

# A comparison of the chromosome G-banding pattern in two *Sorex* species, *S. satunini* and *S. araneus* (Mammalia, Insectivora)

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## Abstract

The G-banded karyotype of *S. satunini* was compared with the karyotype of *Sorex araneus*. Extensive homology was revealed. The major chromosomal rearrangements involved in the evolutionary divergence of these species have been identified as centric fusions and centromeric shifts. From the known palaeontological age of *S. satunini* it is obvious that the vast chromosomal polymorphism of the *S. araneus* group originated during the middle Pleistocene.

## Keywords

G-banding, common shrew, *Sorex araneus*, *Sorex satunini*, karyotype, phylogeny

## Introduction

Within the genus *Sorex* Linnaeus, 1758, the *Sorex araneus* group includes eight species characterized by the sex chromosome complex  $XY_1Y_2$  (Zima et al. 1998). Some of them were raised to species status on a karyological basis. Two species from this group, the common shrew *Sorex araneus* Linnaeus, 1758 and the Caucasian shrew *S. satunini* Ognev, 1922 can be defined as cryptic species that are virtually impossible to distinguish by morphological (cranial) characters (Sokolov and Tembotov 1989).

The common shrew is widely distributed in Europe and Asia up to as far east as Lake Baikal, and the Caucasian shrew is known to be present in the Caucasus and in

the northern parts of Asia Minor (Sokolov and Tembotov 1989, Bukhnikashvili and Kryštufek 2008). In the North Caucasian plains, this species is contiguous with the common shrew (the chromosomal race *Neroosa*) (Stacheev et al. 2010).

The common shrew displays phenomenal variability of the autosomal complement (Wójcik et al. 2002). The Caucasian shrew is monomorphic and can be reliably identified by means of conventionally stained karyotype (Kozlovsky 1973, Sokolov and Tembotov 1989, Macholán 1996). Macholán (1996) recognized in G-banded metaphases of the *S. satunini* the autosomes *af*, *bc* and *tu*, which are invariantly present in the common shrew karyotype. The presence of these Robertsonian fusions in the *S. satunini* corroborates the findings of Zagorodniuk and Khazan (1996) who described the arm combinations of autosomes *af*, *bc*, *gh*, *ik*, *jn*, *lo*, and *tu* in the karyotype of a single female from Kobi (Georgia).

From the plain between the Kuban and Don rivers we described a new subspecies of the Caucasian shrew *Sorex satunini tembotovi* Orlov, Balakirev, Borisov, 2010 (Orlov et al. 2010) that differs from the subspecies *S. s. armenica* Sokolov et Tembotov, 1989 and *S. s. stavropolica* Sokolov et Tembotov, 1989.

In this study the karyotypes of *S. s. tembotovi* and *S. araneus* (chromosome race Moscow) were examined and compared.

## Material and methods

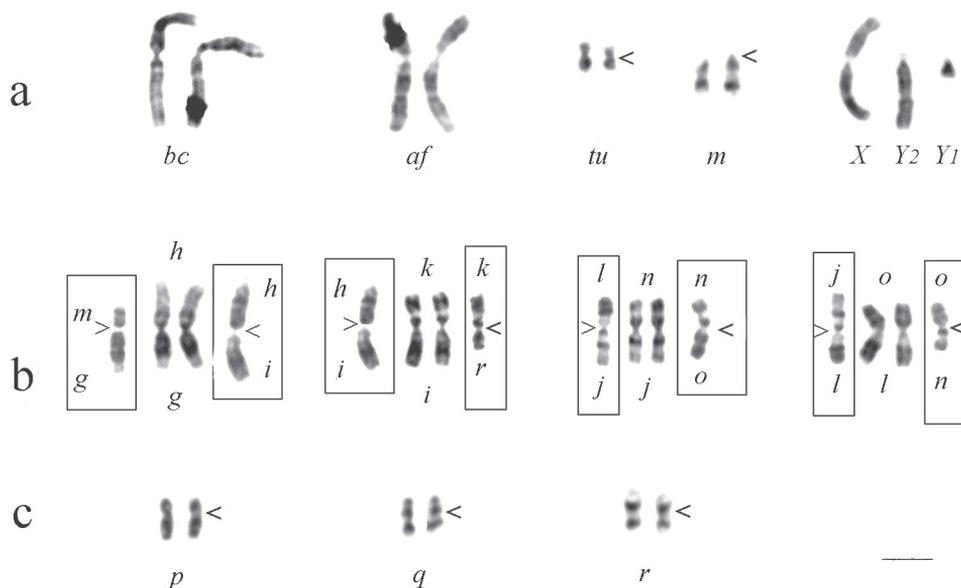
Three females and four males of *S. satunini* were captured in the valley of the Beisoog River (45°40'N, 39°41'E), 90 km N of the Krasnodar city in June 2009. Two shrews of the race Moscow (male and female) were captured in Moscow vicinity.

