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G- AND C-BANDED KARYOTYPES OF THE RHINOPOMATIDAE (MICROCHIROPTERA)

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Bats of the Family Rhinopomatidae (which contains a single genus with three species) are generally considered to be primitive microchiropterans which have retained many of the morphological character states thought to be distinctive of early bats (Miller, 1907; Koopman, 1984). Ray-Chaudhuri et al. (1968) compared the standard karyotypes of *Rousettus leschenaulti* (Pteropodidae, Megachiroptera) and *Rhinopoma hardwicketi* and stated that "such extensive similarities between the chromosome complements of

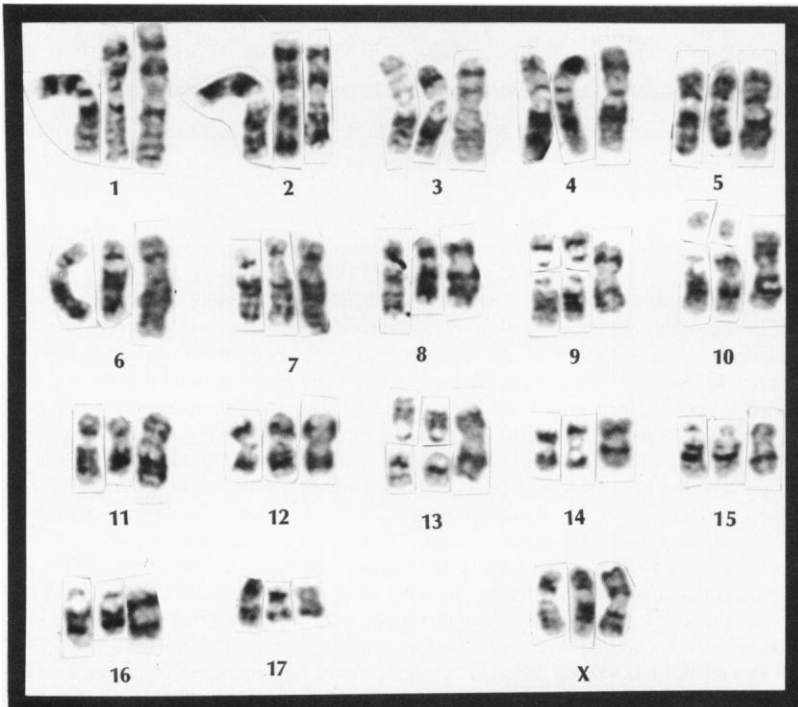


FIG. 1.—Composite haploid genomes of *Rhinopoma microphyllum* (from two cells, on left) and *R. hardwicketi* (one cell, right). The numbers are chromosome numbers for *R. hardwicketi* and each number may represent more than one chromosome in *R. microphyllum*.

