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REG NORMAL **Copy** **Journal**

TITLE:	CYTOGENETICS
PUBLISHER/PLACE:	Karger Basel :
VOLUME/PAGES:	1969;8(3):199-208 199-208
DATE:	1969
AUTHOR OF ARTICLE:	Arrighi FE;Sorenson MW;Shirley LR
TITLE OF ARTICLE:	CHROMOSOMES OF THE TREE SHREWS (TUPAIIDAE).
ISSN:	0011-4537
OTHER NUMBERS/LETTERS:	NLM Unique ID: 0367734 39576111 5802537
SOURCE:	PubMed
MAX COST:	$0.00
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Cytogenetics *8:* 199–208 (1969)

Chromosomes of the tree shrews (Tupaiidae)[1]

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Abstract. Chromosomes from seven species of Tupaiidae, including *Tupaia glis*, *T. chinensis*, *T. longipes*, *T. montana*, *T. minor*, *T. palawanensis* and *Urogale everetti*, were analyzed. The diploid number varied from 68 for *T. montana* to 44 for *U. everetti*. *T. glis* and *longipes* had identical karyotypes and diploid numbers (2n = 60). *T. minor* had a diploid number of 66, and *palawanensis* had one of 52. The number of biarmed chromosomes per cell varied considerably among the species studied.

Introduction

The tree shrews (family Tupaiidae) hold a unique position in mammalian phylogeny. Some taxonomists favor grouping these animals with the insectivores, and others list them as primitive primates. Difficulty has also been encountered in identifying several species within the genus *Tupaia*. This family is, therefore, of special interest to a number of biologists.

The present article reports the karyological data of seven species of Tupaiidae. This information should be useful in evaluating the relationships of the members within this family as well as their relationships with the insectivores and primates.

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[1] Supported in part by Research Grants DRG-269 from the Damon Runyon Memorial Fund for Cancer Research and GB-6657 from the National Science Foundation, by the University of Texas M. D. Anderson Hospital and Tumor Institute at Houston and by the Space Sciences Research Center, University of Missouri, Columbia.

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Materials and methods

The specimens of Tupaiidae analyzed in this study were either trapped in the field by CONAWAY and MOCH of the Zoological Department, University of Missouri, Columbia, or obtained from KOFORD of the Zoology Department, University of California, Davis, or purchased from the Rider Animal Company, Brooksville, Florida (Table I). These animals were maintained by the Zoology Department, University of Missouri, until they were sacrificed on January 25 and 26, 1968. All specimens were deposited at the Zoology Department of the University of Missouri.

TABLE I

Collection records

Species	Locality	Collector	Year	Animal No. ♀	Animal No. ♂
Tupaia glis LYON	Near Kuala Lumpur, Malaya	C. B. KOFORD	1965	730	729
T. chinensis LYON	Near Bangkok, Thailand	R. D. RIDER CO.	1967	726, 727	724
T. longipes LYON	Near Tawau, N. Borneo	C. H. CONAWAY	1962	–	728
T. minor LYON	Near Tawau, N. Borneo	C. H. CONAWAY	1964	–	733, 734
T. montana LYON	Mt. Kinabalu, N. Borneo	C. H. CONAWAY	1965	732	731
T. palawanensis LYON	Palawan Is., Philippines	O. B. MOCH	1967	736	735
Urogale everetti LYON	Mindanao Is., Philippines	O. B. MOCH	1965	737	–

Lung tissue was used for initiating cell cultures for cytological preparations. For safety as well as for comparison, in some cases bone marrows were incubated for one hour in a growth medium containing Colcemid, and flame-dried preparations were made immediately thereafter. In some individuals, where lung cultures were not successful, the bone marrow preparations were used for analysis.

Results

Table II presents the chromosomal characteristics of the seven species of Tupaiidae studied. The diploid number varied from 44 for *Urogale everetti* to 68 for *Tupaia montana*. For convenience in comparing the karyological data, marker chromosomes of some species are classified into three groups, designated A, B and C. Group A consists of metacentric and submetacentric chromosomes with low arm ratios; Group B, submetacentrics with high arm ratios; and Group C, acrocentric chromosomes with a distinct secondary constriction near the

