

## New chromosome races of the common shrew *Sorex araneus* from Eastern Siberia

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Two new chromosome races of the common shrew *Sorex araneus* Linnaeus, 1758 have been discovered in Eastern Siberia (Strelka and Ilga). This finding helps to clarify the geographical limits of other previously-described chromosome races (Tomsk and Baikal) in the same region and to elucidate the chromosome evolution of Siberian common shrews. The diversity of chromosome races in this area can be explained by stepwise accumulation of Robertsonian fusions and whole-arm reciprocal translocations from a Baikal-like ancestral race.

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### Introduction

The common shrew *Sorex araneus* Linnaeus, 1758 demonstrates remarkable inter-population chromosome variation in terms of existence of chromosome races (review: Searle and Wójcik 1998). The full haploid karyotype of this species consists of 18 autosome arms, 12 of which are involved in this racial variation. More than 50 chromosome races have been described (Zima *et al.* 1996) and they are believed to be formed in two ways. One way is through fixation of multiple Robertsonian (Rb) fusions. Alternatively, one chromosome race may evolve into another following modification of metacentrics by whole-arm reciprocal translocations (WARTs) (Winking 1986). It has been suggested that WARTs can generate large series of chromosome races from a single ancestor (Halkka *et al.* 1987, 1994, Wójcik 1993, Fredga 1996, Polyakov *et al.* 1997b).

To further our understanding of the generation of chromosome races in the common shrew, it is desirable to study the species over its whole range. One part of the range that is relatively poorly known is Eastern Siberia, which forms the extreme eastern limit of the species. Only two localities have been studied there before, those that define the Yermakovskoie and Baikal races (Aniskin and Volobouev 1981, Zima *et al.* 1994; Fig. 1). In this paper we present data on shrews from three new sites and define two new races. These results add significantly to our knowledge of chromosome variation in the Asian part of the range of the common shrew and permit us to devise an evolutionary scheme for the chromosome races in that area.

### Material and methods

Common shrews were caught with live traps in the years 1995–1996 at 3 localities shown in Fig. 1. The specimens studied and their geographic origin are shown in Table 1. Chromosome spreads were made in the field from bone marrow (Král and Radjabli 1974, Polyakov *et al.* 1997a). G-band staining was performed in the laboratory according to Radjabli and Kryukova (1973). Chromosome nomenclature follows Searle *et al.* (1991).

### Results and discussion

Since 1995 the population density of the common shrew in Siberia has apparently been low (Polyakov *et al.* 1997a), especially in the marginal eastern areas of the species range. We only managed to obtain samples in a few trapping sites and the sample sizes were small. Here we present data on the three sites where we found two new races: the Ilga and the Strelka.

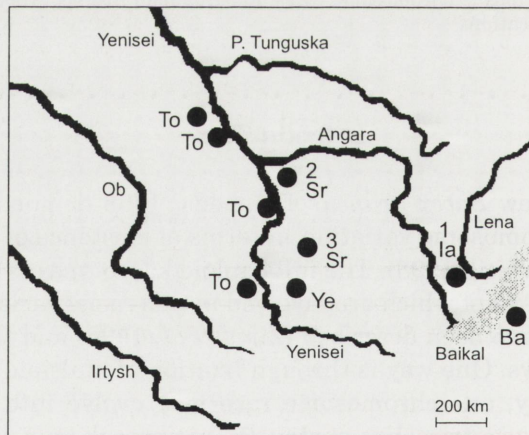


Fig. 1. Map showing the collection sites for the present study (labelled 1–3) and sites where the Baikal (Ba) and Yermakovskoie (Ye) races were previously collected (Aniskin and Volobouev 1981, Zima *et al.* 1994). The easternmost localities of the Tomsk race (To) are also shown (Polyakov *et al.* 1996).

### Ilga race

The easternmost site 1 (Fig. 1) was situated north of the Lake Baikal by the Ilga river near the village of Zhigalovo. One of two males from this site was homozygous for metacentric chromosomes *gk*, *ho*, *im*, *jl*, *nq* and homozygous for acrocentrics *p* and *r*; the other was heterozygous for *gk* (Table 1, Fig. 2). This is a new combination of metacentrics and, following the definition of chromosome races provided by Hausser *et al.* (1994), we tentatively define the Ilga race as follows:

Ilga race (Ia)

XX/XY<sub>1</sub>Y<sub>2</sub> *af*, *bc*, *g/k*, *ho*, *im*, *jl*, *nq*, *p*, *r*, *tu*

Description: this paper

Type locality: Zhigalovo, E Siberia, Russia 54°45'N, 104°56'E

Distribution: Type locality

### Strelka race

Trapping sites 2 and 3 were located near the city of Strelka and the village of Narva on the right bank of the Mana river (right tributary of Yenisei), respectively (Fig. 1, Table 1). At these two sites we trapped 5 shrews characterised by metacentrics *go*, *hi* and *jl* (Fig. 2), which again is a new combination for Eastern Siberia. We describe this as the Strelka race:

