KARYOTYPES AND KARYOTYPIC VARIATION OF
NORTH AMERICAN VESPERTILIONID BATS

ROBERT J. BAKER AND JAMES L. PATTON

ABSTRACT.—Karyotypes of 32 species of North American vespertilionid bats are described. Individual, population, subspecific, specific, and generic karyotypic variation are discussed. The use of karyotypes as a taxonomic tool and phylogenetic indicator in bats is discussed.

The chromosomes of few North American bats have been analyzed. Painter (1925) determined the diploid number \(2n = 48\) of the molossid bat, *Tadarida brasiliensis*. Osborne (1965) studied the chromosome complements of 14 species, including eight (*Myotis thysanodes*, *M. volans*, *M. fortidens*, *Piponyx vivesi*, *Pipistrellus hesperus*, *Eptesicus fuscus*, *Lasius cinereus*, and *Lasionycteris noctivagans*) in the family Vespertilionidae.

In this study 164 specimens representing 10 genera and 32 species of North American vespertilionids were examined. Methods and techniques used were those described by Patton (1967) except that bone marrow was collected from humeri, and vincoleucoblastine (Velban from Eli Lilly and Company) was used in place of colchicine. Diploid number, fundamental number, and chromosome morphology were determined using standard methods (Nadler and Block, 1962; Bender and Chu, 1963; Patton, 1967). Fundamental number \(\text{FN}\) is herein considered to be the total number of arms of the autosomal complement; acrocentrics contain one arm and subtelocentrics, submetacentrics, and metacentrics, two arms.

RESULTS

A summary of the results of this study of vespertilionid karyotypes is presented in Table 1. Locality data and sex of the specimens studied in each species are listed under “Specimens Examined” beyond. A detailed karyotype description for each species is given below.

*Myotis velifer* (Fig. 1).—\(2n = 44\), \(\text{FN} = 50\). The autosomes consist of three large pairs and one small pair of metacentrics, with a graded series of 17 pairs of acrocentrics ranging in size from medium to small (including two pairs of minute chromosomes). The X-chromosome is a medium submetacentric and the Y is a submetacentric that is smaller in size than the smallest pair of metacentric autosomes.

In addition to *M. velifer*, 13 other species of *Myotis* were examined (Table 1). All were found to have karyotypes identical to that described for *M. velifer*. Osborne (1965) studied an additional species, *M. fortidens*. His results agree with those obtained for other species here.

*Myotis* (*Piponyx*) *vivesi* (Fig. 2).—\(2n = 44\), \(\text{FN} = 50\). The karyotype of this species appears to be identical to that described for *M. velifer* above.

*Rhogeessa parvula* (Fig. 3).—\(2n = 44\), \(\text{FN} = 50\). The karyotype is somewhat similar to that of *Myotis*, but *R. parvula* possesses an autosomal complement containing one large, one medium, and one small pair of metacentrics, one pair of medium subtelocentrics, and
Table 1.—Somatic chromosome numbers and types of 32 chiropteran species of the family Vespertilionidae. M = metacentric; SM = submetacentric; ST = subtelocentric; A =acrocentric; FN = fundamental number.

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1 Two males and five females analyzed by T. C. Hsu (personal communication).

17 pairs of acrocentrics grading in size from medium to small. The X-chromosome, like that of Myotis, is a medium submetacentric; the Y is a small submetacentric. Two specimens of R. gracilis examined had karyotypes identical to that of R. parvula.

Rhogeessa tumida (Fig. 4).—2n = 42, FN = 50. This species has a lower diploid
number, but the same fundamental number as *R. parvula* and *R. gracilis*. The karyotype contains one more pair of subtelocentrics and two less pairs of acrocentrics. Compounded with this is a significant change in the size of the largest metacentric.

*Eptesicus fuscus* (Fig. 5).—2n = 50, FN = 48. All autosomes are acrocentric, ranging in size from large to small. The X-chromosome is a submetacentric and the Y is a small acrocentric. The karyotypes of *E. andinus* and *E. furinalis* are identical to that described for *E. fuscus*.

*Nycticeius humeralis* (Fig. 6).—2n = 46, FN = 48. Two large pairs of metacentrics and a series of 20 pairs of medium to small acrocentrics (including three pairs of minute chromosomes) comprise the autosomal complement. The X-chromosome is a medium submetacentric and the Y is a small acrocentric.