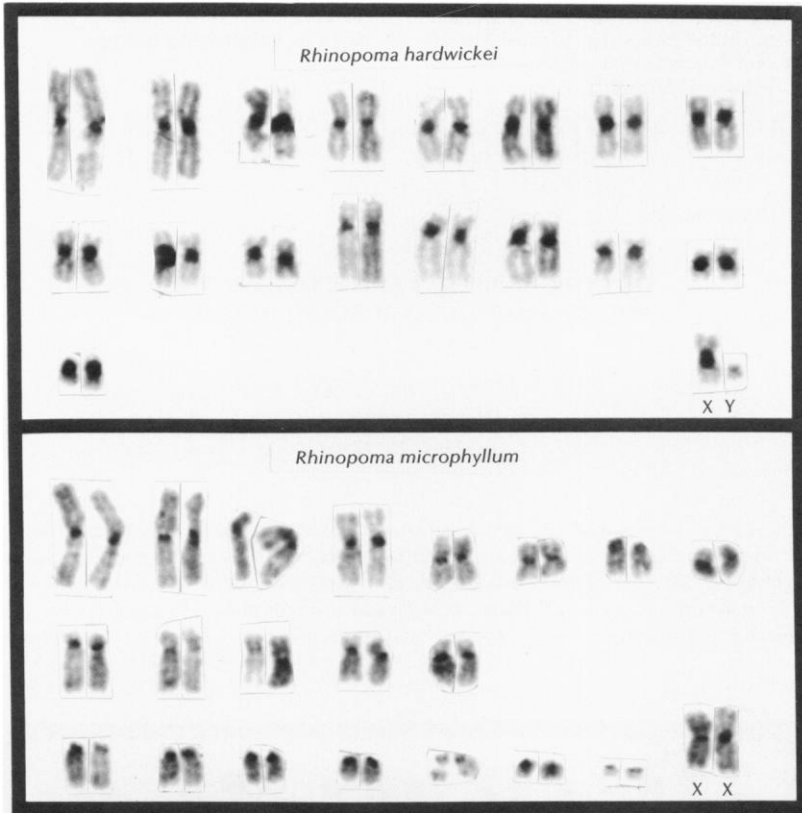


FIG. 2.—C-band karyotype of a male *Rhinopoma hardwickei* (top) and a female *R. microphyllum* (bottom).

these two genera cannot be just accidental, but should reflect close genetic relationships between Pteropidae and Rhinopomatidae.”

The purpose of this study was to examine G- and C-banded karyotypes of *R. hardwickei* and *R. microphyllum* to document the amount and type of chromosomal variation that may exist between the two species and to compare G-band sequences of the rhinopomatids with members of the Megachiroptera and the Microchiroptera to determine the magnitude of shared G-band homology and thereby test the conclusion of Ray-Chaudhuri et al. (1968), which was based on standard (non-differentially stained) karyotypes.

Ear and lung biopsies were obtained in the field and returned to the laboratory where primary cell lines were established as described by Patton and Baker (1978) and Baker and Qumsiyeh (in press). The G-banding procedure was that of Seabright (1971) as modified by Patton and Baker (1978) and the C-banding procedure was as described in Stefos and Arrighi (1971). A minimum of five complete spreads from each individual were examined for each of the G-band, C-band, and standard karyotypes.

Specimens examined.—*Rhinopoma hardwickei*: Palestine, Jericho, Mt. Quarantania (TTU 40638 ♂, TTU 40641 ♂); *Rhinopoma microphyllum*: Jordan, Jordan Valley, Tabqat Fahl (TTU 40521 ♀, TTU 40522 ♀).

The standard karyotype of *Rhinopoma hardwickei* ($2n = 36$, FN = 68) from Palestine is indistinguishable from that described from specimens from India (Ray-Chaudhuri et al., 1968), although our terminology for those same chromosomes is slightly different. Eleven pairs of autosomes are metacentric and six are submetacentric. The X-chromosome is a medium sized metacentric and the Y-chromosome is a very small acrocentric.

The standard karyotype of *Rhinopoma microphyllum* has not been reported previously. The karyotype has $2n = 42$, FN = 66 which is different from that of the morphologically similar species, *R. hardwickei*

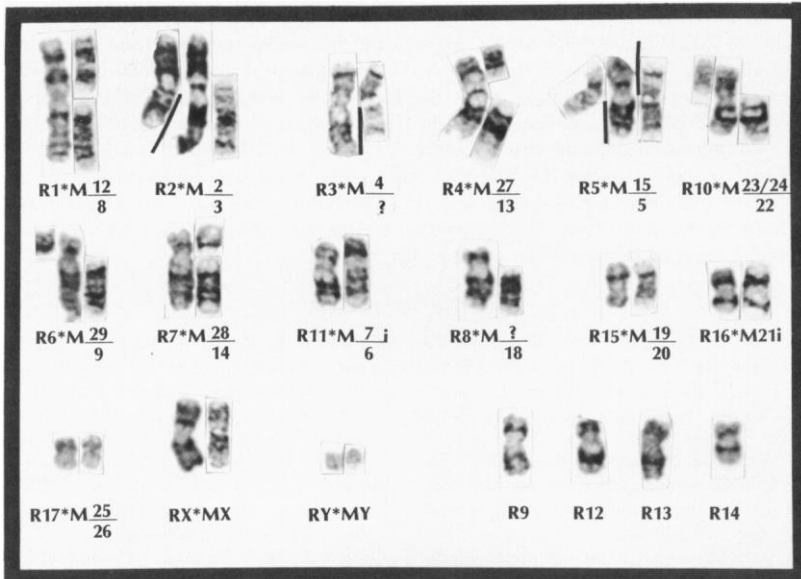


FIG. 3.—Composite haploid complements for *Rhinopoma hardwicki* (left or center) and *Macrotus waterhousii*. Black bars separate nonhomologous arms; “R” refers to *Rhinopoma* chromosome numbers as in Fig. 1 and “M” to *Macrotus* arm numbers proposed by Patton and Baker (1978) and Baker (1979); “i” refers to an inversion difference.