Strelka race (Sr)

XX/XY<sub>1</sub>Y<sub>2</sub> *af*, *bc*, *g/o*, *hi*, *jl*, *k*, *m*, *n*, *p*, *q*, *r*, *tu*

Description: this paper

Type locality: Strelka, E Siberia, Russia 58°07'N, 93°30'E

Distribution: E Siberia, right bank of the Yenisei river

The Tomsk race is characterized by metacentrics *gk*, *hi*, *jl*, *mn* and *qr* and occupies the left bank of Yenisei river (Polyakov *et al.* 1996, Fig. 1). A male from site 2 with the karyotype *gk/go/k/o*, *q/r* was likely a Strelka × Tomsk hybrid, confirming its location at the contact of the two races. Apparently, the Yenisei river marks an eastern border of the Tomsk race. Indeed, on the left bank of Yenisei we found the

Table 1. Karyotypes of the common shrews collected in different localities of eastern Siberia. \* – the site codes are given in accordance with those in Fig. 1, M – male, F – female.

Site and coordinates	Sex and 2n	Karyotype	Race
1. Zhigalovo* 54°45'N, 104°56'E	1M, 2n = 23	<i>gk</i> , <i>ho</i> , <i>im</i> , <i>jl</i> , <i>nq</i> , <i>p</i> , <i>r</i>	Ilga
	1M, 2n = 24	<i>g/k</i> , <i>ho</i> , <i>im</i> , <i>jl</i> , <i>nq</i> , <i>p</i> , <i>r</i>	Ilga
2. Strelka 58°07'N, 93°30'E	1M, 2n = 28	<i>g/o</i> , <i>hi</i> , <i>jl</i> , <i>k</i> , <i>m</i> , <i>n</i> , <i>p</i> , <i>q</i> , <i>r</i>	Strelka
	1M, 2n = 27	<i>go</i> , <i>hi</i> , <i>jl</i> , <i>k</i> , <i>m</i> , <i>n</i> , <i>p</i> , <i>q</i> , <i>r</i>	Strelka
	1M, 2n = 26	<i>gk/go/k/o</i> , <i>hi</i> , <i>jl</i> , <i>q/r</i> , <i>m</i> , <i>n</i> , <i>p</i>	Strelka × Tomsk hybrid
3. Narva 55°26'N, 93°44'E	1M, 2n = 27	<i>go</i> , <i>hi</i> , <i>jl</i> , <i>k</i> , <i>m</i> , <i>n</i> , <i>p</i> , <i>q</i> , <i>r</i>	Strelka
	2F, 2n = 26	<i>go</i> , <i>hi</i> , <i>jl</i> , <i>k</i> , <i>m</i> , <i>n</i> , <i>p</i> , <i>q</i> , <i>r</i>	Strelka

