KARYOTYPIC STUDIES OF SEVEN SPECIES OF AFRICAN MEGACHIROPTERANS (MAMMALIA: PTEROPODIDAE)

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Abstract

Karyotypes of seven species of megachiropterans from Africa are described. Epomops franqueti, Hypsignathus monstrosus, Lissonycteris angolensis, and Myonycteris torquata have a $2n = 36$ and karyotypes that are similar to each other in morphology. Micropteropus pusillus ($2n = 35$) is similar to the above four, but possesses what appears to be an $X/Y, Y$ sex-determining system. Scotonycteris ophiodon ($2n = 34$, $FN = 62$) and Megaloglossus woermanni ($2n = 34$, $FN = 62$) are respectively distinctive from the other taxa studied, but may share several chromosomal characteristics with the other species.

Introduction

The family Pteropodidae is a diverse assemblage of species and is widely distributed in the Old World. The family consists of two subfamilies, 38 genera, and approximately 150 species (Koopman and Jones, 1970). Karyotypic studies within this family have been limited...
Table 1.—A summary of known karyotypic data for the family Pteropodidae. ST—subtelocentric, SM—submetacentric, M—metacentric, and A—acrocentric, O—absent.

<table>
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<th>FN</th>
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<th>Y</th>
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and, at present, published information is restricted to 10 genera and 19 species (Table 1). Most species studied thus far appear to be chromosomally conservative and are characterized by similar diploid and fundamental numbers.

In this study, the karyotypes of seven species, representing new data on six genera, are presented and discussed. The karyotype of *Epomops franqueti* has been described previously (Peterson and Nagorsen, 1975) from females. We illustrate the karyotype of a male. Our results are consistent with the majority of the chromosomal data reported thus far.

**Materials and Methods**

All karyotypes were obtained from bone marrow preparations made in the field by the *in vivo* incubation method as described by Robbins and Baker (1978). Diploid number determinations were based on counts from a minimum of 10 mitotic spreads. Nomenclature of chromosome morphology used is that of Patton (1967). All specimens examined were prepared as standard museum skins and skulls and are housed at the Carnegie Museum of Natural History (CM).

**Specimens Examined**

All specimens were collected in CAMEROON unless otherwise noted.

*Epomops franqueti*.—9 km S, 10 km W Yaounde, 3°47’N, 11°25’E (1♀); 30 km N, 40 km E Obala, 4°22’N, 11°58’E (1♂, 1♀); 13 km S Ngaoundere, 7°12’N, 13°36’E (1♀); 13 km S, 8 km E Ambam, 2°15’N, 11°21’E (1♀).

*Hypsignathus monstrosus*.—30 km N, 40 km E Obala, 4°22’N, 11°58’E (1♀). Zaïre: Bumba Zone; Yalosemba, 2°34’N, 22°10’E (1♀).

*Lissonycteris angolensis*.—4 km S, 2 km E Eseka, 3°36’N, 10°48’E (1♂, 2♀♀).

*Myonycteris torquata*.—13 km S Ngaoundere, 7°12’N, 13°36’E (1♂, 1♀).

*Micropteropus pusillus*.—13 km S Ngaoundere 7°12’N, 13°36’E (3♂♂); 23 km S, 8 km E Garoua, 9°6’N, 13°28’E (1♂).

*Scotonycteris ophiodon*.—3 km S, 3 km W Eseka, 3°37’N, 10°45’E (1♂).

*Megaloglossus woermanni*.—13 km S, 8 km E Ambam, 2°16’N, 11°21’E (1♀); 30 km N, 40 km E Obala, 4°22’N, 11°58’E (1♂).

**Results**

The karyotypes of seven species (representing seven genera and two subfamilies) are presented in Figs. 1–3. Table 1 is a summary of the known karyotypic data for the family, including those reported herein. A brief description of each karyotype is given below.
Fig. 1.—The standard karyotypes of (a) *Epomops franqueti* ♂ (CM 58181), 2n = 36, FN = 68; (b) *Hypsipetes monstrosus* ♀ (CM 58184), 2n = 36, FN = 68; (c) *Micropus pusillus* ♂ (CM 58217), 2n = 35; FN = 64.

**Subfamily Pteropodinae**

*Epomops franqueti*, 2n = 36, FN = 68, Fig. 1a.—The karyotype illustrated here is like that reported by Peterson and Nagorsen (1975). The autosomal complement consists of 13 pairs of metacentric or sub-metacentric elements, ranging in size from large to small, and four
pairs of medium-sized elements which have a submetacentric or sub-telocentric centromere placement. The fifth pair of the complement possesses a secondary constriction proximal to the centromere (marker chromosomes) which is found in other species as well (see below, Dulic and Mutere, 1973; Peterson and Nagorsen, 1975; Yong and Dhaliwal, 1976). The X is a medium-sized subtelocentric and the Y is a small subtelocentric.

