OCCASIONAL PAPERS
THE MUSEUM
TEXAS TECH UNIVERSITY

NUMBER 78 7 MAY 1982

COMMENTS ON THE STATUS OF MUSONYCTERIS HARRISONI (CHIROPTERA: PHYLLOSTOMIDAE)

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Musonycteris harrisoni is a monotypic glossophagine known only from xeric scrub forests in western México (Jalisco southeastward to Guerrero). Although the systematic relationships among many glossophagines are uncertain because of the apparent convergence associated with nectivory, *Musonycteris* appears to be most closely related to *Choeronycteris mexicana*. In the original description of *Musonycteris*, Schaldach and McLaughlin (1960) allied it morphologically with *Choeronycteris* and distinguished between the two using differences in the basicranium and in rostral proportions. However, because differences in rostral proportions between two species, *Choeroniscus godmani* and *C. periosus*, of another genus in the subfamily exceeded those between *Musonycteris* and *Choeronycteris*, Handley (1966) considered *Musonycteris* to be congeneric with *Choeronycteris* so as not "to obscure relationships in this segment of the Glossophaginae." Handley further concluded that *Hylonycteris*, *Scleronycteris*, and *Lichonycteris*, although less specialized for nectivory, also were related to *Choeroniscus* and *Choeronycteris*. Phillips (1971) regarded *Musonycteris* and *Choeronycteris* as distinct genera based on basicranial differences and the expanded metastyle of M^3 of *Musonycteris*, but agreed with Handley concerning the systematic affinities of the other genera.

The karyotypic relationships of these bats were discussed by Baker (1967, 1979) and Gardner (1977). *Choeronycteris* ($2n$=16,

FN=24, plate 22 of Baker, 1979) and *Hylonycteris* (*2n*=16, FN=24, plate 24 of Baker, 1979) appear to have karyotypes that are similar and unique among phyllostomids. Baker (1979) attributed this similarity to a common ancestor with a diploid number of 16 and fundamental number of 24, whereas Gardner (1977) thought the two species independently converged from a *2n*=32, FN=30 progenitor to the present karyotype derived by a series of fusions.

The species of *Choeroniscus* thus far examined have diploid numbers of 18 to 19 or 20 and fundamental numbers of 32 or 36. Although Baker (1967) noted the similarity in the standard karyotype and sex determining mechanisms (XX/XY_1Y_2) in *Choeroniscus* and *Carollia* (subfamily Carolliinae), Stock (1975) found essentially no G or C-band autosomal homologies in those genera. Patton and Gardner (1971) also suggested that a common evolutionary origin of the multiple sex chromosomes of *Carollia* and *Choeroniscus* was doubtful. It also should be noted that the five males of *Choeroniscus godmani* thus far examined had a *2n*=19, whereas the three females had a *2n*=20, suggesting a system in which the Y has been translocated to an autosome rather than an autosome being translocated to the X, as has occurred in *Carollia*. A note of caution, however, should be considered, because the males (from Chiapas) and females (from Costa Rica and Honduras) were taken from separate geographic localities, and different cytotypes might be involved. *Lichonycteris* (*2n*=24, FN=44) is karyotypically distinct among glossophagines; Gardner (1977) assumed it was derived from a *2n*=32, FN=30 progenitor primarily by pericentric inversions. The karyotypes of *Scleronycteris* and *Platalina* are unknown, and that of *Musonycteris* is discussed below.

The autosomal karyotypes of two *Musonycteris harrisoni* (TTU 36153, and 36433, both adult males) from 2 mi. NW Tomatlán, Jalisco, consisted of one large pair of submetacentrics, one large pair of subtelocentrics, a medium pair each of subtelocentrics and submetacentrics, and three small pairs of acrocentrics (Fig. 1). The sex chromosomes are small heteromorphic metacentrics. Thus, the data indicate that the karyotype of *Musonycteris* (*2n*=16, FN=22) resembles those of *Choeronycteris* and *Hylonycteris*, but differs autosomally from both in possessing three small pairs of acrocentrics (rather than two). The X appears to be biarmed and metacentric in *Choeronycteris* (plate 22 of Baker, 1979), *Hylonycteris* (plate 24 of Baker, 1979), and *Musonycteris* (Fig. 1). The Y is biarmed in both *Choeronycteris* and *Musonycteris*. The Y of

FIG. 1.—Karyotype of a male *Musonycteris harrisoni* from Jalisco, México.

