Chromosomes of the Fruit-bat Subfamily Macroglossinae from Peninsular Malaysia

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The karyotypes of the insectivorous bats (Microchiroptera) are well represented (cf. Baker 1970, Capanna and Civitelli 1970, Matthey 1973, Yonenaga, Frota-Pessoa and Lewis 1969). On the other hand, only seven species belonging to four genera of fruit bats (Megachiroptera) have been reported. Of the 14 species of Malayan fruit bats belonging to 11 genera (cf. Medway 1969), only 2 species belonging to a single genus Cynopterus have been studied karyologically (Yong, Dhaliwal, Lim, Teh and Start 1973).

The present paper deals with the fruit-bat subfamily Macroglossinae which is represented by 2 genera, Macroglossus and Eonycteris, in Peninsular Malaysia. Macroglossus comprises two species whilst Eonycteris is monotypic. The common long-tongued fruit bat Macroglossus lagochilus Matschie is widespread in the lowlands particularly in the mangroves. The hill long-tongued fruit bat Macroglossus minimus (Geoffroy) is found only in the foothills and the highlands. The cave fruit bat Eonycteris spelaea (Dobson) is widespread and locally common, particularly the caves, in the mainland.

Materials and methods

The fruit bats were trapped live by means of mist nets. Macroglossus lagochilus was collected from Tanjong Karang, Selangor, M. minimus from the University of Malaya Field Studies Centre, 16 mi Ulu Gombak, Selangor, and Eonycteris spelaea from Batu Caves, Selangor, and Bukit Lanjau, Sg. Buloh, Selangor.

The bat was injected intraperitoneally with 0.01 ml of 0.01% (W/V) colchicine solution per gram of its body weight. After 1 hr the aminal was sacrificed and bone marrow was extracted and incubated in 0.5% potassium chloride solution for 20 mins. The cells were then fixed in a 3:1 methanol:glacial acetic acid solution. After three changes of fixative, slides were prepared by the conventional air-drying technique and stained with Giemsa solution.

Results

Table 1 summarises the karyotypes of the two species of Malaysian long-tongued fruit bats Macroglossus lagochilus and M. minimus as well as the cave fruit bat Eonycteris spelaea.
Table 1. The karyotypes of *Macroglossus lagochilus*, *M. minimus* and *Eonycteris spelaea*

<table>
<thead>
<tr>
<th>Species</th>
<th>Specimens studied</th>
<th>Autosomes*</th>
<th>X</th>
<th>Y</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>male</td>
<td>female</td>
<td>2n</td>
<td>m</td>
</tr>
<tr>
<td><em>M. lagochilus</em></td>
<td>2</td>
<td>3</td>
<td>34</td>
<td>8</td>
</tr>
<tr>
<td><em>M. minimus</em></td>
<td>1</td>
<td>0</td>
<td>34</td>
<td>8</td>
</tr>
<tr>
<td><em>E. spelaea</em></td>
<td>2</td>
<td>3</td>
<td>36</td>
<td>11</td>
</tr>
</tbody>
</table>

* m, metacentric; sm, submetacentric; sa, subacrocentric; a, acrocentric.

Fig. 1. Karyotype of a male *Macroglossus lagochilus*.

Fig. 2. Karyotype of a male *Macroglossus minimus*.
1. *Macroglossus lagochilus* and *Macroglossus minimus*: The karyotypes of these bats, as far as could be ascertained, are similar if not identical. Both possess $2n=34$ with a pair of metacentric 'marker' autosomes bearing a secondary constriction near the centromere (Figs. 1 and 2). There are 8 pairs of metacentric, 4 pairs of submetacentric, 2 pairs of subacrocentric and 2 pairs of acrocentric autosomes. The X-chromosome is metacentric while the Y is acrocentric with a distinct short arm. The X-chromosome constitutes about 6.3% of the female haploid complement and is about the size of the 'marker' autosome. The Y-chromosome is larger than the smallest autosome (acrocentric) and constitutes about 1.3% of the female haploid complement.