Mitotic chromosome spreads were prepared in the field conditions from bone marrow and spleen cells using the air-drying technique after fixation with methanol and glacial acetic acid. For G-banding, the slides were treated with trypsin solution according to Seabright (1971). Chromosome nomenclature used follows Searle et al. (2010).

## Results and comments

The karyotype of *S. satunini* consists of 24–25 chromosomes. The sex chromosomes are a large metacentric X, a small acrocentric Y<sub>1</sub>, and a medium-sized Y<sub>2</sub>. Of 11 autosomal pairs, only a single pair of small chromosomes is acrocentric, all other autosomes are biarmed. Such a karyotype has been described for many populations from the North Caucasian and Transcaucasian regions (Kozlovsky 1973, Sokolov and Tembotov 1989, Macholán 1996).

The Caucasian shrew has the following chromosome formula: XX / XY<sub>1</sub>Y<sub>2</sub>, *af*, *bc*, *gh*, *ik*, *jn*, *lo*, *tu*, *m*, *p*, *q*, *r*, *tu*. The comparison of the G-banded metaphase chromosomes of *S. satunini* and of *S. araneus* (the race Moscow) is presented in Fig. 1. This comparison revealed a considerable homology between individual chromosomal arms. Identical



**Figure 1.** The G-banded karyotype of *Sorex satunini* (male) in comparison with the karyotype of *S. araneus* (the race Moscow, male). The chromosomes of the race Moscow are given in the frameworks. Some chromosomes are identical (a), the others are different because of the arms involved in different fusions (b) or because of the centromeric shift (c). Centromere position is indicated by "<". Bar = 3  $\mu$ m.

banding patterns and centromeric positions were found in two large biarmed autosomes *af* and *bc*, in small metacentric *tu*, in acrocentric pair *m* and in the sex chromosomes (Fig. 1a). The acrocentric *m* is found in the karyotypes of the chromosomal races of *S. araneus* either as an individual acrocentric, or in combination with other acrocentrics.

Seven arms of *S. araneus*, namely *g*, *i*, *k*, *j*, *n*, *l*, and *o*, were also identified in the complement of *S. satunini*. The difference in G-banding of the arm *h* between *S. satunini* and other species of the *S. araneus* group was observed (Fig. 1b). An identical banding pattern and a different centromeric position were found in three autosomal pairs: *p*, *q*, and *r*, suggesting occurrence of centromeric shift. The chromosomes *p*, *q*, and *r* were found to be metacentric in the complement of *S. satunini* (Fig. 1c) and acrocentric in *Sorex araneus*.

The large biarmed chromosome *bc* was also identified in the complement of *S. antinorii* Bonaparte, 1840, and only in *S. coronatus* Millet, 1828 it was substituted by *ci* (Hausser and Jammot 1974). The biarmed chromosome *lo* is found in the karyotypes of *S. coronatus* and *S. antinorii*, the biarmed chromosome *jn* - in the karyotype of *S. coronatus* (Brünner et al. 2002). The metacentric *ik* is known in five chromosomal races of *S. araneus* (Wójcik et al. 2003). The metacentric *gh* was identified only in the complement of *S. satunini* (Fig. 1b).

In karyotype of *S. coronatus* there are only two species-specific chromosome rearrangements (Rb fusions *ci* and *mp*). In karyotype of *S. antinorii* there are only two spe-

cies-specific chromosome rearrangements, too (*hj* and *kn*). In karyotype of *S. satunini* there are five species-specific chromosome rearrangements (Rb fusion *gh*, centromeric shifts in the chromosomes *p*, *q*, *r*, and, probably, a paracentric inversion in the chromosomal arm *h*), i.e. *S. satunini* has more rearranged karyotype than the species of *S. araneus* group in Western Europe.

A number of chromosome rearrangements shared by *S. araneus*, *S. satunini* and *S. antinorii* (centric fusions *bc*), by *S. coronatus*, *S. satunini* and *S. antinorii* (*lo*), by *S. coronatus* and *S. satunini* (*jn*) suggest the existence of a common ancestral species in the Pleistocene of Europe analogous to the modern *S. araneus*.

The known paleontological age points to an early origin of *S. satunini*. At present, the dating of fossils confirmed by the radiocarbhydrate analysis is known only for *S. satunini*. These fossils, morphologically very similar to the recent *S. satunini* were found in the Transcaucasian region (Kudaro caves) in all layers of the middle and late Pleistocene, beginning since 0.36 Myr BP (Osipova 2006).

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