

THE KARYOTYPE OF *Ateles paniscus paniscus* (CEBIDAE, PRIMATES): $2n = 32$

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ABSTRACT

In the present paper we report the karyotype of *Ateles paniscus paniscus*. Four animals from the borders of the Jari and Uatumã rivers, Brazilian Amazon region, presented $2n = 32$ and $FN = 31$. In a review of cytogenetic data about *Ateles*, Kunkel *et al.* (*Int. J. Primatol.* 1: 223-232, 1980) demonstrated that *A. belzebuth belzebuth*, *A. b. hybridus*, *A. fusciceps robustus*, *A. geoffroyi geoffroyi* and *A. paniscus chamek* have $2n = 34$ and $FN = 33$, and that there are differences among taxonomic groups due to inversions. The reduction in chromosome number detected in *A. p. paniscus* is due to fusion between chromosomes 4 and 12. By comparing the above karyotypes, it can be seen that the *Ateles* populations that are geographically closest are also karyotypically closest, in contrast to the classification proposed by Kellog and Goldman (*Proc. United States Nat. Museum* 96: 1-45, 1944).

INTRODUCTION

The genus *Ateles* (Cebidae, Platyrrhini) comprises the primates known as spider monkeys. The most widely accepted classification at the species and subspecies level for this genus is that proposed by Kellog and Goldman (1944). The species *Ateles geoffroyi* (with 9 subspecies) inhabits Central America and the species *A. paniscus* (with 2 subspecies), *A. belzebuth* (with 3 subspecies) and *A. fusciceps* (with 2 subspecies) live in South America. The classification of Kellog and Goldman (1944) was complemented with additional information provided by Hershkovitz (1949) and Heltne and Kunkel (1975). This classification provides a good explanation for the

differences in coat color among *Ateles* specimens, even though Hershkovitz (1972), Hernandez-Camacho and Cooper (1976) and others consider *Ateles* to be a single species. In disagreement with the hypothesis of a single species, Mittermeier and Coimbra-Filho (1981) emphasize the occurrence of sympatry between *A. geoffroy panamensis* and *A. fusciceps rufiventris* with a zone of strict hybridization, suggesting that these are actually distinct species.

The weak point in the classification of Kellog and Goldman (1944) lies in the geographic distribution of the species *A. belzebuth* and *A. paniscus* (Mittermeier and Coimbra-Filho, 1981). The subspecies of *A. belzebuth* (*A. b. belzebuth* and *A. b. marginatus*) are widely separated geographically though they are very close to the subspecies of *A. paniscus* (*A. p. chamek* and *A. p. paniscus*, respectively). On this basis, Thorington (1976) suggested that *A. b. belzebuth* is taxonomically closer to *A. p. chamek* and that *A. b. marginatus* is taxonomically closer to *A. p. paniscus*.

Cytogenetic analysis can be a very useful tool for the clarification of the taxonomic relationships in *Ateles* (Konstant *et al.*, 1985). Studies using standard staining have demonstrated $2n = 34$ and $FN = 33$, the autosomes consisting of 12 metacentrics, 18 submetacentrics and 2 acrocentrics. In all animals studied, the X chromosome was a metacentric but the Y chromosome was either acrocentric or submetacentric (Bender and Mettler, 1958; Chu and Bender, 1961; Bender and Chu, 1963; Egozcue and Hagemenas, 1967; Hsu and Benirschke, 1968; Egozcue *et al.*, 1969; De Boer, 1974). Chromosomal variations have been observed but the lack of banding and the classification errors concerning the animals analyzed (Kunkel *et al.*, 1980) have impaired the cytotaxonomic interpretation of these data.

