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Comparative study of the karyotypes of two Egyptian species of bats, *Taphozous perforatus* and *Taphozous nudiventris* (Chiroptera: Mammalia)

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Abstract. A detailed karyotypic analysis of two Egyptian species of bats, *Taphozous perforatus* and *Taphozous nudiventris*, was made on the basis of conventional data and G-band patterns. No detectable karyotypic difference was found between the two species (2n = 42, F.N. 64). By comparison of G-band patterns, some differences between the two species were seen in the corresponding autosomal pairs. These results are reported for the first time in Egypt.

Key words. Chromosome; karyotype; G-banding; *Taphozous perforatus*; *Taphozous nudiventris*.

Karyological information is available for about 180 species of bats, but the greater part of this information is limited to European, African and American species, apart from a few studies on tropical and subtropical species in Asia[1-4]. G-banding patterns of chromosomes of about 48 bat species have been analysed by Stock[5] and Bickman[6,7]; these studies have revealed that the banding patterns of chromosome arms or segments are strongly conservative, thus the banding patterns can be used to detect karyotypic alterations between species of the same genus and between related genera. Chromosome studies in species of the genus *Taphozous* have been made by several authors, among which those by Capanna and Civitelli[8] and Harada et al.[9] are the most outstanding.

Although a large number of recent reports have dealt with the chromosomes of bats in the different localities of the world, Egyptian bats remain to be studied. So in the present paper, a detailed comparison of the karyological data of the two species *Taphozous perforatus* and *Taphozous nudiventris* is made, using conventional and G-banding staining.

Materials and methods

Specimens of *T. perforatus* (10 males and 8 females) and *T. nudiventris* (13 males and 9 females) were collected from different localities around Qena City in Upper Egypt. The two species are classified following Wassif[10]. To analyse the karyotype, bone marrow cells from the humerus were used in an air-dried preparation, as described by Uchida and Ando[11]. Each animal received an i.p. injection of 0.5% colchicine 2 h before sacrifice. The bone marrow and the testicular tissues were taken out and exposed to 0.75 M KCL for 30 min at a temperature of 37 °C. Cells were fixed in Carnoy's fluid and preparations stained with Giemsa. At least 10 mitotic metaphases were karyotyped from each species to ascertain the karyological data, and more than 50 spreads were counted to determine the diploid number. The G-banding technique of Seabright[12] was applied. The terminology used for centromeric placement was that of Levan et al.[13] The number of arms (F.N.) for each species was calculated excluding the sex chromosomes.

Results and discussion

Conventional staining. The karyotypes of *T. perforatus* (fig. 1, b) and of *T. nudiventris* (fig. 2, b) are identical with each other (2n = 42, F.N. = 64). We grouped the chromosomes of the two species into three series, A, B and C, according to their size and morphology. Group A is composed of 9 pairs of metacentric chromosomes which display differences in size and appear to be arranged in decreasing order of size. The centromeric index of the chromosomes of this group in *T. perforatus* ranges between 44.55 and 48.57 while in *T. nudiventris* it ranges between 44.24 and 49.68. The B group displays 3 pairs of submetacentrics, with a centromeric index ranging between 34.49 and 35.39 in *T. perforatus* and 33.11 and 35.33 in *T. nudiventris*. Group C is composed of 8 pairs of acrocentric chromosomes which display in *T. perforatus* a relative length range from 4.85% (pair n. 13) to 1.46% (pair n. 20) and in *T. nudiventris* a relative length range from 5.07% to 1.49%. Sex chromosomes are easy to identify. X is metacentric while the Y chromosome is an acrocentric one of a very small size as shown in tables 1 and 2.