*Antrozous pallidus* (Fig. 7).—2n = 46, FN = 50. Very similar to the karyotype of *N. humeralis*, that of this species differs in the size of the metacentric autosomes, having one large and one medium instead of two large pairs, plus one pair of small submetacentrics. There are also only 19 pairs of acrocentrics of medium to small size (including two pairs of minute chromosomes). The X-chromosome is submetacentric and the Y is acrocentric.

*Plecotus townsendii* (Fig. 8).—2n = 32, FN = 48. This species possesses 10 pairs of metacentrics and submetacentrics, grading in size from large to small, one pair of medium acrocentrics, and five pairs of small acrocentrics (including three pairs of minute chromosomes). The sex complement is not now known. If the X-chromosome is assumed to be a submetacentric, the FN can be tentatively placed at 48.

*Plecotus phyllochus* (Fig. 9).—2n = 30, FN = 50. Twelve pairs of metacentrics and submetacentrics, grading in size from large to small, one pair of medium acrocentrics, and two pairs of minute acrocentrics make up the chromosome complement of this species. The sex complement is unknown because no males have been examined. However, it is assumed that the X-chromosome is a submetacentric, the type that appears to predominate among this group of bats. The FN is tentatively placed, therefore, at 50.

*Lasiusurus borealis* (Fig. 10).—2n = 28, FN = 46. The autosomes consists of seven pairs of large metacentrics and submetacentrics, three pairs of medium metacentrics, and three pairs of small acrocentrics. The X-chromosome is a medium submetacentric and the Y is a small acrocentric.

Specimens of *L. cinereus* also have been examined. The karyotype of this species is identical to that described above for *L. borealis*.

*Lasiusurus ega* (Fig. 11).—2n = 28, FN = 46. *Lasiusurus ega* presents an unusual situation in that slightly different karyotypes have been recorded from specimens of two different subspecies. The northern subspecies, *L. e. xanthinus*, has a karyotype identical to that described above for *L. borealis* and *L. cinereus*. However, *L. e. panamensis*, although possessing the same autosomal complement as the northern subspecies, has an acrocentric X-chromosome instead of the submetacentric X typical of the northern subspecies and for *L. borealis* and *L. cinereus*.

*Lasiusurus intermedius* (Fig. 12).—2n = 26, FN = 40. This species has seven pairs of large metacentrics and submetacentrics, one pair of medium metacentrics, one pair of medium acrocentrics, and three pairs of small acrocentrics in the autosomal complement. The X-chromosome is a large submetacentric and the Y is a small acrocentric.

*Pipistrellus hesperus* (Fig. 13).—2n = 28, FN = 46. Nine pairs of metacentrics and submetacentrics of large to medium size, one pair of small submetacentrics, and three pairs of small acrocentrics comprise the autosomal complement. For the sex complement, the X-chromosome is a medium submetacentric and the Y is a small acrocentric.

*Pipistrellus subflavus* (Fig. 14).—2n = 30, FN = 56. The autosomes consist of 10 pairs of large to medium metacentrics and submetacentrics, and four pairs of small submetacentrics. The X-chromosome is a medium submetacentric and the Y is a small acrocentric.
Lasionycteris noctivagans (Fig. 15).—$2n = 20$, FN = 28. The autosomes consist of four pairs of large metacentrics and submetacentrics, one pair of small submetacentrics, and four pairs of very small acrocentrics. The X-chromosome is a large submetacentric, whereas the Y is a small acrocentric.

**DISCUSSION**

With recent improvements in cytological techniques, mammalian karyotypes have been shown to be an important adjunct to the classical approaches.
Fig. 3.—*Rhogeessa parvula*. Male, Alamos, Sonora; UA 14913.
Fig. 4.—*Rhogeessa tumida*. Male, Km 184 on Hwy 200 E Huisxtla, Chiapas.
Fig. 5.—*Eptesicus fuscus*. Female, Chiricahua Mts., Cochise Co., Arizona; UA 14914.

Fig. 6.—*Nycticeius humeralis*. Female, 13 mi. NW Warren, Bradley Co., Arkansas; UA 14915.
Fig. 7.—*Antrozous pallidus*. Female, 1 mi. E McDonald Observatory, Davis Mts., Jeff Davis Co., Texas.