_Hypsognathus monstrosus_, 2n = 36, FN = 68, Fig. 1b.—The standard karyotype of the female of this species is indistinguishable from that described above for _Epomops franqueti_.

_Micropteropus pusillus_, 2n = 35, FN = 64, Fig. 1c.—The karyotype of _Micropteropus_ is similar to that of _Epomops_. There are 13 pairs of metacentric or submetacentric chromosomes (small to large), but only three pairs of medium-sized subtelocentric elements. The sex chromosomes of the male consist of a medium-sized subtelocentric X, a small submetacentric Y₁ and a smaller subtelocentric Y₂.

_Myonycteris torquata_, 2n = 36, FN = 66, Fig. 2a.—The autosomal complement consists of 12 pairs of large to small metacentric and submetacentric elements, four pairs of medium-sized subtelocentric elements, and one pair of small acrocentric chromosomes. The fifth pair bears the secondary constriction. The X is a medium-sized subtelocentric and the Y is a small acrocentric.

_Lissonycteris angolensis_, 2n = 36, FN = 66, Fig. 2b.—The standard karyotype of _L. angolensis_ is indistinguishable from that described above for _Myonycteris torquata_.

_Scotonycteris ophiodon_, 2n = 34, FN = 62, Fig. 3.—The field preparations for _Scotonycteris ophiodon_ were difficult to analyze. In _Scotonycteris_, approximately 200 spreads were examined and the majority (95%) of all spreads counted gave a diploid number of 33. However, the unpaired element was not the same in each case and spreads with each element unpaired were found. The karyotype presented here for this species is based on conclusions derived from a study of G-bands (in progress) in which homologous pairs can be identified and complete spreads with 2n = 34 were found. The pair designated by an asterisk is a composite, with one element having been taken from a different spread. There are 11 pairs of metacentric or submetacentric elements, ranging from large to small in size and five pairs of subtelocentric or acrocentric elements. The X is a medium-sized submetacentric and the Y is a small acrocentric. The karyotype of this species is distinctive in several respects. First, the marker pair with the secondary constriction is absent or at least not apparent. Second, the largest subtelocentric chromosome was not found in the complements of other species. If this pair is homologous to the largest pair of the other species, then it has undergone a pericentric inversion.
Fig. 2.—The standard karyotypes of (a) Myonycteris torquata δ (CM 58253), 2n = 36, FN = 66; (b) Lissonycteris angolensis ♀ (CM 58196), 2n = 36, FN = 66; (c) Megaloglossus woermanni δ (CM 58261), 2n = 34, FN = 62.
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*Megaloglossus woermanni*, 2n = 34, FN = 62, Fig. 2c.—The autosomal complement is similar to that of *Myonycteris*. However, there is one additional pair of large metacentric chromosomes and one of the small metacentric pairs is lacking. The X is a medium-sized metacentric and the Y is a small metacentric.

Discussion

The karyotypes of the seven species reported here agree well with the general karyotypic trend thus far reported in the family Pteropodidae (Table 1). The works of several authors (Pathak, 1965a, 1965b, 1966, and 1972; Dulic and Mutere, 1973; Peterson and Nagorsen, 1975; Yong and Dhaliwal, 1976) have shown that, in most species of both subfamilies, karyotypes are characterized by similar diploid numbers (34–38) with most elements being biarmed. The species examined here possess diploid numbers of 34, 35, and 36 and hence represent chromosomal complements like those which appear most commonly in the family (Table 1). Despite the overall similarity, there are certain differences worthy of note which may be of systematic significance.

The karyotypes of *Lissonycteris angolensis* and *Myonycteris torquata* (Figs. 2a, 2b) are indistinguishable from each other and differ from that illustrated by Dulic and Mutere (1973) for *Rousettus aegyptiacus* only in the morphology of the Y chromosome (which may be an artifact of preparation). These three genera have been considered closely related or congeners (Andersen, 1912; Rosevear, 1965) and the karyotypic data certainly supports a close relationship.

