

Banded chromosomes of *Sorex daphaenodon* : a comparison with *S. araneus* (Mammalia, Insectivora)

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**Banded chromosomes of *Sorex daphaenodon*:
A comparison with *S. araneus*
(Mammalia, Insectivora)**

BY

J. ZIMA¹

Summary.—ZIMA J., 1991. Banded chromosomes of *Sorex daphaenodon*: A comparison with *S. araneus* (Mammalia, Insectivora). *In*: J. HAUSSER, ed. The cytogenetics of the *Sorex araneus* group and related topics. Proceedings of the ISACC's Second International Meeting. *Mém. Soc. vaud. Sc. nat.* 19.1: 119-124.

The chromosome number found in the karyotype of a female of *Sorex daphaenodon* was $2n = 28$. The complement consisted of twenty-six autosomes and two sex chromosomes ($NFa = 42$). Three pairs of large submetacentric autosomes, one pair of medium-sized submetacentric autosomes, five pairs of small acrocentric autosomes, four pairs of small biarmed autosomes, and two large metacentric X chromosomes were found in the set. The analysis of the G-band chromosome pattern showed that the large and medium-sized submetacentric autosomes were composed of the common shrew arms *af*, *bh*, *cg*, and *lm*. An equivalent of the common shrew biarmed chromosome *tu* was also present, as well as acrocentrics corresponding to the chromosome arms *i*, *j*, *k*, *n*, *r*. The banding pattern of the other small biarmed autosomes suggested their possible origin by inversion or centromere shift from the common shrew arms *o*, *p*, *q*. The X sex chromosomes were very similar to those of *S. araneus*. Thus, the comparison of *S. daphaenodon* and *S. araneus* karyotypes indicates an extensive homology of their chromosome banding pattern.

Résumé.— ZIMA J., 1991. Chromosomes de *Sorex daphaenodon* par la technique des bandes G: Une comparaison avec *S. araneus* (Mammalia, Insectivora). *In*: J. HAUSSER, dir. The cytogenetics of the *Sorex araneus* group and related topics. Proceedings of the ISACC's Second International Meeting. *Mém. Soc. vaud. Sc. nat.* 19.1: 119-124.

Un nombre diploïde de 28 a été trouvé dans le caryotype de la femelle de *Sorex daphaenodon*. La garniture présente vingt-six autosomes et deux chromosomes

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sexuels (NFa = 42). Le caryotype est composé de trois paires de grands autosomes submétacentriques, d'une paire d'autosomes submétacentriques assez grands, de cinq paires de petits autosomes acrocentriques, de quatre paires de petits autosomes métacentriques et de deux grands chromosomes X métacentriques. L'analyse des bandes G a montré que les submétacentriques grands et moyens recombinaient les bras *S. araneus* pour former les combinaisons *af*, *bh*, *cg*, et *lm*. On a constaté la présence de l'équivalent du petit chromosome métacentrique *tu* de *S. araneus* ainsi que des éléments acrocentriques correspondant aux bras *i*, *j*, *k*, *n* et *r*. Les bandes des petits autosomes métacentriques témoignent de la possibilité de leur dérivation des bras de *S. araneus* *o*, *p* et *q* par les inversions péricentriques ou par des déplacements centriques. Les chromosomes sexuels de *S. daphaenodon* sont très semblables à ceux de *S. araneus*. La comparaison des caryotypes de *S. daphaenodon* et de *S. araneus* montre donc une homologie considérable au niveau des bandes G.

INTRODUCTION

The large-toothed shrew, *Sorex daphaenodon* Thomas, 1907, is an Asiatic species distributed primarily in Siberia, from east of the Urals to the Kolyma river (CORBET 1978, see also Fig. 1). FEDYK and IVANITSKAYA (1972) studied the karyotype of this species for the first time, and revealed the presence of the XY₁Y₂ sex chromosome complex in the male. That finding substantiated the inclusion of the large-toothed shrew into the *Sorex araneus* species complex (MEYLAN and HAUSSER 1973, HAUSSER *et al.* 1985). Further chromosomal studies have confirmed previous observations and indicate the existence of karyotypic polytypy between different geographical populations caused by a single autosomal Robertsonian rearrangement (IVANITSKAYA and MALYGIN 1985, IVANITSKAYA *et al.* 1986; see Fig. 1).

In this paper, I shall describe the karyotype of a female obtained in north-eastern Mongolia, and make an attempt to compare the G-banding chromosome pattern of *Sorex daphaenodon* with those of *S. araneus*.