Fig. 8.—*Plecotus townsendii*. Female, El Tigre Mine, Chiricahua Mts., Cochise Co., Arizona; UA 14917.

to systematics. Recent publications (Patton, 1967; Singh and McMillan, 1966; and Nadler and Hughes, 1966) have indicated not only karyotypic variation between species of the same genus in the order Rodentia, but also the occurrence of polymorphic karyotypes within a given species. This type of variation within a single species or between species of the same genus is not always the case, as Hsu *et al.* (1963) reported remarkable homogeneity between the karyotypes of nine species and two genera of Felidae.

Considering this information, it is necessary to evaluate interspecific as
well as intraspecific karyotypic variation for any given group before karyotypes can be used as a taxonomic tool or as an indicator of phylogenetic relationships for that group. Such an evaluation has never been made for bats. Osborne (1965) examined more than one species in only one genus (Myotis), and in only one species were specimens from widely separate localities utilized.

In our study specimens of 16 species were examined from widely separate localities, and more than one species was examined from six genera.

**Individual variation.**—Because bone marrow was the major tissue used in our analysis, variation in chromosome complements between different tissues of the same individual could not be analyzed. However, Dr. T. C. Hsu (per-
sonal communication) has analyzed a number of the same species reported on here using fibroblasts from lung tissue culture. In no case did there appear to be differences between the karyotypes from these two tissue types for the same species.

Intrapopulation variation.—As indicated under Specimens Examined, several specimens of a given species were examined from the same locality to
check for intrapopulation variation. Utilizing diploid number, fundamental number, and chromosome morphology as criteria, no variation has been found between members of the same population.

Subspecific and interpopulation variation.—Bats of the same species were examined from separate localities to check for interpopulation and, in some cases, subspecific variation. As mentioned previously, subspecific variation was found only in *Lasius ega*, with the slight variation between *L. e. panamensis* and *L. e. xanthinus* lying in the relative position of the centromere on the X-chromosome.
Specimens of 15 species other than _L. ega_ (see list of specimens examined) have been sampled from populations that range from 300 miles apart (_M. grisescens_) to more than 2000 miles apart (_E. fuscus_). No variation has been recorded in these widely located samples. It would seem, therefore, that inter-population variation in vespertilionid bats is indeed a rare phenomenon.

**Taxonomic and phylogenetic implications below the generic level.**—The close relationship of the nominate _Pizonyx_ Miller to _Myotis_ has been shown by Hamilton (1949) from comparative studies of bacula and by Miller (1907) on the basis of dental and other morphological criteria. This closeness in relationship is further indicated by the fact that _Pizonyx_ has a karyotype indistinguishable from the 14 other species of North American _Myotis_ examined to date (compare Figs. 1 and 2). Most authors have followed Miller (1906) in recognizing _Pizonyx_ as a genus distinct from _Myotis_, although it was originally described as a member of the latter genus (Menegaux, 1901). The differences given by Miller (1906, 1907) for erecting the genus are (1) length of foot and claw as long as tibia, (2) great lateral compression of the claws, (3) glandular mass on the forearm, (4) small anterior cusp on the lower canine cingulum, and (5) inner cusp of the lower molars usually well developed. To these can be added the fact that (6) the ventral hairs on the distal half of the uropatagium grow anteriorly. Differences 1, 2, and 6 are structural modifications for catching small fish and crustaceans beneath the surface of the water, and should perhaps not be assigned generic significance. Moreover, when the total amount of variation between species of North American _Myotis_ is considered—for example, foot length compared to tibia length between _M. leibii_ and _Myotis lucifugus_, condition of uropatagial hair between _M. leibii_ and _M. thysanodes_, and tooth variation when _M. fortidens_ and _M. occultus_ are compared with other _Myotis_—only the glandular
mass of *Pizonyx* is unique. Outweighing this single character are several characters indicating close relationship between *Pizonyx* and *Myotis* (e.g., karyotype, tooth number 38 as in majority of *Myotis*, presence of sharp-pointed and elongated tragus, and similar baculum). After considering the magnitude of variation within the genera *Lasiusurus* and *Plecotus*, and between the genera *Plecotus* and *Euderma* (Handley, 1959), it seems more important to recognize the close phylogenetic relationship of *Pizonyx* to the genus *Myotis* by considering the two congeneric, than to emphasize structural food-gathering modifications by recognizing the genus *Pizonyx*.

A possible polyphyletic origin for the genus *Myotis* has been suggested by Handley (1959) and others. Karyotypic data, however, indicates that the North American species of *Myotis* examined to date must have developed from a single line. The identical karyotypes of these species make untenable any other stand, for convergence of this magnitude would be difficult indeed to accept. Since we have not yet examined any Old World species, we do not deny the possible polyphyletic origin for the genus as now recognized.