![Fig. 3. Karyotype of a male Eonycteris spelaea.](image)

2. *Eonycteris spelaea*: The diploid number $2n=36$ is composed of 11 pairs of metacentric, 3 pairs of submetacentric, 2 pairs of subacrocentric and 1 pair of acrocentric autosomes, metacentric X and metacentric Y sex-chromosomes (Fig. 3). A pair of medium-sized metacentric autosome is characterised by the presence of a secondary constriction near the centromere. The only pair of acrocentric autosome is the smallest in the complement. The X-chromosome comprises about 5.7% of the female haploid complement and is about the size of the 'marker' autosome. The Y-chromosome is the smallest element in the complement and comprises about 1.9% of the female haploid complement.

Discussion

*Macroglossus* and *Eonycteris* are the two genera of fruit-bats belonging to the subfamily Macroglossinae (Ellerman and Morrison-Scott 1951). They are charac-
terised by distinct diploid number; $2n=36$ for *Eonycteris* and $2n=34$ for *Macroglossus*. Such variations in diploid number for bat genera belonging to the same subfamily, however, are not uncommon.

The karyotypes of *Macroglossus* and *Eonycteris*, though distinct, show considerable similarities, particularly the ‘marker’ autosome pair, the smallest acrocentric autosome and the X-chromosome. The additional pair of autosome found in *Eonycteris* belongs to the small sized group, and the different number of each morphological class (metacentric, submetacentric, subacrocentric and acrocentric) may be explained in terms of pericentric inversions. It is, however, premature at this stage to postulate the evolutionary relationship of these two genera.

Although the diploid number of *Macroglossus* is similar to *Cynopterus*, the karyotypes of these two genera can be distinguished by 1) the ‘marker’ autosome:—this is the 4th longest in the complement for *Cynopterus* (Yong, Dhaliwal, Lim, Teh and Start 1973) but the 9th pair in *Macroglossus*, 2) the presence of a large acrocentric autosome in *Macroglossus*, 3) the presence of only a single pair of very small acrocentric autosome in *Macroglossus* whereas there are 2 such pairs in *Cynopterus*, and 4) the X-chromosome is metacentric in *Macroglossus* but subacrocentric in *Cynopterus*. Similarly, the karyotype of *Eonycteris* is distinct from that of *Rousettus* with $2n=36$.

The identical karyotypes of *Macroglossus lagochilus* and *M. minimus* substantiates close evolutionary relationship of these bats. Like the majority of closely related bats, karyotypes do not help in distinguishing *M. lagochilus* and *M. minimus*. The identifications of these animals still depend on morphological characters.

Chromosomes are presumably also not important as an isolating mechanism since these two species overlap in their distribution. On the other hand, two very closely-related sympatric insectivorous species, occurring in the same locality as *Macroglossus* have been found to possess very different diploid number due to Robertsonian translocations, which indicates the importance of chromosomes as an isolating mechanism (Yong, Dhaliwal and Teh 1971).

The karyotypes of *Macroglossus* and *Eonycteris* can also be distinguished from those of other Malaysian fruit bats of which *Pteropus hypomelanus* Temminck has $2n=38$, *Penthetor lucasi* (Dobson) with $2n=48$, and *Balionycteris maculata* (Thomas) with $2n=24$ (Yong Hoi-Sen unpubl. data).

The present findings for *Macroglossus* and *Eonycteris* bring the total number of genera of fruit bats with $2n=34$ to three viz. *Cynopterus*, *Eidolon* and *Macroglossus* and those with $2n=36$ to two (*Eonycteris* and *Rousettus*). It appears the karyotypes with $2n=34$, 36 and 38 are more ‘typical’ for the fruit bats (Megachiroptera), whilst those with $2n=24$ (*Balionycteris*) and $2n=48$ (*Penthetor*) are unusual.

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References