Using G banding, Garcia *et al.* (1975) analyzed a male and two females of *A. geoffroyi*. Benirschke (1975) described the G-banding idiogram of *A. paniscus belzebuth* and *A. p. robustus* from Colombia. These species are not included in the classification currently accepted for *Ateles*. On the basis of the site of specimen collection and of the G-banding pattern described by Benirschke (1975), Kunkel *et al.* (1980) assume that these species correspond to *A. belzebuth hybridus* and *A. fusciceps rufiventris*, respectively. Kunkel *et al.* (1980) described the G-banding pattern of *A. p. chamek* (3 males and 3 females), *A. b. belzebuth* (1 male and 1 female), *A. b. hybridus* (1 female), *A. geoffroyi* (1 male and 5 females), and *A. f. rufiventris* (2 males and 4 females). All of these *Ateles* specimens had $2n = 34$ and $FN = 33$, with intra- and intertaxon differences due to chromosome inversions. The conclusion reached by Kunkel *et al.* (1980) was that the intertaxon differences support the taxonomy proposed by Kellog and Goldman (1944) but the intrataxon differences support the hypothesis of a single species, with the consequent impossibility of accepting either one of the two hypotheses.

In the present study we describe the karyotype of *A. paniscus paniscus* and compare it with those previously described in the literature.

MATERIAL AND METHODS

Two specimens (a male and a female) of the genus *Ateles* were collected from the borders of the Jari river (0°32'S; 52°40'W) and two (a male and a female) from the borders of the Uatumã river in the region of the Hydroelectric Plant of Balbina (1°54'S; 59°28'W). On the basis of coat color and geographic distribution, these specimens belong to the species *Ateles paniscus*, subspecies *A. p. paniscus* (Kellog and Goldman, 1944).

Blood (3 ml) was collected by femoral puncture with heparinized syringes and chromosome preparations were obtained by the culture method of Moorhead *et al.* (1960). G bands were obtained by the technique of Scheres (1972), C bands by the technique of Sumner (1972), and NOR bands by the technique of Howell and Black (1980).

Karyotypes were mounted by arranging the chromosomes in the order proposed by Kunkel *et al.* (1980). The fundamental number (FN) was obtained by considering the total number of chromosome arms in an autosomal haploid lot plus an X chromosome.

The phenogram of the *Ateles* species was mounted with the aid of a Microtax program (Sandro and Charles Bonatto, 1984, Porto Alegre, RS, Brazil) using the mean taxonomic distance as a coefficient of similarity and the UPGMA as a cluster method.

RESULTS AND DISCUSSION

The specimens analyzed had $2n = 32$ and $FN = 31$, with 14 biarmed autosomes and 1 acrocentric pair. The X chromosome is metacentric and the Y acrocentric. Pair no. 8 presents a sharp secondary constriction. When compared with the karyotypes of other *Ateles*, the present karyotype shows a reduction in chromosome number as well as a large pair of metacentric chromosomes unlike any observed in other *Ateles* animals.

Comparison of the G-banding patterns of *A. p. paniscus* with those of previously described *Ateles* karyotypes shows that the reduction in diploid number is due to a fusion between chromosomes 4 and 12 in the numeration of Kunkel *et al.* (1980) (Figure 1). This fusion gave origin to a metacentric pair specifically found in *A. p. paniscus*, the short arm and part of the long arm of this metacentric corresponding to chromosome 4 and the remaining part of the long arm to chromosome 12. A G-positive band was observed on the distal half of the arm of the Y chromosome.

The difference in diploid number between *A. p. paniscus* and *A. p. chamek* strongly suggests that these are different taxa. On the basis of skull morphology and facial pattern, Froelich *et al.* (1987) suggested that *A. b. belzebuth*, *A. p. chamek* and *A. b. marginatus* form a circular species with clinal variation between taxa, with *A. p.*