MATERIAL AND METHODS

A female of *Sorex daphaenodon* was live-trapped in north-eastern Mongolia (Chentei region, Dadal Sum village, 112° 30' E; 49° 00' N), and karyotyped in the field by the standard method of direct treatment of the bone marrow and spleen cells. G-banded mitotic preparations were obtained by a trypsin technique as described by RADJABLI and KRYUKOVA (1973). The specimen studied is preserved as a skull and skin in the collection of the Institute of Systematic and Ecological biology, Czechoslovak Academy of Sciences, in Brno.

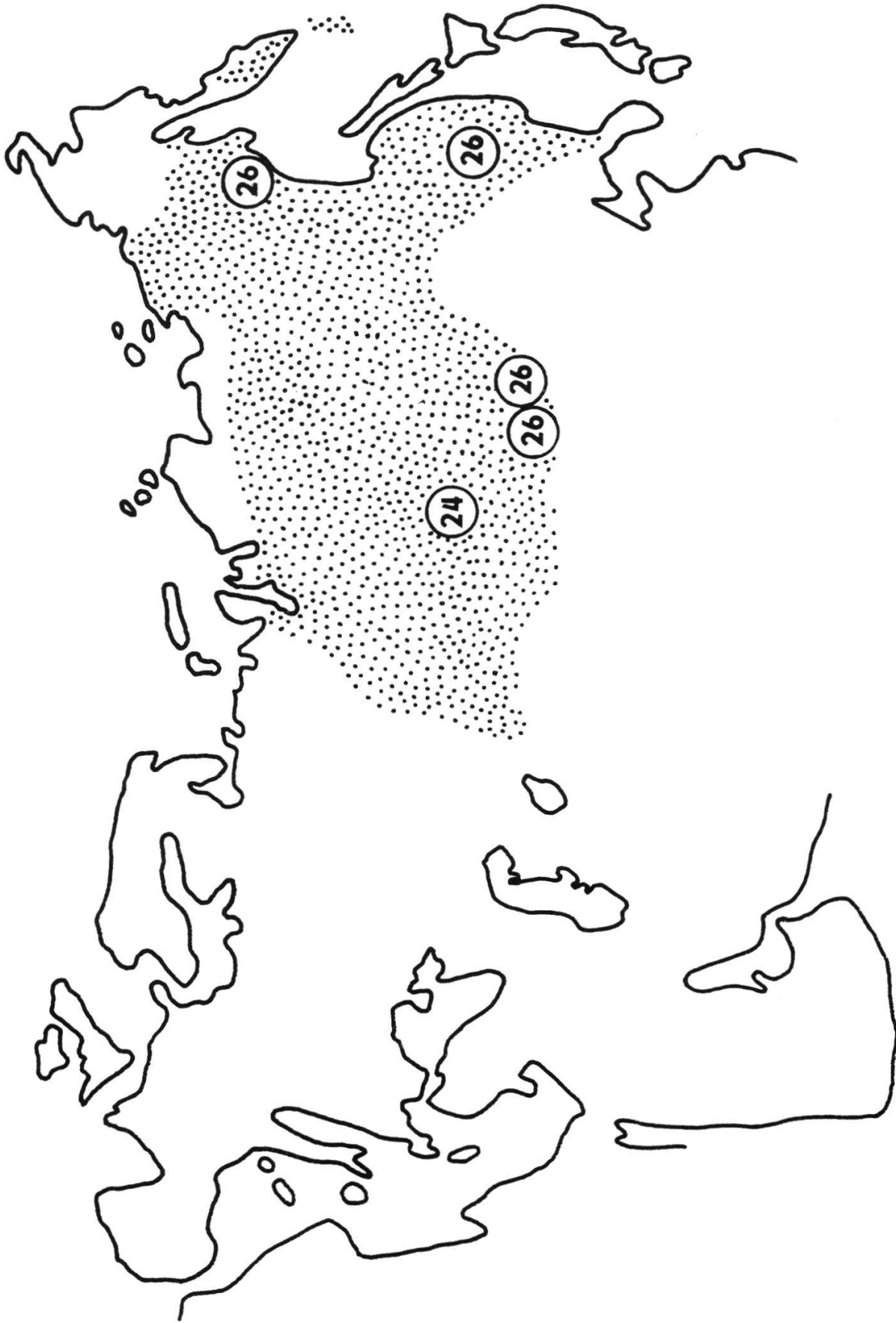


Figure 1.—The distribution of *Sorex daphaenodon* (according to CORBET 1978), and the variation in autosome number. Data (from left to right) from FEDYK and IVANITSKAYA (1972), IVANITSKAYA and MALYGIN (1985), this paper, IVANITSKAYA *et al.* (1986).

