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Karyotypes of three species of molossid bats (Molossidae, Chiroptera) from India and western Africa

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A b s t r a c t . Conventional and G- banded karyotypes are reported for three species of molossid bats from India (*Chaerephon plicatus*) and Senegal (*Ch. pumilus, Mops condylurus*). The chromosome diploid number 2n = 48 and the number of chromosomal arms FN= 54 were recorded, similarly as in the previous published reports on karyology of molossid bats from Thailand, East Malaysia, and Africa. A synopsis of karyotypes of bats of the family Molossidae is presented with comments on their chromosomal evolution.

Key words: karyotype evolution, chromosome banding

Introduction

Bats of the family Molossidae are widely distributed in warm regions of both the Old World and the New World. The family comprises two subfamilies, 16 genera, and about 100 species (S i m m o n s 2005). There are 40 species recorded in Africa (V a n C a c k e n b e r g h e & S e a m a r k 2008) and about 17 species in southern and southeastern Asia (C o r b e t & H i l l 1992, B a t e s & H a r r i s o n 1997).

After a pioneer study by P a i n t e r (1925), many species of molossid bats were examined karyologically. Karyotype data are currently available for molossid bats from America (e.g. W a r n e r et al. 1974, B a k e r et al. 1982), Africa (e.g. Đ u l i ć & M u t e r e 1973, P e t e r s o n & N a g o r s e n 1975, N a g o r s e n et al. 1976, S m i t h et al. 1986, R a u t e n b a c h et al. 1993), Australia (V o l l e t h et al. 2002), Thailand (T s u c h i y a et al. 1979, H a r a d a et al. 1982), Malaysia (H a r a d a & K o b a y a s h i 1980), central and eastern Asia (Z h a n g 1985, O n o & O b a r a 1989, Z i m a et al. 1991, W u et al. 2004), and Europe (D u l i ć & M r a k o v č i ć 1980, A r r o y o N o m b e l a et al. 1986). The molossid bats were investigated in chromosome banding studies (B a k e r et al. 1982,

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Arroyo Nombela et al. 1986, Morielle et al. 1988, Ono & Obara 1989, Freitas et al. 1992, Morielle-Versute et al. 1994, 1996, Leite-Silva et al. 2003), as well as in comparative studies using chromosome in situ hybridization (Finato et al. 2000, Faria & Morielle-Versute 2002, 2006, Volleth et al. 2002, Leite-Silva et al. 2003).

The karyotype of *Chaerephon plicatus* was reported previously from Thailand and East Malaysia (Tsuchiya et al. 1979, Harada & Kobayashi 1980, Harada et al. 1982). However, the present study provides the first karyological report on molossid bats from the Indian subcontinent, including the description of the G-banded karyotype. The karyotypes of the other two species studied in Senegal, *Chaerephon pumilus* and *Mops condylurus,* were reported previously from eastern, and southern Africa (Đulić & Mutere 1973, Peterson & Nagorsen 1975, Smith et al. 1986, Rautenbach et al. 1993).

Material and Methods

Only one male specimen of *Chaerephon plicatus* (Buchannan, 1800) was collected in the mist net at Kolar, India (13° 09´ N; 78° 10´ E) and the voucher specimen was deposited at National Institute of Virology, Pune. The examined specimens of *Ch. pumilus* (Cretzschmar, 1830–1831) and *Mops condylurus* (A. Smith, 1833) were collected in four sites in Senegal, western Africa: Simenti (13° 01´ N; 12° 18´ W), Dar Salam (13° 16´ N; 13° 12´ W), Gue de Sambeillou (12° 39´ N; 13° 20´ W) and Niokolo (13° 04´ N; 12° 43´ W), and they are deposited in the collections of the Institute of Vertebrate Biology AS CR, Brno (Table 1). The bats were collected with the permission and under supervision of the Senegal's National Parks General Management.

Chromosome preparation was done following the bone marrow direct methods modified after Baker (1970). G-bands were developed adopting the procedure of Seabright (1971).