There is a difference between the fundamental numbers of *Pipistrellus hesperus* and *P. subflavus* (46 and 56, respectively), which can be accounted for, in part, by pericentric inversions involving the three small pairs of autosomes. The significant difference between the karyotypes of the two species, however, is that *P. hesperus* lacks one of the large pairs of metacentrics found in *P. subflavus*. These differences appear to be extremely significant, especially when one considers the generally conservative nature of karyotypes at the generic level in vespertilionid bats (for example, *Myotis, Eptesicus*, and *Lasiusurus*). These karyotypic data essentially agree with Hamilton’s (1949) studies on the baculum of the two species. He suggested generic or at least subgeneric differences. It would seem doubtful that these two species are very closely related, for such would necessitate the complete loss of a major chromosome in the evolution of *P. hesperus* from *P. subflavus* or a common ancestor. Possibly, the two species are distantly related, acquiring their distinctive karyotypes through a series of changes from the karyotype of some remote ancestor.

As with the North American *Myotis*, the three species of *Eptesicus* examined are karyotypically identical. The great morphological diversity between members of this genus has led investigators to suspect that it may not be a natural assemblage. Following the same reasoning as for the genus *Myotis*, the three species considered here must have evolved from a common ancestor within the genus.

Three easily recognizable chromosomal features distinguish *Rhogeessa parvula* and *R. gracilis* from *R. tumida*: *parvula* and *gracilis* possess only one subtelocentric whereas *tumida* has two; *parvula* and *gracilis* have two pairs of acrocentric autosomes lost in *tumida*; the conspicuously large metacentric chromosome pair in *parvula* and *gracilis* has been reduced to a chromosome
on the same order of size as the rest of the complement in *tumida*. The first
two differences are slight and can be accounted for by a single centric fusion
involving the two extra acrocentrics in *R. parvula* and *R. gracilis* which
formed the second subtelocentric in *R. tumida*. The third difference is,
however, of some significance, for the loss or rearrangement of such an
amount of genetic material indicates a distant relationship of *tumida* to
*parvula* and *gracilis*.

As indicated previously, no differences exist in the chromosome comple-
ments of *Lasiusurus borealis*, *L. cinereus*, and *L. ega xanthinus*. Subspecific dif-
fferences in the morphology of the X-chromosome between *L. ega xanthinus*
(submetacentric X) and *L. ega panamensis* (acrocentric X) have been found.
Since the relative sizes of these X elements are the same in both karyotypes,
a pericentric inversion would be apparent in converting one X-chromosome
into the other. It is impossible to tell in which direction the change took
place, but it probably went from the condition in *L. e. xanthinus* to that in
*L. e. panamensis*, for the submetacentric X-chromosome is characteristic for
all other members of the genus studied.

Significant differences do exist between *L. intermedius* and the rest of the
lasiusines. It contains the same seven large pairs of biarmed chromosomes as
the others, but possesses only one pair of medium-sized metacentrics instead
of the three pairs typical for the other species. The two relatively large pairs
of acrocentrics unique to *intermedius* could be the two lost pairs of meta-
centrics whose centromere positions have been changed through pericentric
inversions. If this is true, then the pair of chromosomes which *intermedius*
lacks (giving it a diploid number of 26 rather than 28 as for the others) would
be one of the small acrocentric pairs. *Lasiusurus intermedius* is, therefore, set
far apart with regard to its chromosomal complement from the other three
species of *Lasiusurus*.

These chromosomal data substantiate the interpretation of Handley (1960)
that *Lasiusurus* and *Dasypetes* are congeneric. More karyotypic variation is
found to occur between species of the formerly recognized genus *Dasypetes*
(*L. ega* and *L. intermedius*) than occurs between the two groups (*L. borealis*
and *L. cinereus* on one hand and *L. ega* on the other).

Although the fundamental numbers of the two species of *Plectotus* examined
are quite close (48 for *P. townsendii* and 50 for *P. phyllostus*), several major
differences between these two species do exist. A single centric fusion involv-
ing two pairs of small acrocentrics in *P. townsendii* would give a karyotype
nearly identical to that of *P. phyllostus*. However, the remaining single, small
pair of acrocentrics in *P. townsendii* and the extra small metacentric pair in
*P. phyllostus* indicate that several rearrangements must have occurred in the
evolution of these species from a common ancestor. The magnitude of the
chromosomal differences between the two species suggests that they have
been separated for some time. Handley (1959), on morphological bases,
considered *P. townsendii* and *P. phyllostus* to be the most distantly related
members of the genus. He emphasized this by placing them in separate subgenera. Karyotypic variation, so far as known, confirms his arrangement.