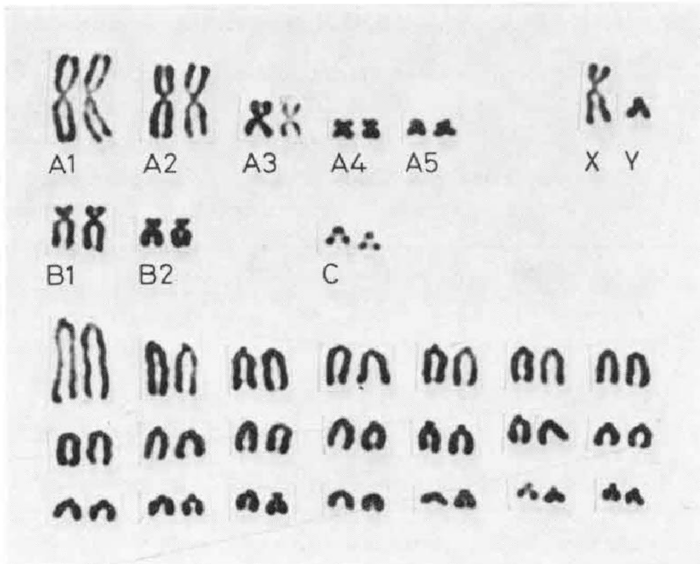

Fig. 1. A complete karyotype of a male *Tupaia glis* from lung culture (2n = 60).

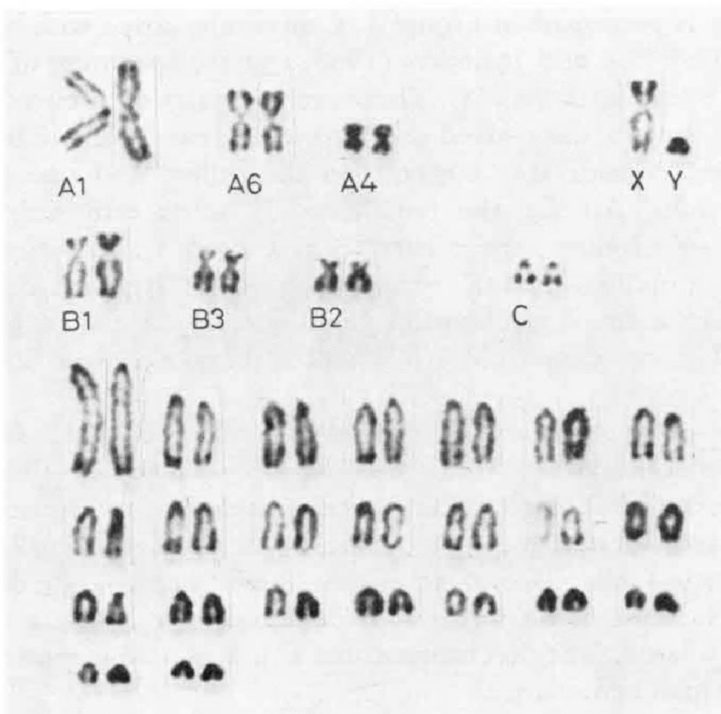

Fig. 2. A complete karyotype of a male *Tupaia chinensis* from lung culture (2n = 62).

TABLE II

Karyological characteristics of the Tupaiidae[1]

Species	No. of specimens ♀	♂	Total	2n	No. of acrocentrics	No. of biarmed chromosomes	No. of arms
Tupaia chinensis LYON	2	1	3	62	48	14	76
T. glis LYON	1	1	2	60	44	16	76
T. longipes LYON		1	1	60	44	16	76
T. minor LYON		2	2	66			
T. montana LYON	1	1	2	68	62	6	74
T. palawanensis LYON	1	1	2	52	30	22	74
Urogale everetti LYON	1		1	44	8	36	80

[1] All computations were based on female karyotype only.

centromere. Each chromosome pair is given a letter and number according to the descending length order within each group.

The diploid number of individuals of *Tupaia glis* is 60. A male karyotype is presented in Figure 1. Our results agree well with those presented by HSU and JOHNSON (1963) and the specimen of CHU (see HSU and BENIRSCHKE, 1968). There are five pairs of A chromosomes, two large, one medium-sized and two small; two pairs of B chromosomes, one considerably larger than the other; and one pair of C chromosomes. Among the remaining 21 acrocentric pairs, one is outstandingly longer; the others form a graded size series without distinct groupings. The X chromosome is a large submetacentric, and the Y, a small acrocentric. Identification of the Y element is equivocal since several pairs of small acrocentrics exhibit the same morphology.

The diploid number and karyotype of a male *T. longipes* are identical with those of individuals of *T. glis*. The diploid number of individuals of *T. chinensis* is 62. A male karyotype is presented in Figure 2. There are three pairs of chromosomes in Group A, two large and one small; three pairs in Group B, one larger than the other two; and one pair in Group C. Among the remaining 23 acrocentric pairs, one is outstandingly large. The X chromosome is a large submetacentric, and the Y, a small acrocentric.