G-banding pattern. The G-bands on individual autosomal elements of *T. perforatus* (fig. 3, a and b) and *T. nudiventris* (fig. 3, c and d) exhibit a well-differentiated appearance, so that the homologous pairs in the autosomal complements of both species can be identified pre-

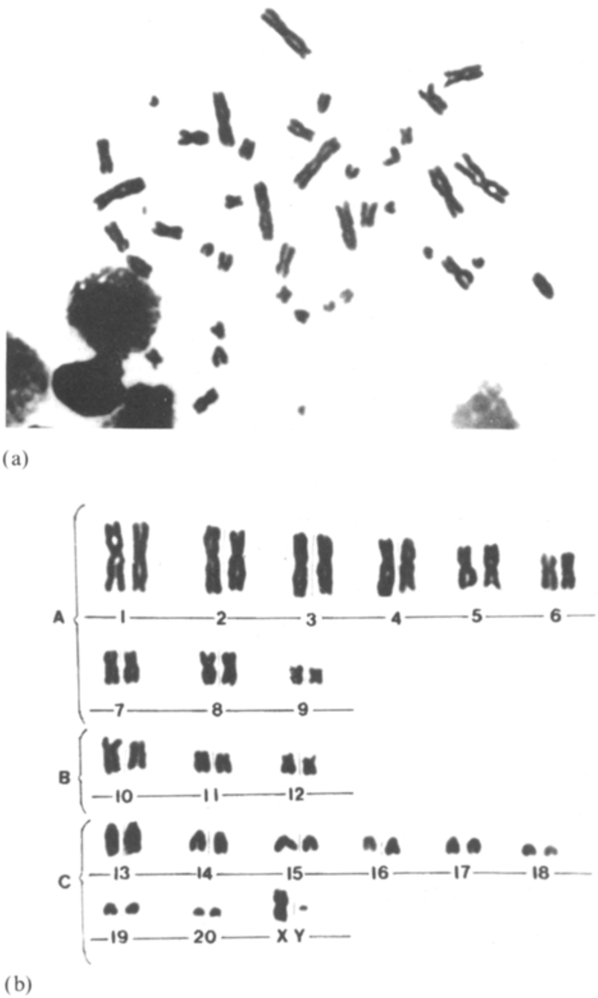

Figure 1. Mitotic metaphase spread (*a*) and karyotype (*b*) of male *T. perforatus* 2n = 42.

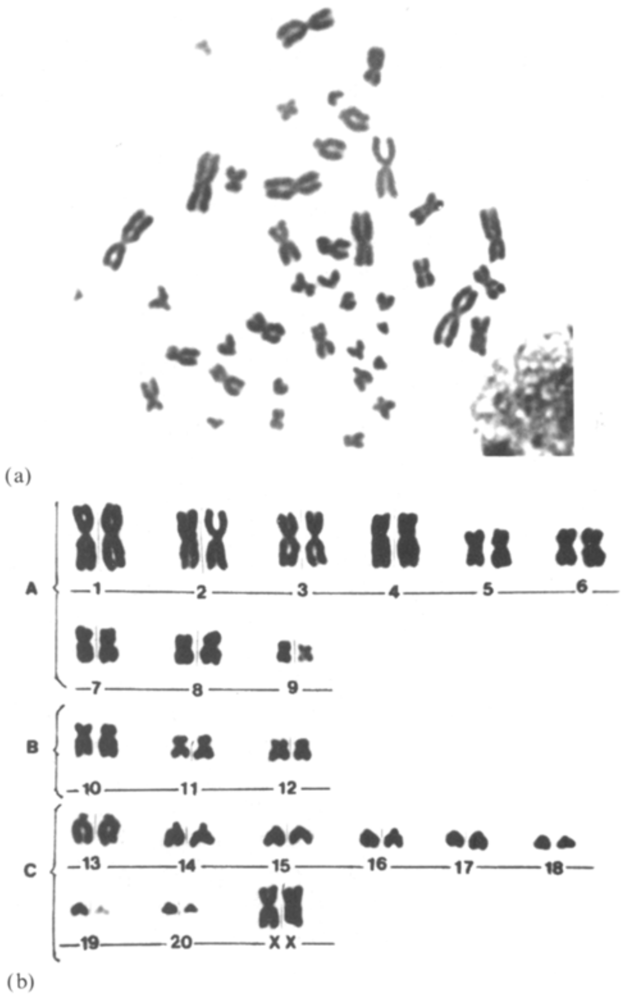

Figure 2. Mitotic metaphase spread (*a*) and karyotype (*b*) of female *T. nudiventris* 2n = 42.