*Phylogenetic relationships at the generic level.*—Because direct homologies cannot be shown between the chromosome pairs of any two species, or genera, only a few general comments can be made concerning possible relationships between most genera. The problem is compounded because variation at the generic level is certainly much greater than at the specific level. The genera examined can be divided, however, into four groups based on karyotypes, but, as such, the groupings are subject to the dangers of being based on a single character.

Group 1 includes *Myotis, Rhogeessa, Antrozous, Eptesicus,* and *Nycticeius.* These genera share the characters of a low number of biarmed autosomes and a high number of uniarmed chromosomes. The fundamental number varies only slightly (between 48 and 50) for all species, and the X-chromosome is a submetacentric in all cases.

Group 2 includes the single genus *Plecotus.* It is characterized by the same range in fundamental number as in Group 1 genera, but the differences in the number of biarmed and uniarmed autosomal pairs distinguishes *Plecotus* from Group 1.

Group 3 includes *Lasiusurus* and *Pipistrellus.* These genera are somewhat related karyotypically to *Plecotus* of Group 2 as several features are shared (for example, a low diploid number, and a high number of metacentrics and submetacentrics and a low number of acrocentrics in the complement). Group 3 is separated from Group 2 by the lack of the number of very small acrocentrics characteristic of *Plecotus.*

Except for differences in the size of some of the chromosomes, the karyotype of *P. hesperus* is indistinguishable from that of the majority of *Lasiusurus.* This relationship is probably due to convergent or parallel evolution, but the two genera are classed together on chromosomal data.

Group 4 includes only *Lasionycteris,* which, with its low diploid number and fundamental number (20 and 28, respectively) is significantly distinct from other members of the family examined to date. While Tate (1942) considered this monotypic genus "essentially a *Myotis,*" and Miller (1907) pointed out the similarity of *Lasionycteris* to *Myotis,* Miller did call attention to the great degree of specialization of the skull, ear, and tragus of *Lasionycteris* when compared to *Myotis.* The studies of the baculum by Hamilton (1949) and our karyotypic data seem to point to a more distant relationship of this bat to the genus *Myotis* and probably to all other vespertilionids.

**Conclusions**

From the few studies of mammalian karyotypes that have thus far been made, it appears obvious that the degree of karyotypic variation encountered at a given taxonomic level (subspecies, species, genus), is in itself highly variable from mammalian group to group (see Patton, 1967; Singh and McMillan, 1966; Nadler and Hughes, 1966; Nadler, 1966; and Hsu et al. 1963).
Thus, it is obvious that an analysis of variation between and within populations must be made for each mammalian group before attempts are made to use karyotypic configurations in interpreting phylogeny.

From this study, involving 164 specimens of 32 species, several conclusions can be made:

1. Karyotypes of vespertilionid species within a given genus, for the most part, have not evolved since the speciation of present North American groups. Therefore, karyotypes of most North American vespertilionid bats will generally not be useful as subspecific characters, and often may not separate species within a single genus (*Myotis* and *Eptesicus*, for example).

2. Karyotypes of recent vespertilionid bats are remarkably homogenic and present fairly stable characters below the generic level. Thus, the evolution of such karyotypes has generally not paralleled the course of speciation within each generic group. Karyotypes of bats in this family appear, therefore, to be good indicators of relationships between groups at the level of subgenus, genus, or subfamily. Since bats are one of the oldest and most divergent mammalian groups, and since phylogenetic relationships are often obscured by adaptive radiation, karyotypes may prove an important tool in delineating these aspects of bat phylogeny.

3. Karyotypes are nonadaptive—at least they are not adaptive to the same degree as morphological characteristics involving flight and feeding. Consequently, karyotypes may provide more of a clue in determining whether convergence or parallelism is involved than do the more classical approaches to taxonomy.

4. It is possible that the amount of chromosomal homogeneity within a genus depicts the relative closeness of relationship among its members. For example, all species of *Myotis* (including *Pizonyx*) studied may show a closer relationship to each other than does *Pipistrellus hesperus* to *P. subflavus*, or *Plecotus townsendii* to *P. phyllotus*.