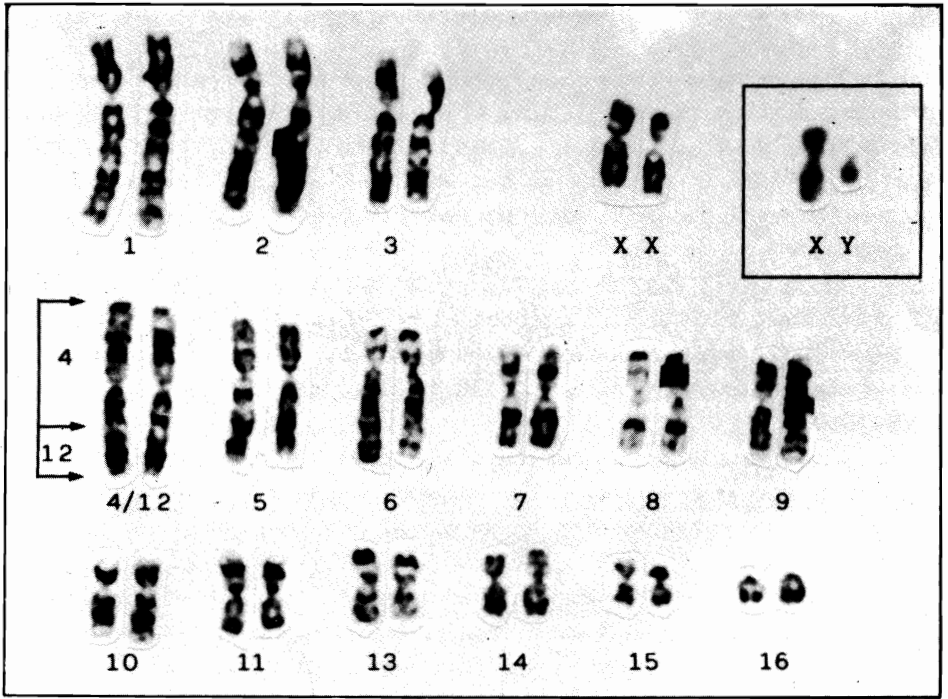


Figure 1 - G-banding pattern of *Ateles paniscus paniscus*. The X and Y chromosomes appear in the square inset.

paniscus forming a separate group. The cytogenetic data described here are consistent with this interpretation.

As shown in Figure 2, all chromosomes have a centromeric C-banding pattern. In addition, chromosomes 3, 6, 8, 11 and 14 have telomeric bands and chromosomes 3, 5 and 8 have interstitial bands. Pair 15 is fully heterochromatic except at the ends. Chromosome Y is almost fully heterochromatic.

NOR analysis showed that pair 8, with a sharp secondary constriction, is the nucleolar organizer (Figure 3). Silver staining was not observed in any other chromosomes. The presence of this chromosome with a secondary constriction in other *Ateles* animals suggests that this is the NOR-bearing chromosome in the other animals also.

When comparing the karyotypes of the *Ateles* species described in their article, Kunkel *et al.* (1980) detected differences due to pericentric inversions that led to different chromosomal forms, which were designated with different letters. Thus, chromosomes 1, 5, 7, 14 and Y present two forms, "a" and "b", for the autosomes and "a" and "s" for the Y. Chromosome 6 has four forms (a, b, c, d). These data are summarized in Table I together with those described here for *A. p. paniscus*. These