Table 1. A synopsis of the specimens examined. F – female; M – male.

species	collection site	specimens examined
Ch. plicatus	Kolar	1M
Ch. pumilus	Dar Salam	1F, 1M
	Simenti	6F, 5M
M. condylurus	Gue de Sambeillou	1M
	Simenti	1F, 1M
	Niokolo	1M

Results and Discussion

The diploid number of all the specimens examined was 2n = 48 chromosomes, the fundamental number of autosomal arms (FNa) was about 54. The autosomes were categorized into one pair of large metacentrics, three pairs of medium sized meta- to submetacentrics and 19 pairs of medium to small sized acrocentrics. Short chromosomal arms were distinctly apparent in various acrocentric autosomes; however, these arms were not considered in calculation of the

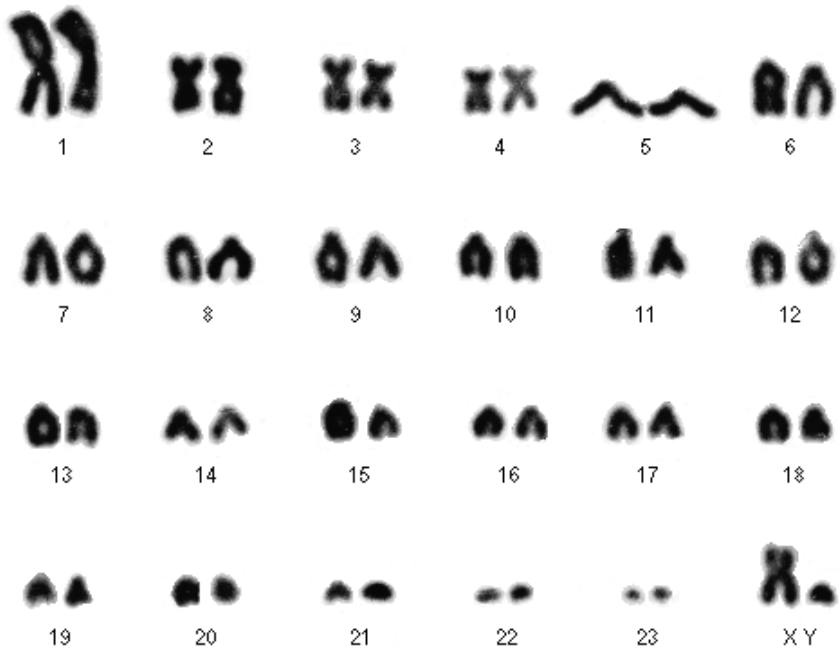

Fig . 1. Karyotype of *Chaerephon plicatus* from India arranged from conventionally Giemsa-stained chromosomes.

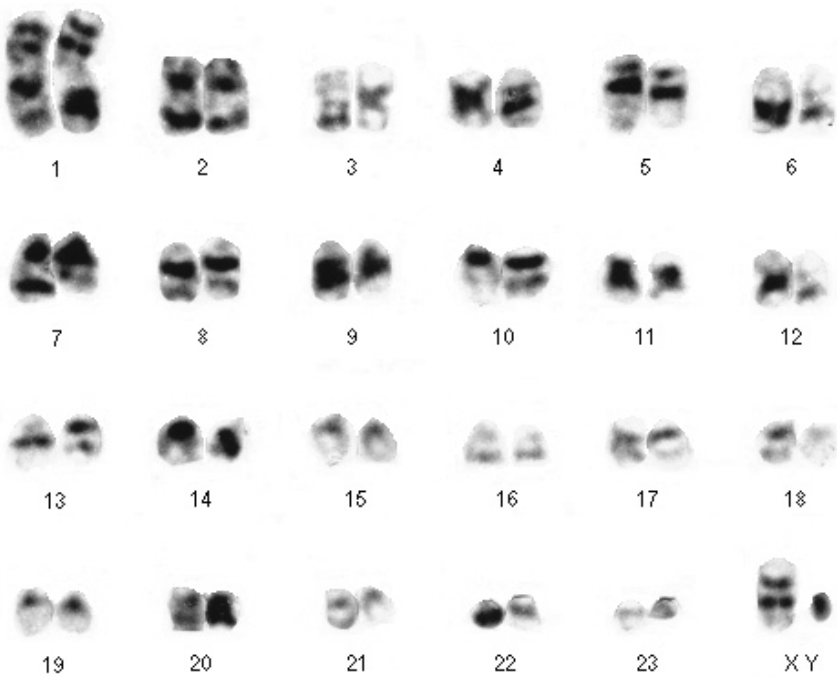

Fig. 2. Karyotype of *Chaerephon plicatus* from India arranged from G-banded chromosomes.