**Specimens Examined**

All specimens and their corresponding microscope slides are deposited at the Department of Biological Sciences (Zoology), University of Arizona, unless otherwise designated. Results of specimens examined by T. C. Hsu (TCH) are at M. D. Anderson Hospital and Tumor Institute, Houston, Texas.

*Myotis lucifugus.*—Arizona: Coconino Co., 16 miles N Flagstaff (1 female), 30 miles W Flagstaff (1 female, 4 males). Kentucky: Carter Cave State Park, Carter Cave (3 females, 2 males). New Mexico: Catron Co., 9 miles E Mogollon (2 males).


*Myotis austroriparius.*—Florida (1 male, 2 females).

*Myotis grisescens.*—Oklahoma (5 females, 2 males) (TCH). Missouri (5 males).

*Myotis velifer.*—Sonora: Tajitos (1 female, 3 males). Veracruz: 2 km S Cuautlapan (2 females). Morelos: 47 km E Mexico City on Hwy 95 (1 male, 1 female).


Myotis sodalis.—Kentucky: Carter Cave State Park, Carter Cave (3 females, 3 males).


New Mexico: Catron Co., 9 miles E Mogollon (1 male).


Myotis leibii.—Arizona: Coconino Co., 30 miles W Heber (1 male), 30 miles W Flagstaff (1 male). New Mexico: Catron Co., 9 miles E Mogollon (1 male).

Myotis nigricans.—Veracruz: Ojo de Agua de Atayac (1 male, 1 female).

Myotis elegans (see Hall, 1962).—Chiapas: km 184 on Hwy 200 E Huixtla (1 male, 1 female).

Myotis vivesi.—Sonora: Isla Partida (3 females); Guaymas (1 female, 2 males).

Rhogeessa parcula.—Sonora: Alamos (2 females, 3 males). Nayarit: 4 km N Ouichimichis (4 females, 1 male).

Rhogeessa gracilis.—Guerrero: Ojo de Agua de Chiapa (1 male, 1 female).

Rhogeessa tumida.—Chiapas: km 184 on Hwy 200 E Huixtla (3 males, 2 females).

Eptesicus fuscus.—Arizona: Pima Co., Sabino Canyon (1 female, 1 male), Madera Canyon (1 female, 2 males); Coconino Co., 30 miles W Flagstaff (1 male), 7 miles S Flagstaff (1 female); Cochise Co., Southwestern Research Station (1 female). Kentucky: Scott Co., Georgetown (3 females, 2 males). Sinaloa: 1 km W Palmito (1 female).

Morelos: 47 km E Mexico City on Hwy 95 (1 female). Chiapas: 42 km W Cintalapa (1 male, 1 female).

Eptesicus andinus (see Davis, 1966).—Veracruz: Ojo de Agua de Atayac (1 male, 1 female).

Eptesicus furinalis (see Davis, 1966).—Chiapas: km 184 on Hwy 200 E Huixtla (1 female).

Nycticeius humeralis.—Arkansas: Bradley Co., 13 miles NW Warren (1 female, 4 males).


Lastius borealis.—Arkansas: Bradley Co., 13 miles NW Warren (1 male). Sonora: Rio Cuchijaqui, 7 miles S Alamos (1 female, 1 male).

Lastius cinereus.—New Mexico: Catron Co., 9 miles E Mogollon (2 males). Texas: Jeff Davis Co., 1 mile E McDonald Observatory (1 male). Sinaloa: 2 km W Palmito (1 male).

Lastius ega.—Sonora: 8 miles E Alamos (1 male). Morelos: Oaxtepec (1 female). Chiapas: 42 km W Cintalapa (2 males); km 184 on Hwy 200 E Huixtla (1 male).

Lastius intermedius.—Chiapas: 42 km W Cintalapa (1 male, 1 female).

Pipistrellus hesperus.—Arizona: Pima Co., Lower Sabino (1 male). Texas: Jeff Davis Co., 1 mile E McDonald Observatory (2 males). Sonora: vicinity of Alamos (2 males).

Pipistrellus subflavus.—Kentucky: Carter Cave State Park, Carter Cave (2 females, 3 males). Oklahoma: Adair Co. (2 females, 2 males) (TCH).

Lasionycteris noctivagans.—Arizona: Cochise Co., Southwestern Research Station (2 females); Pima Co., Madera Canyon (1 female); Coconino Co., 30 miles W Heber (1 male). Arkansas: Bradley Co., 13 miles NW Warren (2 males).


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LITERATURE CITED


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