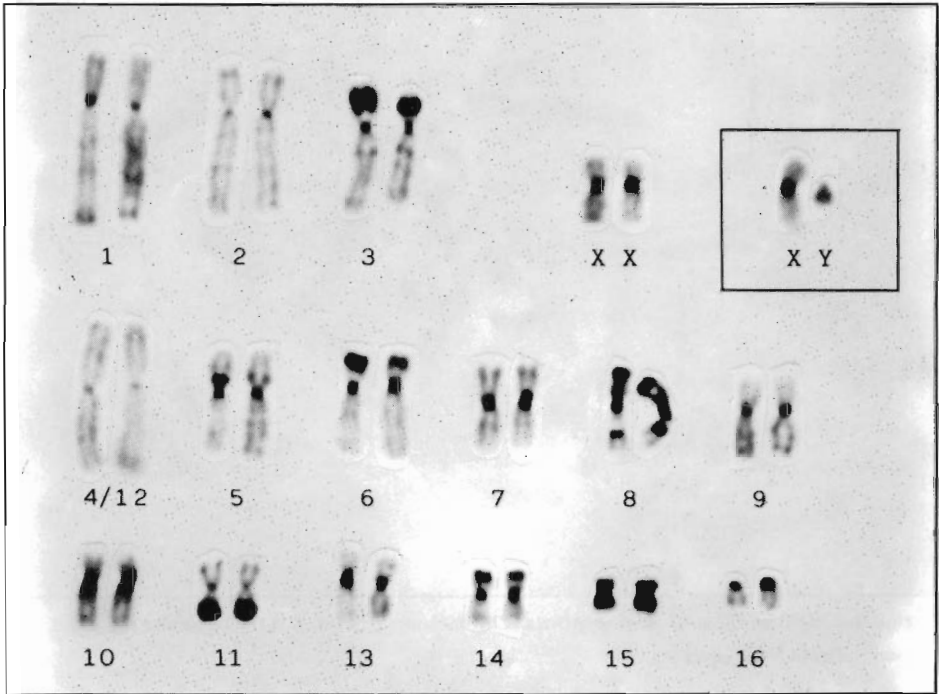


Figure 2 - C-banding pattern of *A. p. paniscus*. The X and Y chromosome appear in the square inset.

cytogenetic data were transformed into a data matrix which was analyzed by the Microtax program (see Material and Methods). In the construction of this matrix we did not consider the “a” forms of chromosomes 1 and 14 because they are shared by all taxa and therefore do not represent diagnostic traits. We also disregarded the morphological variation of chromosome Y since, considering that the largest portion of chromosome Y is heterochromatic and that the region of pairing with the X is small, probably corresponding to the terminal regions, inversion may easily occur and be maintained in the population, thus possibly occurring several times in an independent manner in the various populations. This analysis was used to construct a phenogram (Figure 4) with a cophenetic correlation coefficient of 0.794223061. It is interesting to note in this phenogram that *A. p. paniscus*, *A. p. chamek* and *A. b. belzebuth* form a grouping, whereas *A. f. rufiventris*, *A. geoffroyi* and *A. b. hybridus* form a separate group. It should be pointed out that:

– *A. b. hybridus* is very close to *A. geoffroyi* and was separated from *A. b. belzebuth*.

– *A. p. chamek* is closer to *A. b. belzebuth* than to *A. p. paniscus*.



Figure 3 - NOR labelling of *A. p. paniscus*. Chromosome pair no. 8 is the nucleolar organizer. The arrows indicate NOR silver staining.

Table I - Summary of the cytogenetic information obtained by G-banding for the genus *Ateles*. The letters below chromosomes 1, 5, 6, 7 and 14 refer to the chromosome forms described by Kunkel *et al.* (1980). Chromosome 4/12: a) separate chromosomes; b) fused chromosome. Y: s = submetacentric; a = acrocentric.

Species	Chromosomes							Reference
	1	5	6	7	4/12	14	Y	
<i>Ateles geoffroyi</i>	a	a	c	b	a	a	s	Kunkel <i>et al.</i> , 1980
<i>Ateles geoffroyi</i>	a,b	a	c	b	a	a,b	s	Garcia <i>et al.</i> , 1975
<i>Ateles fusciceps rufiventris</i>	a	b	d	b	a	a	s	Kunkel <i>et al.</i> , 1980
<i>Ateles fusciceps rufiventris</i>	a	b	d	b	a	a	s	Benirshke, 1975
<i>Ateles belzebuth hybridus</i>	a	a	a	b	a	a	?	Kunkel <i>et al.</i> , 1980
<i>Ateles belzebuth hybridus</i>	a,b	a	a	b	a	a	s	Benirshke, 1975
<i>Ateles belzebuth belzebuth</i>	a	a	c,d	a	a	a	a	Kunkel <i>et al.</i> , 1980
<i>Ateles paniscus chamek</i>	a	a	b	a	a	a	s	Kunkel <i>et al.</i> , 1980
<i>Ateles paniscus paniscus</i>	a	a	a	a	b	a	a	This study