The genera *Epomops*, *Hypsognathus*, *Epomophorus*, and *Micropteropus* constitute a closely related assemblage of species based on morphology (Rosevear, 1965; Ellerman et al., 1953). Simpson (1945) had regarded these as congeners but the work of Ellerman et al. (1953) re-established them as separate genera. Chromosomally, these four genera appear to be similar as well. The small pair of acrocentrics characteristic of *Lissonycteris* and *Myonycteris* is absent in all four and all possess 13 rather than 12 pairs of metacentric-submetacentric elements. The karyotypes of *Epomophorus wahlbergi* and *E. anurus* figured by Dulic and Mutere (1973) are indistinguishable from those of *Epomops franqueti* (Peterson and Nagorsen, 1975; and this paper) and *Hypsognathus monstrosus*, and further supports the contention of a close relationship.

*Micropteropus pusillus* is similar to *Epomops* and *Hypsognathus* but is chromosomally distinctive. This species does possess the 13 pairs of metacentric-submetacentric elements, but it is lacking one pair of medium-sized subteloctentric chromosomes. Additionally, the males
(only males were examined) possess a different sex-determining system which consists of three unpaired chromosomes—a subtelocentric X, a submetacentric Y₁, and a small subtelocentric Y₂. This suggests that Micropteropus is derived relative to the other genera, but the exact relationship is unclear at present.

The genus Scotonycteris also has been considered congeneric with Epomops (Simpson, 1945). However, the karyotype of Scotonycteris ophiodon is distinctive, not only relative to Epomops but to the other species examined as well. This species possesses 11 pairs of metacentric-submetacentric elements, as does Megaloglossus woermanni but, in addition, there are four pairs of subtelocentric elements, one of which is the second largest member of the complement. The pair of small acrocentric chromosomes may represent a character shared with Lissonycteris, Myonycteris, and Megaloglossus, but this remains to be conclusively demonstrated.

The karyotype of Megaloglossus woermanni is similar to those figured by Yong and Dhaliwal (1976) for Macro glossus lagochilus, M. minimus, and Eonycteris spelaea. Megaloglossus, however, differs in possessing additions to the short arms of two of the subtelocentric elements, leaving only two pairs in the subtelocentric condition. Whereas the diploid number of Megaloglossus is the same as that of Macro glossus, the morphology of the Y (metacentric) is like that of Eonycteris. The X for all three genera apparently is the same.

The species examined in this study can be separated into four groups based on chromosomal data. Lissonycteris angolensis and Myonycteris torquata make up the first group, characterized by the presence
of the small acrocentric pair and only 12 pairs of metacentric-submetacentric elements. *Megaloglossus* shares some features (the acrocentric pair) with this group, but is distinctive in possessing one fewer small and one additional large metacentric pair, and comprises the second group. *Epomops, Hypsignathus,* and *Micropteropus* make up a third group which is identified by the common absence of the small acrocentric pair and the presence of 13 pairs of metacentric-submetacentric elements. *Micropteropus* is distinctive, however, with a presumably derived sex-determining system, and one fewer subtelo-centric pair. *Scotonycteris* makes up the fourth group, and is chromosomally distinct. However, this species may share characteristics with the other three groups.

Within the family Pteropodidae, diploid and fundamental numbers are similar in most cases and only two species are radically different (*Balionycteris, 2n = 24 and Penthetor, 2n = 48; Yong and Dhaliwal, 1976*). Because of the high degree of karyological similarity among taxa, chromosomal studies of these bats involving nondifferentially stained preparations will be of limited utility. At the species level, it is probable that most or all species within a genus will display the same or very similar chromosomal characteristics. At the generic level or higher, however, some conclusions may be reached based on standard karyotypes, as illustrated in the present study.

The family Phyllostomatidae (Microchiroptera) represents a parallel to the situation in the megachiropterans. Within this family, many taxa possess karyotypes with diploid numbers of 30 or 32 and fundamental numbers of 56 to 60 (Baker, 1970, 1973, 1979). The widespread occurrence of similar karyotypes was taken as an indication of shared homology between taxa. That this is not the case was demonstrated by studies utilizing G- and C-banding (Patton and Baker, 1978; Baker and Bass, 1979; Baker et al., 1979). G-banding allows for the more accurate identification of homologous segments and it has been demonstrated that although the number and general morphology of linkage groups (chromosomal arms) may be similar in many taxa, they have been derived independently and are not homologous (Patton and Baker, 1978).

In the megachiropterans, the high incidence of diploid numbers of 34–36 and fundamental numbers of 58–68 may be misleading in that the homology suggested by overall similarity of karyotypes may be lacking. G-banding will allow a more accurate assessment of homology which will be of utility in systematic studies within this family. Comparisons of G-band homology will be of systematic importance in the study of relationships between species and higher taxa and should provide insight into the types and sequences of rearrangements involved in the evolution of megachiropterans.
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Literature Cited


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