Hylonycteris (TTU 36152, adult male from 3 km. E Teapa, Grutas de Cocona, Tabasco) is approximately half the size of the X but has extremely reduced arms above the centromere.

The following points are critical in evaluating the evolutionary relationships of *Musonycteris* as indicated by karyotypes. A synthesis of G-banded chromosomal, albumin immunological, and electrophoretic data suggests that a $2n=32$, FN=60 karyotype such as that found in *Glossophaga* was primitive for the clade of the Glossophaginae containing *Glossophaga, Monophyllus, Leptonycteris, Anoura, Choeronycteris,* and *Hylonycteris* (Baker *et al.*, 1981). Therefore, the most parsimonious conclusion is that taxa with morphologically similar $2n=16$ karyotypes possess a highly derived chromosomal phenotype, most features of which were established in the common ancestor for the three genera (*Choeronycteris, Musonycteris,* and *Hylonycteris*). However, standard karyotypes of the three are not identical, and a schematic representation of how the karyotypes of each might be modified into those of the other two is shown in Fig. 2. The significant point to be derived from this diagram is that no data from standard karyotypes document that *Musonycteris* and *Choeronycteris* are more closely related to each other than either is to *Hylonycteris*. It is probable that the differences noted in those genera do not result from heterochromatic additions, a rare event in phyllostomid bats (see Baker and Bickham, 1980: table 1).

Morphological and karyotypic similarities indicate that *Musonycteris* and *Choeronycteris* are closely related, but we are reluc-

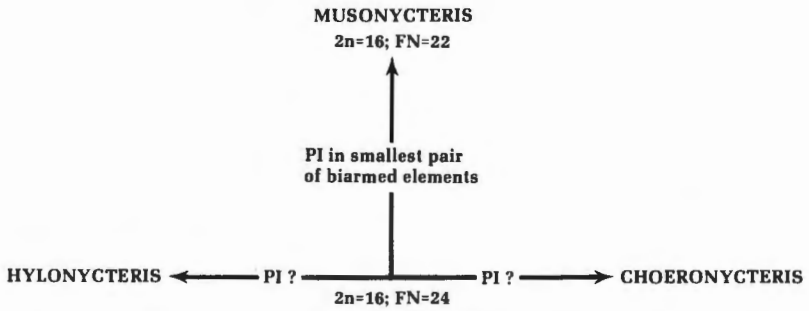

FIG. 2.—The most parsimonious path of change to explain differences in autosomes of *Choeronycteris*, *Musonycteris*, and *Hylonycteris*. The pair of autosomes possibly inverted (PI) in the lineages of *Hylonycteris* and *Choeronycteris* is the second pair of row 2 in plates 22 and 24 of Baker (1979). Also, it should be noted that the two pairs of acrocentric autosomes in *Choeronycteris* are unequal in size, whereas they are equal in *Hylonycteris*.

tant to consider them congeric for several reasons. Clearly, the well-developed basisphenoid ridge, smaller braincase, narrower and more elongate (but domed) rostrum, expanded metastyle on M^3, and reduced depth of the mandibular ramus in *Musonycteris* separate it from *Choeronycteris*, and are as diagnostic as characters that discriminate between *Choeroniscus* and *Hylonycteris*. Furthermore, the standard karyotypic data do not indicate a closer relationship between *Musonycteris* and *Choeronycteris* than between either and *Hylonycteris*.

We wish to thank Avelino B. Villa S., Direccion General de Fauna Silvestre, and Jorge E. Mendoza, Proyectos Tecnicos Faunisticos, México, for their kind assistance in obtaining collecting permits. Field work was supported by the Institute of Museum Research, Texas Tech University, and NSF Grant DEB-8D-04293 to R. J. Baker.

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ISSN 0149-175X
Texas Tech Press
Lubbock, Texas 79409