Table 1. Averages of ten cell spreads of chromosomes; measurements and classification. *Taphozous perforatus.*

Chromosome pair number	Chromosome length (Mean + SD)			Relative length %(Mean + SD)			Arm ratio (Mean + SD)	Centromeric index (Mean + SD)	Classification
	Long arm	Short arm	Total	Long arm	Short arm	Total			
1	0.64 + 0.13	0.60 + 0.12	1.24 + 0.25	5.13 + 0.51	4.84 + 0.42	10.00 + 0.83	1.05 + 0.08	48.57 + 2.03	M
2	0.64 + 0.13	0.53 + 0.09	1.17 + 0.22	5.15 + 0.61	4.28 + 0.29	9.35 + 0.86	1.20 + 0.14	45.48 + 3.04	M
3	0.60 + 0.11	0.49 + 0.10	1.09 + 0.19	4.84 + 0.39	3.96 + 0.49	8.82 + 0.51	1.23 + 0.20	44.91 + 4.08	M
4	0.58 + 0.12	0.46 + 0.08	1.04 + 0.17	4.66 + 0.43	3.76 + 0.50	8.43 + 0.44	1.25 + 0.25	44.55 + 4.98	M
5	0.44 + 0.12	0.38 + 0.08	0.83 + 0.20	3.59 + 0.63	3.10 + 0.32	6.70 + 0.77	1.16 + 0.20	46.49 + 4.03	M
6	0.37 + 0.09	0.33 + 0.08	0.70 + 0.17	2.97 + 0.30	2.69 + 0.41	5.67 + 0.59	1.12 + 0.18	47.44 + 3.76	M
7	0.34 + 0.08	0.30 + 0.05	0.64 + 0.13	2.71 + 0.22	2.41 + 0.16	5.14 + 0.26	1.12 + 0.11	47.32 + 2.55	M
8	0.29 + 0.08	0.24 + 0.06	0.53 + 0.14	2.33 + 0.55	1.93 + 0.38	4.27 + 0.89	1.19 + 0.17	45.69 + 3.53	M
9	0.20 + 0.04	0.17 + 0.03	0.37 + 0.06	1.62 + 0.27	1.41 + 0.22	3.04 + 0.38	1.17 + 0.31	46.71 + 5.65	M
10	0.41 + 0.08	0.22 + 0.05	0.64 + 0.13	3.40 + 0.63	1.81 + 0.40	5.22 + 0.99	1.90 + 0.24	34.63 + 2.88	S.M
11	0.33 + 0.09	0.18 + 0.05	0.51 + 0.13	2.69 + 0.62	1.48 + 0.42	4.17 + 0.97	1.85 + 0.34	35.39 + 4.28	S.M
12	0.26 + 0.03	0.13 + 0.03	0.40 + 0.06	2.12 + 0.28	1.11 + 0.18	3.24 + 0.42	1.91 + 0.23	34.49 + 2.88	S.M
13	0.59 + 0.09	0.00	0.59 + 0.09	4.85 + 0.35	0.00	4.85 + 0.35	∝	0.00	Acro.
14	0.42 + 0.08	0.00	0.42 + 0.08	3.41 + 0.32	0.00	3.41 + 0.32	∝	0.00	Acro.
15	0.35 + 0.05	0.00	0.35 + 0.05	2.86 + 0.23	0.00	2.86 + 0.23	∝	0.00	Acro.
16	0.32 + 0.05	0.00	0.32 + 0.05	2.61 + 0.11	0.00	2.61 + 0.11	∝	0.00	Acro.
17	0.29 + 0.05	0.00	0.29 + 0.05	2.39 + 0.18	0.00	2.39 + 0.18	∝	0.00	Acro.
18	0.26 + 0.05	0.00	0.26 + 0.05	2.09 + 0.29	0.00	2.09 + 0.29	∝	0.00	Acro.
19	0.22 + 0.04	0.00	0.22 + 0.04	1.82 + 0.22	0.00	1.82 + 0.22	∝	0.00	Acro.
20	0.17 + 0.01	0.00	0.17 + 0.01	1.46 + 0.25	0.00	1.46 + 0.25	∝	0.00	Acro.
X	0.29 + 0.09	0.29 + 0.09	0.58 + 0.17	2.32 + 0.45	2.29 + 0.43	4.64 + 0.88	1.01 + 0.03	49.49 + 0.94	M
Y	—	—	0.11 + 0.02	—	—	0.89 + 0.03	—	—	Micro.
Sum			12.39 + 2.14						

M, Metacentric; S.M., Submetacentric; Acro., Acrocentric; Micro., Microchromosomes.