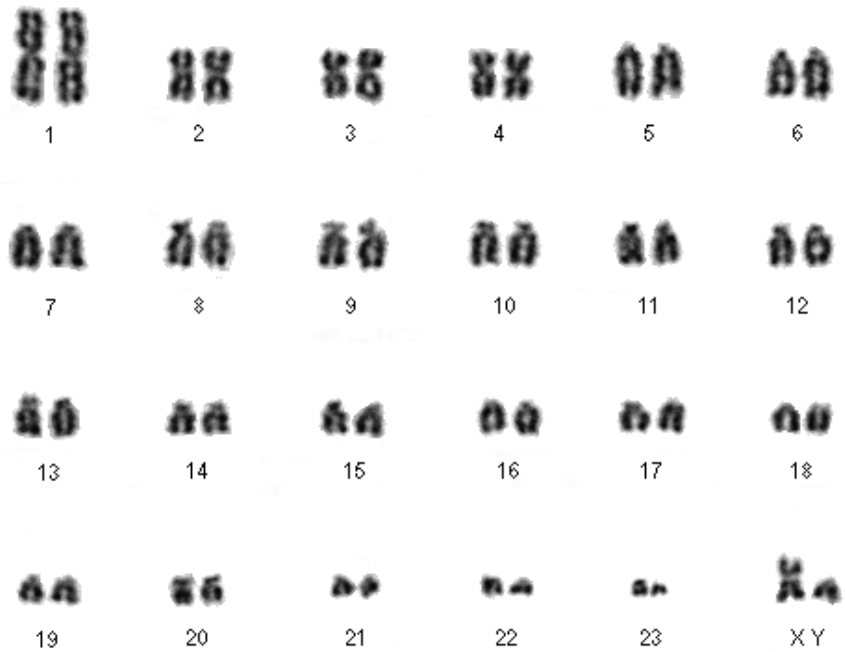

Fig. 3. Karyotype of *Chaerephon pumilus* from Senegal arranged from conventionally Giemsa-stained chromosomes.

fundamental number. The X was a medium sized metacentric and the Y a small acrocentric chromosome (Figs 1, 2, 3).

Such chromosomal complements resemble closely the karyotypes of the species examined published elsewhere, including that of *Ch. plicatus* reported from Thailand and East Malaysia (Tsuchiya et al. 1979, Harada & Kobayashi 1980, Harada et al. 1982), and *Ch. pumilus* and *M. condylurus* from Africa (Đulić & Mutere 1973, Peterson & Nagorsen 1975, Smith et al. 1986, Rautenbach et al. 1993). All the karyotypes have the same diploid number (2n = 48), and the similar number of autosomal (FNa approximately 54). The X chromosome is biarmed (submetacentric or metacentric), and the Y chromosome is a tiny acrocentric.

The karyotypes of molossid bats so far studied are reviewed in Table 2. The karyotype of molossid species is usually recognizable by the presence of one large and three medium sized biarmed autosomes, but the comparative ZOO-FISH analysis did not revealed any unequivocal synapomorphic feature for the family Molossidae compared to related families of bats (Volleth et al. 2002). Warner et al. concluded in the paper from 1974 that "considerable divergence in cranial and external features within the taxa of molossids examined has not been accompanied by major chromosomal rearrangements". However, extensive chromosomal research within the family has revealed distinct variation in both the diploid number and the number of autosomal arms. Considerable variation was also reported in the number and position of nucleolar organizer regions (Baker et al. 1992, Morielle-Versute et al. 1996, Leite-Silva et al. 2003), and the NORs seem to be an important karyotype marker of the molossid bats.

The most common karyotype with 48 chromosomes is found in various species of the genera *Chaerephon, Molossus, Mormopterus, Nyctinomops, Platymops,* and *Tadarida*.

Table 2. Karyotypes of molossid bats. 2n – diploid number of chromosomes; FNa – number of autosomal arms; X – morphology of the X chromosome; M – metacentric, SM – submetacentric; ST – subtelocentric; A – acrocentric. The nomenclature of species adopted after Simmons (2005).

