per individual. This was followed by a sudden reduction in parasite load to a stabilised rate of 5.9 ± 0.98 parasites per individual at the end of the postnatal period. The average ectoparasite load for all neonates over 42 days of the postnatal period was 11.5 ± 0.81 . No significant difference was noted as regards average parasite load for neonate males (11.9 ± 1.11) and females (10.8 ± 1.06). In contrast, the average parasite load for lactating females (at 8.6 ± 0.93) was significantly higher than the corresponding figure for pregnant females (4.1 ± 0.39). The average parasite loads for lactating females and neonates do not differ significantly. Where reference was made to the ratio of body mass to length of forearm, no significant correlation was found between parasite load and body condition among either male or female neonates, or pregnant, lactating and non-pregnant females. The study therefore confirms that host-parasite interactions between the bat *M. emarginatus* and the wing mite *S. emarginata* is tuned proximally in such a way that bat hosts at any stages of their life cycle (male and female pups, pregnant, lactating, and non-productive females and adult males) resist parasites without paying the costs of parasitism in terms of reduced body mass or length adjusted body mass (W/FA).

Key words: *Spinturnix emarginata*, *Myotis emarginatus*, ectoparasite load, wing mite

Dietary composition of four common chiropteran species in a bottomland hardwood forest

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Understanding foraging habits can be important for elucidating the ecology of any species and for designing appropriate conservation strategies. Common methods for determining bat diets, such as morphological examination of fecal material or recovery of prey fragments under feeding roosts, can be biased towards larger prey with harder exoskeletons by underestimating frequency/occurrence of smaller, softer bodied prey items. Our objectives were to determine prey selection for several common chiropteran species of bottomland hardwood forests in east Texas and to evaluate the use of DNA barcoding for dietary studies by comparing dietary composition to prey availability in four species of bats. We amplified the cytochrome c oxidase subunit 1 gene from fecal samples collected from 19 bats of four species and identified arthropods by comparison to the Barcode of Life Data System database. We compared frequency of occurrence in fecal samples to frequency in concurrent night-flying insect sampling. We identified nine insect species from three orders consumed by *Perimyotis subflavus*, nine species from four orders consumed by *Lasiurus seminolus*, seven species from three orders consumed by *Nycticeius humeralis*, and 11 species from two orders consumed by *Lasiurus borealis*. Coleoptera was the most abundant order available by biomass, but beetles were never found in fecal samples from *L. seminolus* ($n = 5$) or *L. borealis* ($n = 7$) bats. However, Coleoptera comprised a substantial portion of prey identified from *P. subflavus* ($n = 2$) and *N. humeralis* samples ($n = 5$). Lepidopteran prey items were found in 13 of 19 bat fecal samples across all species but represented < 7% of arthropod biomass. Although dipteran species were a negligible portion (< 1%) of the available biomass, large numbers of dipterans were identified in fecal samples from all species of bats (13 of 19 samples across all species). *Lasiurus seminolus* and *L. borealis* may be selecting prey based on digestibility rather than availability; whereas, both *N. humeralis* and *P. subflavus* exhibited a more opportunistic approach to foraging. Based on comparison to other studies of bat diets, traditional techniques for analyzing diet from fecal samples are likely underrepresenting soft-bodied arthropods like dipterans.

Key words: diet, foraging theory, insects, bats, molecular scatology, predator-prey interactions, trophic interactions

The wrinkle-lipped free-tailed bat (*Chaerephon plicatus* Buchanan, 1800) feeds mainly on brown planthoppers in rice fields of central Thailand