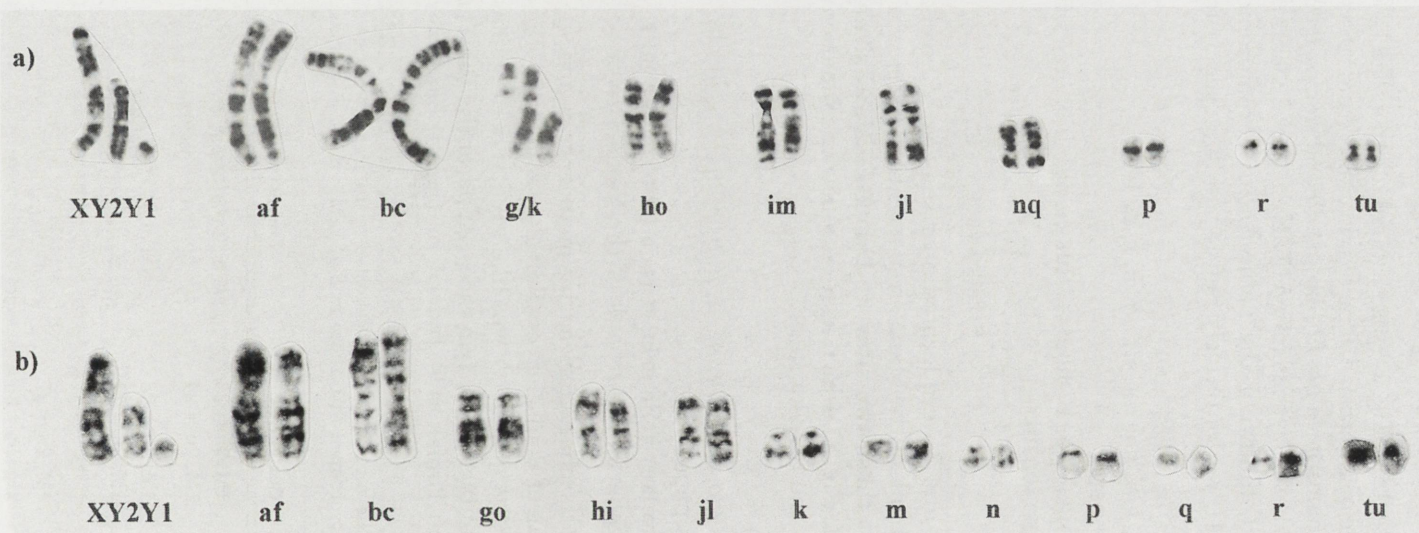


Fig. 2. G-band karyotypes of the Ilga (a) and Strelka (b) chromosome races.

Tomsk race in all three sites studied (Polyakov *et al.* 1996). Earlier Aniskin and Volobouev (1981) also described one more site with Tomsk race individuals from the left bank. On the right bank we found the Strelka race at two sites (Fig. 1) and Aniskin and Volobouev (1981) described the Yermakovskoie race at one site. Finding a Strelka  $\times$  Tomsk hybrid on the right bank of Yenisei indicates that the migration of shrews across the river is possible at least at site 2.

#### Pattern of chromosomal evolution in Siberia

The discovery of two new chromosome races in Eastern Siberia allows us to reconsider the chromosomal evolution of common shrews in Siberia overall. Of the races that have been described so far, the Baikal has the fewest metacentrics and can be considered closest to the ancestral condition (Zima *et al.* 1994). Among the variable chromosomes only *hi* and *jl* are present as metacentrics. Starting with this race it is possible to derive all the other races by assuming that races evolve from neighbouring ancestral forms by stepwise accumulation of Rb fusions and WARTs (Fig. 3). Such accumulation could accompany range changes in association with the last glaciation and its ending. For example, on range expansion at the end of the glaciation, a metacentric (formed by Rb fusion or a WART) may become fixed at the leading edge. The new race formed will become the new leading edge, which may

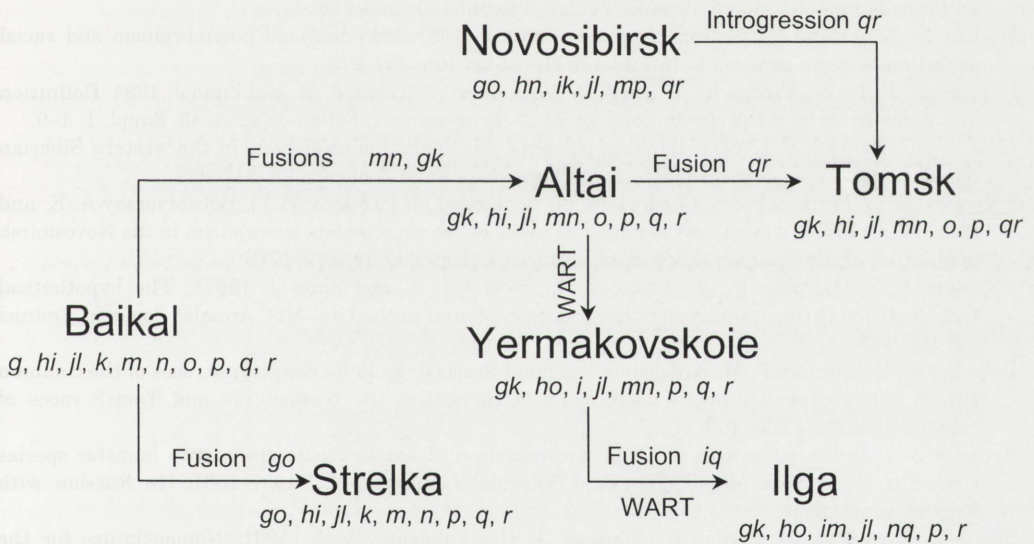


Fig. 3. Tentative scheme for the evolution of chromosome races of the common shrew in Siberia. The Baikal race has the fewest metacentrics and is considered the ancestral form. In this scheme, neighbouring races can be derived from each other by one or two Rb fusions and/or WARTs. The Tomsk race is thought to have derived metacentric *qr* by introgression from the neighbouring Novosibirsk race or by fusion of acrocentrics at the northern edge of the range of the Altai race (Polyakov *et al.* 1996).

itself be the site of fixation of a second metacentric, generating a second new race, and so on.

Clearly, much more work is required to confirm the evolutionary scheme in Fig. 3. Substantially more chromosome survey work is required to establish the widespread occurrence of the Strelka, Ilga and other chromosome races. Molecular studies are needed to provide a phylogeographic framework for the chromosome variation (work in progress) and, if possible, to demonstrate particular chromosomal rearrangements that have been hypothesised.

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