The karyotype of a female of *T. montana* (2n = 68) is shown in Figure 3. Group A consists of only one pair, possibly A6, and Group

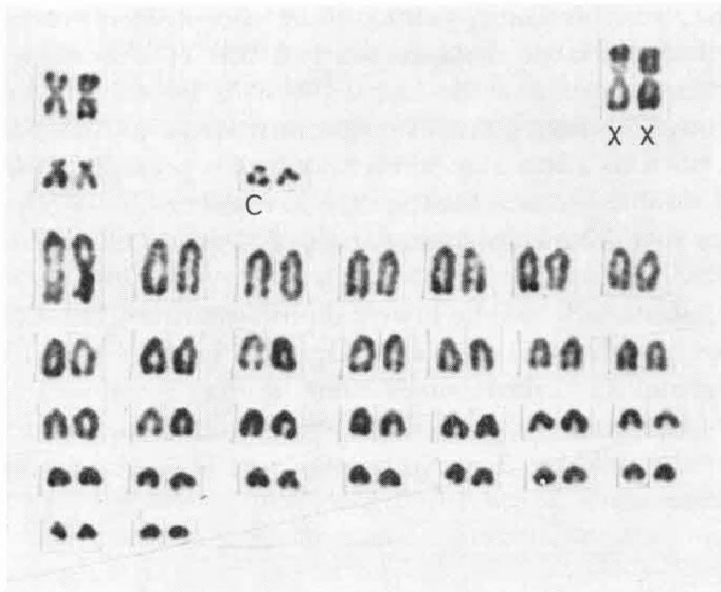

Fig. 3. A complete karyotype of a female *Tupaia montana* from lung culture (2n = 68).

Fig. 4. A complete karyotype of a male *Tupaia palawanensis* from bone marrow culture (2n = 52).

B, one pair, possibly B2. A pair of C chromosomes is present. The X chromosome is a large metacentric, and the Y, a small acrocentric. Again, it is not possible to identify the Y by morphology alone.

Cells from both lung cultures and bone marrow of males of *T. minor* were too poor to allow the construction of a presentable karyotype. However, a reliable count for the diploid number (2n = 66) was made from more than 12 metaphases. A pair of C group chromosomes was present.

Tupaia palawanensis has the lowest diploid number (2n = 52) among the species of this genus so far analyzed (Fig. 4). From 10 cells examined, group C chromosomes were noticeably absent; however, because of the quality of the slides, this observation cannot be considered totally definite. The X chromosome is a submetacentric, and the Y, a minute.

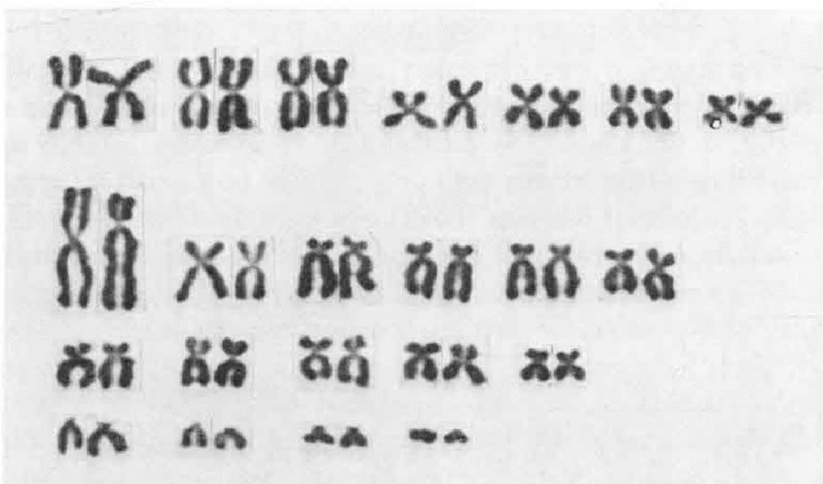

Fig. 5. A complete karyotype of a female *Urogale everetti* from lung culture (2n = 44).

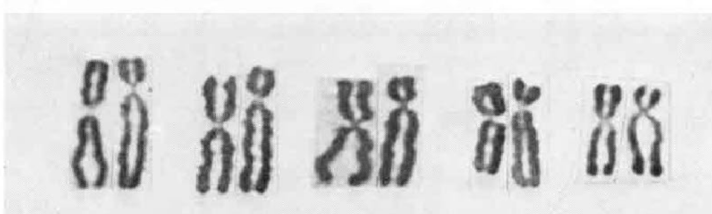

Fig. 6. The largest pair of biarmed chromosomes of *Urogale everetti* taken from five different cells from lung cultures, showing consistent polymorphism. No bone-marrow preparations were made from this animal.

Urogale everetti has a diploid number of 44 (Fig. 5). In this female individual the largest chromosome pair is distinctly polymorphic, one with nearly equal arms, and the other with highly unequal arms. Figure 6 presents five cut-out pairs from different cells to illustrate this heteromorphism. Since the two chromosomes are approximately equal in length, it is assumed that a pericentric inversion has taken place in one of the homologs. The sex chromosomes cannot be cytologically identified in this female specimen, and autoradiographic studies were not performed.