Table 2. Averages of ten cell spreads of chromosomes; measurements and classification. *Tophozous nudiventris.*

Chromosome pair number	Chromosome length (Mean + SD)			Relative length %(Mean + SD)			Arm ratio (Mean + SD)	Centromeric index (Mean + SD)	Classification
	Long arm	Short arm	Total	Long arm	Short arm	Total			
1	0.59 + 0.09	0.53 + 0.11	1.13 + 0.20	5.47 + 0.48	4.90 + 0.30	10.38 + 0.57	1.01 + 0.36	47.28 + 2.67	M
2	0.58 + 0.13	0.47 + 0.09	1.05 + 0.20	5.34 + 0.80	4.29 + 0.32	9.64 + 0.65	1.25 + 0.26	44.24 + 4.42	M
3	0.55 + 0.12	0.44 + 0.09	0.99 + 0.19	5.02 + 0.40	4.04 + 0.43	9.07 + 0.51	1.25 + 0.18	44.58 + 3.74	M
4	0.51 + 0.12	0.42 + 0.10	0.93 + 0.21	4.67 + 0.44	3.85 + 0.51	8.52 + 0.65	1.23 + 0.19	45.06 + 4.10	M
5	0.36 + 0.07	0.33 + 0.08	0.69 + 0.15	3.34 + 0.39	3.01 + 0.38	6.35 + 0.68	1.11 + 0.12	47.40 + 2.85	M
6	0.34 + 0.07	0.27 + 0.06	0.61 + 0.12	3.12 + 0.22	2.52 + 0.32	5.64 + 0.47	1.24 + 0.11	44.63 + 2.48	M
7	0.30 + 0.07	0.26 + 0.03	0.56 + 0.10	2.75 + 0.25	2.40 + 0.16	5.16 + 0.20	1.15 + 0.16	46.71 + 3.59	M
8	0.19 + 0.04	0.18 + 0.04	0.36 + 0.08	1.76 + 0.35	1.64 + 0.27	3.31 + 0.49	1.07 + 0.14	49.68 + 3.38	M
9	0.17 + 0.03	0.16 + 0.02	0.33 + 0.05	1.58 + 0.18	1.50 + 0.18	3.16 + 0.40	1.05 + 0.10	48.78 + 2.43	M
10	0.36 + 0.07	0.18 + 0.03	0.54 + 0.11	3.28 + 0.16	1.69 + 0.14	4.96 + 0.19	1.94 + 0.22	33.11 + 3.69	S.M
11	0.31 + 0.06	0.17 + 0.04	0.48 + 0.09	2.89 + 0.28	1.50 + 0.24	4.44 + 0.27	1.91 + 0.43	34.85 + 4.91	S.M
12	0.20 + 0.02	0.11 + 0.02	0.31 + 0.04	1.90 + 0.33	1.03 + 0.16	2.95 + 0.38	1.89 + 0.48	35.33 + 6.56	S.M
13	0.55 + 0.12	0.00	0.55 + 0.12	5.07 + 0.41	0.00	5.07 + 0.41	$\propto$	0.00	Acro.
14	0.37 + 0.06	0.00	0.37 + 0.06	3.49 + 0.38	0.00	3.49 + 0.38	$\propto$	0.00	Acro.
15	0.29 + 0.07	0.00	0.29 + 0.07	2.67 + 0.24	0.00	2.67 + 0.24	$\propto$	0.00	Acro.
16	0.26 + 0.05	0.00	0.26 + 0.05	2.43 + 0.15	0.00	2.43 + 0.15	$\propto$	0.00	Acro.
17	0.25 + 0.05	0.00	0.25 + 0.05	2.27 + 0.21	0.00	2.27 + 0.21	$\propto$	0.00	Acro.
18	0.20 + 0.02	0.00	0.20 + 0.02	1.89 + 0.22	0.00	1.89 + 0.22	$\propto$	0.00	Acro.
19	0.17 + 0.02	0.00	0.17 + 0.02	1.60 + 0.26	0.00	1.60 + 0.26	$\propto$	0.00	Acro.
20	0.16 + 0.02	0.00	0.16 + 0.02	1.49 + 0.14	0.00	1.49 + 0.14	$\propto$	0.00	Acro.
X	0.31 + 0.08	0.29 + 0.06	0.60 + 0.15	2.89 + 0.78	2.71 + 0.65	5.62 + 1.40	1.05 + 0.07	48.50 + 1.78	M
Y	—	—	0.11 + 0.01	—	—	1.14 + 0.32	—	—	Micro.
Sum			10.89 + 2.08						