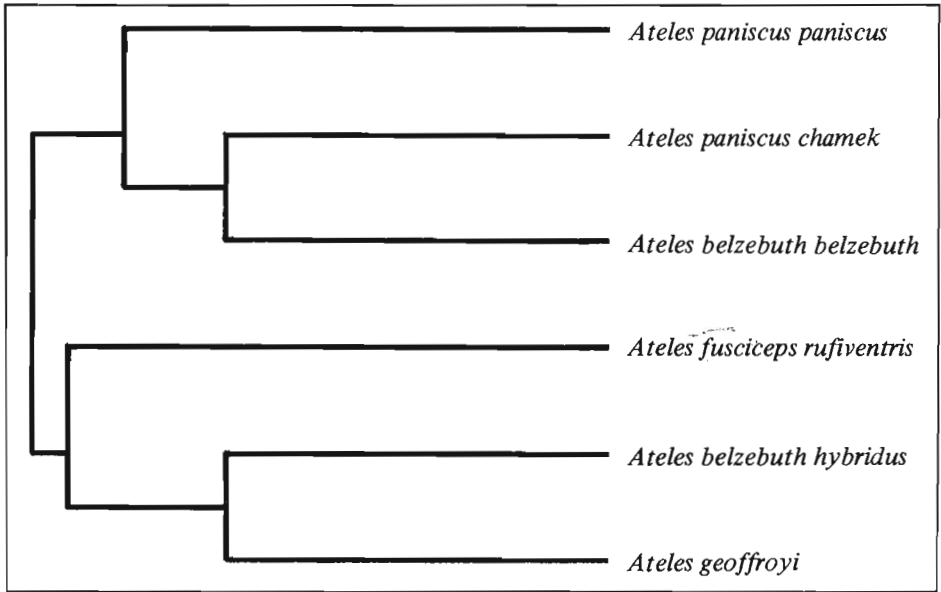


Figure 4 - Phenogram for the *Ateles* species and subspecies which have been studied cytogenetically thus far.

These data disagree with the classification of Kellog and Goldman (1944) but are consistent with the geographic distribution of the taxa, with one group located in Central America and Northeastern South America and the other in the Amazon basin.

Froelich *et al.* (personal communication), in a study of morphometric skull traits, obtained a similar phenogram except that *A. paniscus paniscus* forms an isolated branch which became separated before the differentiation between the Central American group and the Amazon basin group.

The suggestions proposed here require more in-depth analysis using a larger sample of the *Ateles* species studied thus far, as well as a cytogenetic study of *A. b. marginatus* and the study of other genetic markers such as enzymes and blood groups and of morphological traits in order to test these hypotheses.

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RESUMO

No presente trabalho é apresentado o cariótipo de *Ateles paniscus paniscus*. Foram analisados quatro animais provenientes das margens do rio Jari e do rio Uatumã, na Amazônia brasileira. Os exemplares apresentam $2n = 32$ e $NF = 31$. Kunkel et al. (*Int. J. Primatology* 1 (3): 223-232, 1980) revisaram os dados citogenéticos em *Ateles* e demonstraram que *A. belzebuth belzebuth*, *A. b. hybridus*, *A. fusciceps robustus*, *A. geoffroyi geoffroyi* e *A. paniscus chamek* apresentam $2n = 34$ e $NF = 33$, havendo diferenças entre grupos taxonômicos devido a inversões. A redução no número cromossômico em *A. p. paniscus* deve-se a uma fusão entre os cromossomos 4 e 12. Comparando os cariótipos acima citados, observa-se que os *Ateles* mais próximos geograficamente também o são cariotipicamente, contrariando a classificação de Kellog and Goldman (*Proc. of the United States Nat. Museum* 96: 1-45, 1944).

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