species	collection site	2n	FNa	X	references
Chaerephon aloysiisabaudiae	Cameroun	48	66	SM	Smith et al. 1986
C. ansorgei	Cameroun	48	66	ST	Smith et al. 1986
	South Africa	48	68	SM	Rautenbach et al. 1993
C. bemmeleni	Kenya	48	54	SM	Nagorsen et al. 1975
C. bivittatus	Kenya	48	54?	SM	Peterson & Nagorsen 1975
C. chapini	Namibia, Zimbabwe	48	64	ST	Rautenbach et al. 1993
C. nigeriae	Namibia, Zimbabwe	48	62	SM	Rautenbach et al. 1993
C. plicatus	Thailand	48	54	SM	Tsuchiya et al. 1979
	Borneo	48	54	SM	Harada & Kobayashi 1980
	Thailand	48	54	SM	Harada et al. 1982
C. pumilus	Kenya, Uganda	48	58	M	Đulić & Mutere 1973
	Zimbabwe	48	54?	SM	Peterson & Nagorsen 1975
	Cameroun, Somalia	48	58	SM	Smith et al. 1986
		48	66	M	Rautenbach et al. 1993
Cynomops abrasus	Peru	34	60	ST	Warner et al. 1974
	Peru	34	60	ST	Gardner 1977
	Brazil	34	64	SM	Morielle-Versute et al. 1996
C. greenhalli	Venezuela	34	56	M	Linares & Kiblisky 1969
	Trinidad	34	60	ST	Baker 1970
	Trinidad, Costa Rica	34	60	ST	Warner et al. 1974
	Mexico, Costa Rica	34	60	ST	Gardner 1977
C. planirostris	Brazil	34	60	SM	Leite-Silva et al. 2003
Eumops ater	Mexico, Trinidad	48	58	SM	Warner et al. 1974
	El Salvador	48	-	-	Baker et al. 1992
	Brazil	48	54	SM	Morielle-Versute & Varella-Garcia 1994
	Brazil	48	54	SM	Morielle-Versute et al. 1996
	Brazil	48	64	SM	Leite-Silva et al. 2003

Table 2. continued

E. auripendulus	Trinidad	42	62	SM	Warner et al. 1974
	Brazil	42	60	A	Varella-Garcia et al. 1989
	Brazil	52	52	A	Trierveiler et al. 2002
E. glaucinus	Colombia	40	64	M	Warner et al. 1974
	Costa Rica, Mexico, Honduras	38	64	SM/A	Warner et al. 1974
	Brazil	40	64	-	Morielle et al. 1988
	Cuba	38?	-	-	Baker et al. 1992
	Brazil	40	64	SM	Morielle-Versute et al.1996
	Brazil	40	64	SM	Finato et al. 2000
	Brazil	40	-	-	Faria & Morielle-Versute 2002
E. perotis	Mexico	48	56	SM	Baker 1970
	South America	48	58	-	Wainberg et al. 1974
	Mexico	48	56	SM	Warner et al. 1974
	Brazil	48	58	SM	Finato et al. 2000, Morielle-Versute et al. 1996
E. underwoodi	USA	48	56	SM	Warner et al. 1974
Molossops temminckii	Colombia	42	52	ST	Gardner 1977
	Brazil	48	68	ST	Morielle-Versute et al. 1996
Molossus aztecus	Mexico, Costa Rica	48	58	SM	Warner et al. 1974
M. molossus	Puerto Rico	48	56	SM	Baker & Lopez 1970
	South and Central America	48	58	SM	Warner et al. 1974
	Cuba, El Salvador	48	-	-	Baker et al. 1992
	Brazil	48	54	M	Freitas et al. 1992
	Brazil	48	54	SM	Morielle-Versute & Varella-Garcia 1994
	Brazil	48	64	SM	Leite-Silva et al. 2003, Morielle-Versute et al. 1996
M.cf. pygmaeus	El Salvador	48	58	SM	Warner et al. 1974
M. rufus	South America	48	-	-	Wainberg et al. 1974
	Brazil	48	64	-	Faria & Morielle-Versute 2002
M. sinaloae	Nicaragua, Honduras	48	58	SM	Warner et al. 1974
Mops brachypterus	Cameroun	48	54	SM	Smith et al. 1986

Table 2. continued

M. condylurus	Uganda	48	56	SM	Đulić & Mutere 1973
	Somalia	48	66	SM	Smith et al. 1986
	South Africa	48	66	SM	Rautenbach et al. 1993
M. demonstrator	Cameroun	48	54	SM	Smith et al. 1986
M. midas	Somalia	48	66	SM	Smith et al. 1986
	South Africa	48	66	SM	Rautenbach et al. 1993
M. mops	Malaysia	48	-	-	Volleth et al. 2002
M. nanulus	Cameroun	48	54	SM	Smith et al. 1986
M. petersoni	Cameroun	48	54	SM	Smith et al. 1986
M. spurrelli	Cameroun	48	64	SM	Smith et al. 1986
M. thersites	Cameroun	48	62	SM	Smith et al. 1986
Mormopterus jugularis	Madagascar	48	54	-	Volleth et al. 2002
M. kalinowskii	Peru	48	56	SM	Warner et al. 1974
M. planiceps	Australia	48	-	-	Volleth et al. 2002
Nyctinomops aurispinosus	Mexico	48	58	SM	Warner et al. 1974
N. femorosaccus	Mexico	48	58	SM	Warner et al. 1974
N. laticaudatus	Mexico	48	58	SM	Warner et al. 1974
	Brazil	48	64	SM	Morielle-Versute et al. 1996
N. macrotis	Mexico	48	56	SM	Baker 1970
	Mexico	48	58	SM	Warner et al. 1974
Otomops martiensseni	Kenya	48	56	M	Đulić & Mutere 1973
	Kenya	48	58	SM	Warner et al. 1974
Platymops setiger	Kenya	48	54	SM	Warner et al. 1974
Promops centralis	Trinidad	48	54	SM	Warner et al. 1974
P. davisoni	Peru	48	58	SM	Warner et al. 1974
P. nasutus	South America	40	54	A	Wainberg 1966
Sauromys petrophilus	Namibia, South Africa	48	62	SM	Rautenbach et al. 1993
Tadarida aegyptiaca	Kenya	48	54	SM	Nagorsen et al. 1975
	Namibia, South Africa	48	68	M	Rautenbach et al. 1993