M, Metacentric; S.M., Submetacentric; Acro., Acrocentric; Micro., Microchromosome.

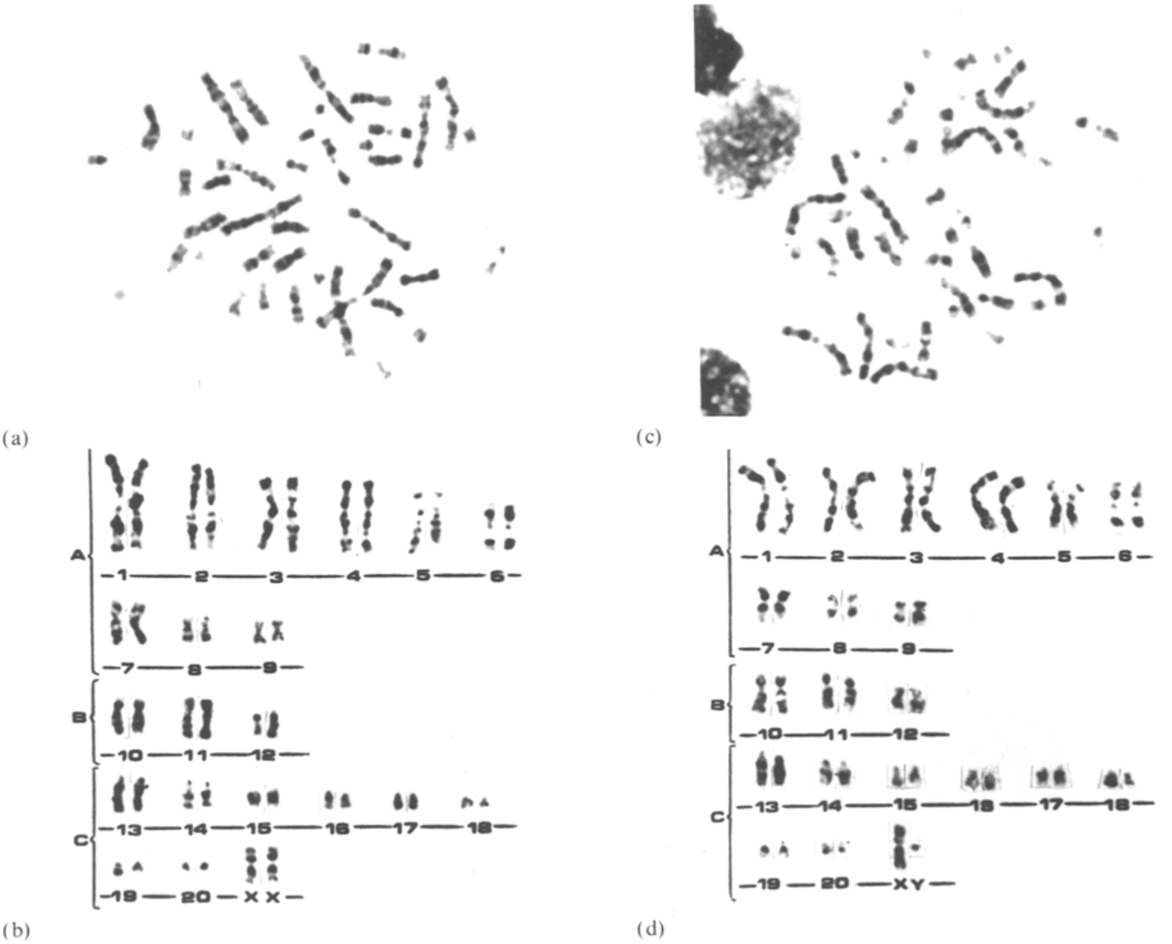

Figure 3. G-band mitotic metaphase spread (*a*) and karyotype (*b*) of female *T. perforatus* and spread (*c*) and karyotype (*d*) of male *T. nudiventris.*