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The brown planthopper (*Nilaparvata lugens*) is one of the major insect pests of rice fields in Southeast Asia. They have been widely acknowledged for causing significant rice yield losses. However, the wrinkle-lipped free-tailed bat (*Chaerephon plicatus* Buchanan, 1800) is a known agent of pest suppression for white-backed planthoppers (*Sogatella furcifera*), and may also suppress brown planthopper populations. Hence, it is important to investigate the diet of *C. plicatus* in areas where brown planthoppers are common to determine whether these bats feed on these insects. To accomplish this objective, we analyzed the diet of *C. plicatus* from two caves that differed in the percentage of surrounding land area occupied by rice fields (70% versus 22%). Bat fecal pellets were collected monthly for a year. A total of 720 fecal pellets were analyzed, and the results revealed that *C. plicatus* feeds on at least eight insect orders, including Coleoptera, Homoptera, Hemiptera, Diptera, Lepidoptera, Odonata, Hymenoptera and Orthoptera. Specifically, homopterans comprised the greatest diet volume in the rice growing season, whereas coleopterans were most abundant in the diet when rice fields were fallow. Moreover, most homopterans were identified as brown planthoppers. To estimate the relative numbers of brown planthoppers consumed during each month, the number of genitalia of male brown planthoppers was counted. We recorded the greatest numbers of genitalia during the rice planting period, with an average of four genitalia per fecal pellet. Examining both the percent volume and percent frequency of each insect order in the diet of *C. plicatus* revealed that the two study caves were no significantly different, even though the proportion of surrounding active rice fields was different. Our results suggest that tens of millions of brown planthoppers are consumed by this bat species each night. The similar diets of the two study colonies may be due to their high altitude foraging and preference for migratory insects. Our results indicate that the wrinkle-lipped free-tailed bat is an important biological suppression agent of brown planthoppers in rice fields.

Key words: biological pest suppression, economic pest, insectivory, diet, high altitude foraging, Homoptera, percent volume, percent frequency

Diet of *Tadarida brasiliensis* (Mammalia: Chiroptera) in Northwestern Argentina

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In Argentina, the study of feeding habits of bats was practically restricted to frugivorous species, whereas data on the insectivorous bat diet was scarce and anecdotal. Thus, the aim of this study was to analyze the diet of *Tadarida brasiliensis* along the Yungas Forest, Argentina, at sites with different degrees of disturbance. Through the analysis of feces, arthropod orders were identified, volume and frequency of occurrence were estimated for each food item, and the niche breadth was estimated for the species. Finally, the diet was compared between capture sites, sexes, and seasons; finding variations among sites and seasons. The diet of *T. brasiliensis* contains arthropods belonging to nine orders and one undetermined taxon. Lepidoptera, Hymenoptera, and Coleoptera represent the highest volume proportions in the diet. The results add new and important information about the biology of *T. brasiliensis* in the southern part of its distribution.

Key words: foraging activity, insectivorous bats, Molossidæ, Yungas Forests

Terrestrial behavior and trackway morphology of Neotropical bats

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Bats (Chiroptera) are unique among flying animals in being the only mammal capable of powered flight and the only extant group that is quadrupedal. Extant bats demonstrate varying levels of terrestrial competency, however, the terrestrial abilities of many groups are unknown. Here we examine the terrestrial ability and resultant traces produced by bats belonging to the families Phyllostomidae and Emballonuridae. Five different subfamilies of phyllostomids and the emballonurid *Saccopteryx bilineata* were video recorded and analyzed for their terrestrial locomotor behaviors over a sand medium, with resultant tracks and trackways cast and measured. Behaviors and traces were compared to morphological criteria previously hypothesized to constrain terrestrial abilities of bats. Type 1 species (presumed poor walkers) generally performed only a breaststrokelike crawl and nonambulatory searching behavior, whereas the terrestrially adept Type 3 *Desmodus rotundus* performed a diagonal sequence walk and bound. Behaviors and traces produced by the intermediate Type 2 *S. bilineata* were indistinguishable from those of the Type 1 bats. Results only partially support the hypothesized morphological basis for terrestrial ability in bats and indicate that ecological differences or as yet unrecognized morphological variations may be the cause of behavioral variations in bats of the same morphotype. This research fills gaps in our knowledge of the terrestrial behaviors of nondesmodontine phyllostomid bats, and is the first study to examine the terrestrial behaviors of any species of emballonurid. Results of this research can be used for comparison to potential bat traces recorded in the geologic record, allowing for a better understanding of bat evolution and dispersal patterns.