($2n = 36$, FN = 68). The autosomes of *R. microphyllum* include eight metacentric pairs, five submetacentric pairs and seven acrocentric pairs. The X-chromosome is a medium-sized metacentric (Fig. 1).

Figure 1 shows a comparison of haploid complements from *Rhinopoma microphyllum* and *R. hardwicki*. Thirteen chromosomes (numbers 1–8, 11, 12, 14, 17, and X) are identical in both species. Biarmed chromosome pairs 9, 10, and 13 in *R. hardwicki* represent translocation differences with six pairs of chromosomes in *R. microphyllum*. In the case of chromosomes 9 and 13, the events are centric fissions/fusions. Chromosome 10 of *R. hardwicki* is represented in *R. microphyllum* by a very small acrocentric chromosome plus a submetacentric chromosome indicating a tandem fusion event. Chromosomes 15 and 16 are metacentric in *R. hardwicki* but acrocentric in *R. microphyllum*, a difference that can be explained by a pericentric inversion. The differences recorded above for the two species are minimal and the present G-band resolution does not consistently show other differences. *Rhinopoma hardwicki* and *R. microphyllum* have been difficult to distinguish morphologically (see Hill, 1977; Qumsiyeh, in press) and the karyotype can be added to the characters used to distinguish the two.

The C-banded karyotypes of both species show that heterochromatin is limited to the centromeric regions on all chromosomes (Fig. 2). *Rhinopoma hardwicki* appears to have larger quantities of C-band positive material on some autosomes and the X-chromosome.

To test the conclusion of Ray-Chaudhuri et al. (1968) we have compared the G-banded karyotypes of *Rhinopoma hardwicki* (Figs. 1 and 3) and *Rousettus aegyptiacus* (from Haiduk et al., 1981—fig. 3), and found that they share five pairs of the long chromosomal arms. The remaining 29 pairs of arms have different G-band patterns or are so small that their homology cannot be determined with the resolution available in our preparations. *Rhinopoma hardwicki* and *Rousettus aegyptiacus* have almost identical standard karyotypes and our results again demonstrate that standard karyotype similarities can be misleading (Baker and Bickham, 1980; Haiduk et al., 1981). The five arms shared between *Rhinopoma* and *Rousettus* are also shared with *Macrotus waterhousii* which has a karyotype proposed as primitive for the family Phyllostomidae and possibly the superfamily Phyllostomoidea (Patton and Baker, 1978; Baker, 1979). These arm numbers according to the *Macrotus* standard karyotype are 4, 5, 8, 12, and 21. There are several other long chromosomal arms of *R. hardwicki* shared with those of *Macrotus waterhousii* (Fig. 3). The number of homologous arms between these two distant groups of bats is striking and suggests that during the

evolution of the Microchiroptera some euchromatic linkage groups were conserved. Additionally, the chromosomes that are shared between the Megachiroptera and *Rhinopoma* and *Macrotus* can be proposed as primitive for all living bat species and the additional linkage groups shared by *Rhinopoma* and *Macrotus* can be proposed as characteristic of the ancestor that gave rise to most families of Microchiroptera.

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MOLAR CUSP PATTERNS IN THE BAT GENUS *BRACHYPHYLLA*: SOME FUNCTIONAL AND SYSTEMATIC OBSERVATIONS

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The bat genus *Brachyphylla* has had a controversial taxonomic history. Gray (1834) originally suggested a close affinity to *Glossophaga*, based on similarities of the lip and tongue. Subsequently, many taxonomists placed the genus in their equivalent of today's subfamily Stenodermatinae (Peters, 1865a, 1865b; Miller, 1907). Others initially suggested that *Brachyphylla* was closely related to other groups of phyllostomid bats (notably to desmodontines; Dobson, 1875; Winge, 1892), although later most became convinced that *Brachyphylla* was a stenodermatine bat (Dobson, 1878; Winge, 1941). Most interesting in light of modern systematic thinking was Allen's (1898) placement of *Brachyphylla* and *Phyllonycteris* in the group Brachyphyllina, which he apparently intended to be a transitional group between the stenodermatines and glossophagines.