RESULTS AND DISCUSSION

The chromosome number in the female studied was $2N = 28$. The karyotype is illustrated in Fig. 2 A. The chromosome complement consisted of one pair of large metacentrics, three pairs of large submetacentrics (N°1, 2, 3), one pair of medium-sized submetacentrics (N° 4), five pairs of small acrocentrics (N°5, 6, 7, 8, 10), and four pairs of small biarmed elements (N° 9, 11, 12, 13). In accordance to published data (FEDYK and IVANITSKAYA 1972, IVANITSKAYA *et al.* 1986), and after an assessment of the banding pattern, the large metacentric pair was identified as the X sex chromosomes. Short arms were clearly visible in all acrocentric autosomes. Conspicuous short arms, resembling satellites by their faint staining, were observed on the acrocentric pair N° 5. The biarmed pair N° 9 could be evaluated as submetacentric, while the other small biarmed pairs were metacentric. The same karyotype with 26 autosomes was found in *Sorex daphaenodon* from a locality north of Ulan Bator in Mongolia (IVANITSKAYA and MALYGIN 1985), in the vicinity of the Evoron lake in Chabarovsk region in the Far East, and in the Magadan region in north-eastern Asia (IVANITSKAYA *et al.* 1986). A karyotype containing only 24 autosomes was ascertained in Krasnoyarsk region by FEDYK and IVANITSKAYA (1972). The geographical distribution of these populations is shown in Fig. 1. The difference between the two karyomorphs described is apparently the result of a Robertsonian translocation. Two of large acrocentric pairs are presumably involved in this rearrangement.

The G-band karyotype of *Sorex daphaenodon* is shown in Fig. 2 B, C. The quality of G-banding did not allow a high resolution chromosome analysis, and certain minor changes might remain undetected in comparison with the *S. araneus* karyotype. The banding pattern in the large and medium-sized biarmed autosomes of *S. daphaenodon* has great similarity to the *S. araneus* arms *af* (chromosome N° 1), *bh* (N° 2), *cg* (N° 3), and *lm* (N° 4). The long arm of the acrocentric N° 5 was identical to the arm *j* of *S. araneus*, but the homology of the short satellited arm was not ascertained. The other acrocentric pairs resembled the *S. araneus* arms *i* (N° 6), *k* (N° 7), *n* (N° 8), and *r* (N° 10). The metacentric N° 11 corresponded to the *tu* chromosome of *S. araneus*. The homology of biarmed autosomes N° 9, 12 and 13 could not be exactly determined, but their origin from *S. araneus* arms *o*, *p*, and *q* by inversions and/or centromeric shifts is a tentative possibility.

VOLOBOUEV (1989) proposed that Robertsonian translocations, centromere-telomere translocations and centromeric shifts are the most important types of chromosomal rearrangement in the karyotypic evolution of the species of *Sorex araneus* complex. The evolutionary divergence of karyotypes of *Sorex daphaenodon* and *S. araneus* can readily be explained by these types of chromosome change. The presence of the *af* fusion in *Sorex daphaenodon* karyotype indicates the position of this species in a chromosome phylogeny proposed by Volobouev (1989). *Sorex daphaenodon* ought to be part of the lineage leading from a *S. granarius*-like ancestor to the recent species *S. araneus* and *S. coronatus*. The *Sorex daphaenodon* lineage should have diverged after the fusions $a + f$ and $t + u$, and before the fusion $b + c$ had