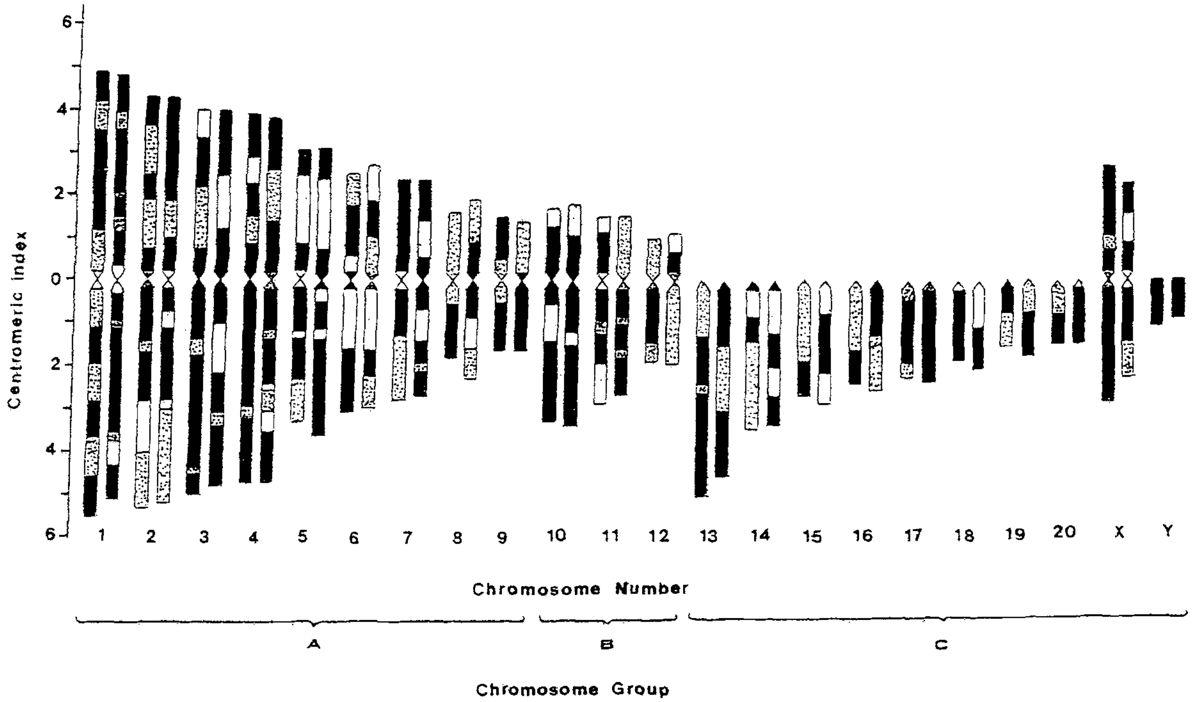

Figure 4. A diagramatic representation of pair matching of G-banded chromosomes between male *T. nudiventris* (left) and male *T. perforatus* (right). The intensity of staining is represented by black, dotted or unshaded for darkly stained, slightly stained and unshaded regions respectively.

cisely by using their band features. There are some differences in the G-band pattern in the corresponding autosomal pairs between *T. perforatus* and *T. nudiventris* as shown in figure 4. The X chromosomes of both species have clearly differentiated bands, and the G-bands on their Y chromosome are both obscure.

From the present study, in spite of the fact that the two species *T. perforatus* and *T. nudiventris* have the same diploid chromosome numbers (2n = 42, F.N. = 64) and karyotypes, they have some differences in the G-band patterns. This confirms the importance of using banding patterns in detecting differences between the karyotypic patterns of species of the same genus.

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