Table 2. continued

T. brasilensis	USA	48	58	-	Painter 1925
	USA	48	54	SM	Kniazeff et al. 1967
	USA	48	56	SM	Warner et al. 1974
	South America	48	56	-	Baker et al. 1982
	Cuba	48	-	-	Baker et al. 1992
T. fulminans	Zimbabwe	48	54?	M	Peterson & Nagorsen 1975
	South Africa	48	66	M	Rautenbach et al. 1993
T. insignis	Japan	48	54	SM	Ono & Obara 1989
	China	48	58	SM	Zhang 1985
T. teniotis	Yugoslavia	48	76	SM	Đulić & Mrakovčić 1980
	Spain	48	58	ST	Arroyo-Nombela et al. 1986
	Kyrghyzstan	48	60	SM	Zima et al. 1991
	Sichuan, China	48	62	SM	Wu et al. 2004
	Turkey	48	78	SM	Karataş et al. 2006

These genera (except of *Molossus*) were formerly included in the single genus *Tadarida* (cf. Freeman 1981, Legendre 1984, Simmons 2005). In certain species of the genera *Eumops, Molossops*, and *Promops*, the lowered diploid number was found, ranging from 34 to 42 chromosomes. Within *Eumops* and *Promops*, species with the standard 48 chromosomes were also found, and different chromosome races were recorded even within single species, *Eumops glaucinus*. The diploid number of 52 chromosomes and only a single large biarmed autosomal pair was reported in *Eumops auripendulus major* from southern Brazil (Trierveiler et al. 2002). Such a complement may be considered ancestral for the molossid bats providing that the autosomal fusions were the source of karyotype differentiation. Morielle-Versute et al. (1996) and Finato et al. (2000) concluded that Robertsonian and tandem fusions, as well as inversions and changes in heterochromatin and nucleolus organizer regions, were the major events in the karyotypic evolution in the molossid bats. The interspecific comparison among G-banded karyotypes revealed extensive homologies between certain species, however, a lesser degree of homology was indicated for instance in *Molossops temmincki* and *Eumops glaucinus* (Morielle-Versute et al. 1996). The Robertsonian variation was reported only for American species and it is possible that it is inherent to only a particular phylogenetic lineage of molossid bats.

Variation in the fundamental number of autosomal arms is occurring because of the varying proportion of uniarmed and biarmed chromosomes in the karyotype. These differences are apparent in the medium sized and small autosomes. Minor variation can be assumed in the centromeric position of certain acrocentric and/or subtelocentric autosomes (Volleth et al. 2002), and/or in the presence or absence of small autosomal arms. These changes can be explained by minor pericentric inversions followed by heterochromatin accumulation in short arms. Nevertheless, we can also suppose that differences in the fundamental number of autosomal arms might originate artificially because of the difficult assessment of the centromeric position in acrocentric autosomes. Currently, there is no unequivocal phylogenetic signal that could be derived from this kind of chromosomal variation. Similar differences can be recorded in the centromere position in the sex X chromosome that is reported as acrocentric, subtelocentric, submetacentric, or metacentric. The true nature of this variation is not clear, and difficulties in identification of the X chromosome in conventionally stained karyotypes should be taken into consideration in this respect.

It is difficult to compare directly the published data on banded karyotypes because the resolution level of staining in chromosomes seems considerably different in respective studies, and this apparently does not allow any precise assessment of chromosomal homology. It will be desirable to study longitudinally differentiated chromosomes in order to unravel the possible cryptic chromosomal variation within the family Molossidae.

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