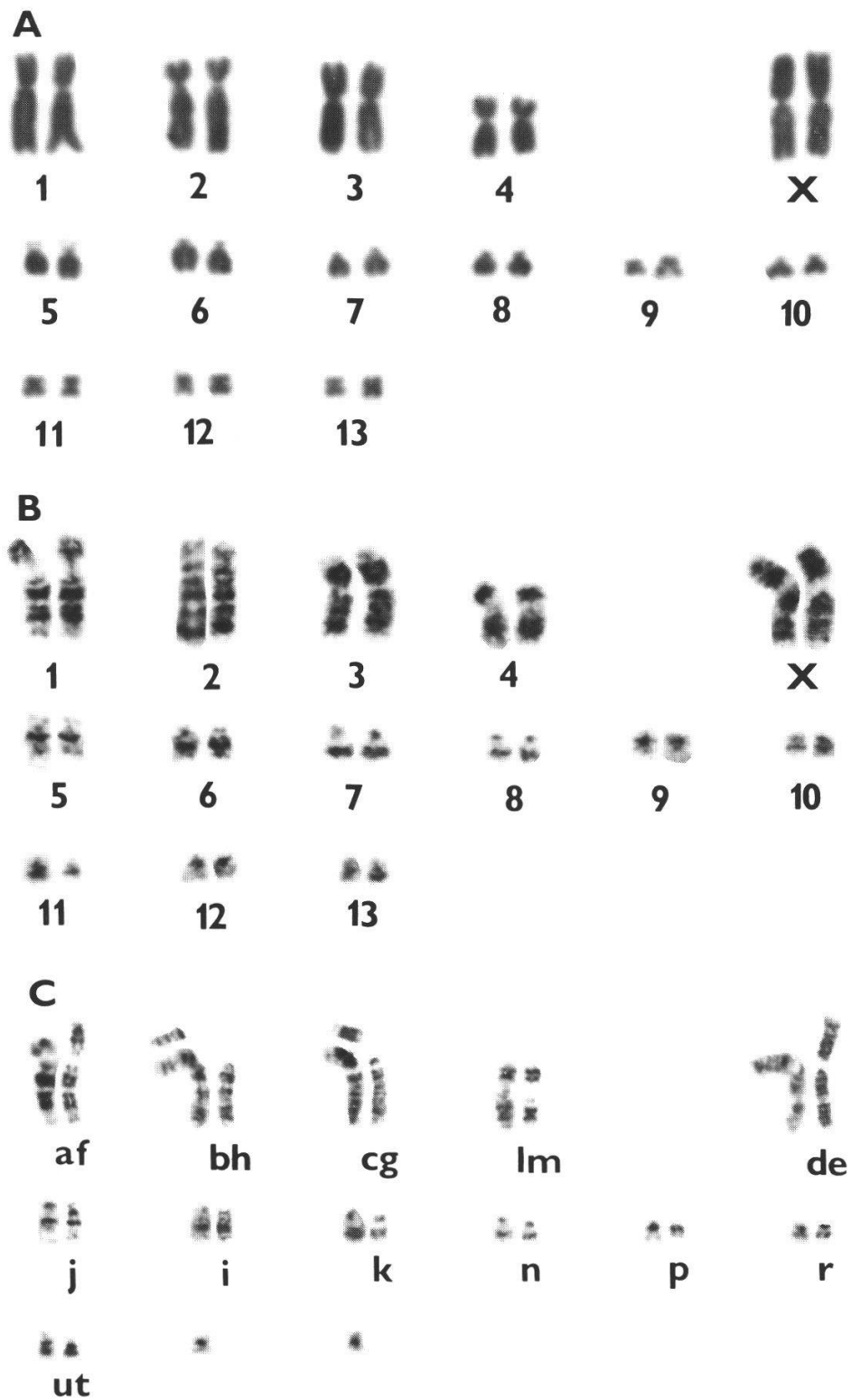


Figure 2.—A: Conventionally stained karyotype of female *Sorex daphaenodon*, B: G-banded karyotype, C: comparison of banded chromosomes from *S. daphaenodon* (left) and *S. araneus* (right).

taken place, i.e. at the same time at which the lineage of *S. coronatus* differentiated. It should be emphasized that the arms *b* and *h*, forming a large submetacentric in *Sorex daphaenodon*, are present as free chromosomes in the *S. coronatus* karyotype.

The comparison of banded karyotypes from *S. daphaenodon* and *S. araneus* provides further confirmation of a direction of karyotype evolution from high to low chromosome numbers, as well as the priority of large arms in entering the Robertsonian fusion process. The proposal of Volobouev (1989) that the *a + f* centric fusion originated in a Central-european population becomes more doubtful considering the recent distribution of *Sorex daphaenodon*. The possibility of parallel and independent evolution of the same karyotype patterns in different areas has to be taken into account, as well. The solution of these problems may, i.a., come from chromosome banding studies in *Sorex caucasicus* and *S. asper*, which remain the last species of the *Sorex araneus* complex with unknown G-band karyotypes.

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