Discussion

Chromosomal differences, including numerical differences, have been found in many natural populations. In human populations, for example, numerous cases of aneuploid individuals have been reported. Thus, chromosomal difference itself does not constitute a strong basis for separation of species or subspecies. However, if other morphological, anatomical or physiological criteria have already suggested a distinction between two taxa, then a consistent cytological difference would certainly substantiate such a conclusion, even though the cytological data alone do not warrant a change of status, say, from subspecies to species or *vice versa*.

A few recently described examples illustrate the above-mentioned principle. The golden mouse, for example, has been placed in the genus *Peromyscus* as a monotypic subgenus *Ochrotomys*. However, a number of mammalogists consider *Ochrotomys nuttalli* as remotely related to *Peromyscus* as some other genera, such as *Baiomys* and *Reithrodontomys*, so that a promotion from a subgenus to a genus status was suggested. All species of *Peromyscus* so far studied have a diploid number of 48 (HSU and ARRIGHI, 1968), but PATTON and HSU (1967) found that *Ochrotomys* had one of 52.

Within the genus *Peromyscus*, HSU and ARRIGHI (1968) found that cytological characteristics distinctly suggest two separate species for *P. truei*. This suggestion supports the conclusion of HOFFMEISTER (1951) from morphological studies.

Several previous reports on the chromosomes of *Tupaia* do not agree with one another. HSU and JOHNSON (1963) reported a diploid number of 60 from a single female, *T. glis*. BENDER and CHU (1963) also reported 60 as the diploid number for this species. However, KLINGER (1963) and EGOZCUE *et al.* (1968) found that *T. glis* had a diploid number of 62. More recently, BORGAONKAR (1967) listed 62 as the diploid number for *T. chinensis*. From the present study it is clear that those with a diploid number of 60 should either be *glis* or *longipes* and those with 62 should be *chinensis*. From the karyotypes presented by KLINGER and by EGOZCUE *et al.*, their specimens were probably *chinensis*.

Although certain recent authors have reduced the number of species and genera of tree shrews (CHASEN and KLOSS, 1931; FIEDLER, 1956;

a *b* *c*

Fig. 7. Photographs of three species of Tupaiidae. *a. Tupaia longipes. b. Tupaia chinensis. c. Tupaia minor.*

DAVIS, 1962; MEDWAY, 1965), the fact remains that an actual examination of all but one species has not been made since the work of LYON in 1913. LYON described *T. glis*, *T. chinensis* and *T. longipes* as discrete species. His decisions were based on methods of classical taxonomists, *e.g.*, the number of mammae (*T. glis* has four, *T. chinensis* and *T. longipes* have six) and distribution of animals. *T. glis* is native to the South Malay Peninsula, Sumatra and adjacent islands. *T. chinensis* occurs on the China mainland from near the Bramaputra river to as far east as Tonkin. *T. longipes* is restricted to Borneo. None of these species overalp. Figure 7 shows three species of Tupaiidae.

Until a critical re-examination of the tupaiids is made, LYON's opinions cannot be discounted. Moreover, observations on the social behavior of individuals of the above groups show distinct species differences (SORENSON and CONAWAY, 1966).

A visual inspection of the karyotypes of individuals of *T. glis* (Fig. 1) and *T. chinensis* (Fig. 2) should readily reveal that the differences cannot be explained by Robertsonian translocations alone. However, from *T. montana* ($2n = 68$) to *U. everetti* ($2n = 44$), the Robertsonian process definitely played a significant role because the number of biarmed elements increased and the diploid number decreased. The lack of intermediate forms prevents us from making interpretations beyond saying that both translocation and pericentric inversions might have occurred.

The small acrocentrics with secondary constrictions (Group C) are interesting. This pair of chromosomes was found in *glis*, *chinensis*, *longipes*, *montana* and *minor*. A pair of chromosomes with similar morphology was found in several species of lemurs, most of which contain diploid numbers in the same range as Tupaiidae (CHU and BENDER, 1962; CHU, personal communication; EGOZCUE, 1967). Whether these are homologous is, of course, not known. It is also an interesting observation that this pair of chromosomes was not observed in individuals of *T. palawanensis* and *U. everetti*.

Acknowledgements

The authors wish to thank Dr. T. C. HSU for his continued interest in this study and his assistance in many ways. Acknowledgement is also extended to Dr. C. H. CONAWAY and Mr. O. B. MOCH of the Zoology Department, University of Missouri, Columbia, and Dr. C. B. KOFORD, presently at the University of California, Davis, for their help in procuring the animals.

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Manuscript received 22 August 1968; accepted for publication 26 November 1968.