Key words: neoichnology, terrestrial locomotion, *Desmodus*, *Saccopteryx*, *Carollia*, quadruped gait, bound, Phyllostomidae

Reproductive dynamics of the nectarivorous Geoffroy's tailless bat *Anoura geoffroyi* (Glossophaginae) in a highland Neotropical area of Brazil, with evidence of a mating period

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This study investigated the reproductive dynamics of a colony of Geoffroy's tailless bat (*Anoura geoffroyi*), an important pollinating bat, in a highland area of Southeastern Brazil. The colony was monitored each month from November 2014 to December 2015 with 154 males and 117 females captured. Testicular and ovarian histological data from 31 adult males and 22 adult females were obtained. Body condition index of male and female, and gonadosomatic index, epididymis-somatic index and Sertoli cell efficiency were analyzed. Females with spermatozoa in uterine crypts, embryos in oviducts, gravid uteri, and pregnant females were registered during the rainy season (November–March) and into the beginning of the following dry season (April), indicating asynchrony of births. The ovaries showed all types of ovarian follicles, and a polarized ovary cortex was found, differing from the organization pattern of most mammals. The testes showed continuous spermatid activity, but testicular parameters analyzed showed significantly higher values during the rainy season. A shorter mating period during the beginning of this season was detected, when values of the gonadosomatic and epididymis-somatic indexes, and Sertoli cell efficiency showed more pronounced differences in relation to the remaining period of study. Unlike polyestry known for some Neotropical phyllostomids, the reproductive cycle of *A. geoffroyi* was characterized as seasonal monoestrous, with the main reproductive events occurring during the rainy season, as the best time for females to reproduce, but with offspring recruitment occurring predominantly during the dry season, a period with fewer food resources.

Key words: *Anoura*, asynchrony of births, Chiroptera, mating period, monoestry, seasonal reproduction

CCTV enables the discovery of new barbastelle (*Barbastella barbastellus*) vocalisations and activity patterns near a roost

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We monitored a barbastelle (*Barbastella barbastellus*) maternity roost for four months using a portable CCTV system, time synchronised with ultrasound recorders. We discovered three patterns of vocal activity not previously described. When barbastelles investigated the roost entrance, calls resembling the approach phase of echolocation were produced consisting of a group of 10 or more broadband pulses of low amplitude, not detected more than a few metres from the roost. The other two distinct vocal patterns were produced during swarming around the roost tree. The first consisted of broadband pulses which were similar to those in the approach pattern, but which tended to be produced in a dynamic group rather than a fixed pattern. They were of higher amplitude than the approach echolocation pulses and were considered to be swarming echolocation pulses. This pattern frequently morphed into sequences containing social calls with a quasi-constant frequency (QCF) tail of very high amplitude. These social calls were likely produced to warn approaching bats on a potential collision course, similar to calls previously described in other species as ‘honking’. In addition to these three vocalisations, standard echolocation pulses were emitted, as well as hooked calls presumably having a social context. These latter two vocalisations were less commonly recorded in our study. Pulse duration was shortest for approach echolocation and longest for the hooked social calls. Amplitude was lowest for approach echolocation and highest for swarming honking calls. The QCF tail in swarming honking was steeper than for swarming social calls. CCTV video evidence (by motion detection) proved invaluable for relating behaviour to call type.

Key words: *Barbastella barbastellus*, CCTV, approach echolocation, swarming echolocation, honking, social calls

Hematological parameters in hibernating *Eptesicus nilssonii* (Mammalia: Chiroptera) collected in Northern European Russia

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The Northern bat, *Eptesicus nilssonii*, is the most common species among northern chiropteran populations. The species is noted for its long hibernation period with low mortality rate. We investigated the morphology of *E. nilssonii* blood cells during hibernation, hematological parameters including hemoglobin level, red blood cell (RBC) count, total white blood cell (WBC) count, and differential WBC count. The study revealed changes of several hematological parameters in hibernating bats, with some variation during the hibernation season. Hibernating *E. nilssonii* were found to have a low total WBC count similar to other hibernators; no significant variation in WBC count was noted during hibernation. Differential leukocyte count showed a significant reduction in total monocytes in winter (in the middle of the hibernation period). Total lymphocyte, band neutrophil, and basophil counts increased in spring (termination of the hibernation period).

Key words: *Eptesicus nilssonii*, hibernation, WBC, differential leukocyte counts, RBC