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The hypothetical Old-Northern chromosome race of *Sorex araneus* found in the Ural Mts.

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Chromosomes of two populations of the common shrew, *Sorex araneus* L. (Mammalia, Insectivora, Soricidae), from the northern Ural Mts. were investigated. In both sites, homozygous, all-metacentric autosomal complements were revealed, with the autosomal arm combinations *af, bc, go, hn, ip, jl, km, qr, tu*. This karyotype is identical to that predicted by Halkka *et al.* (1994) as the hypothetical “Old-Northern” race connecting the northern and eastern racial groups of *Sorex araneus* in Eurasia.

1. Introduction

The extensive chromosomal evolution recorded in the common shrew (*Sorex araneus*) has been reported and analysed in numerous papers (cf. Hausser 1991, Zima *et al.* 1994). The known chromosome races have been arranged into several major phylogenetic units, the West European, East European, and North European karyotypic groups (Searle 1984, Wójcik 1993, Hausser *et al.* 1994), with additional chromosome races in southern Europe (Hausser *et al.* 1991), European Russia (Ivanitskaya 1985, Aniskin & Lukianova 1989, Gabitova 1992), and Siberia (Aniskin & Volobouev 1981, Král *et al.* 1981). The pattern of chromosome variation reported from northern Europe and, particularly, from Finland, is extremely com-

plicated and apparently relates to the postglacial geological history of Fennoscandia (Halkka *et al.* 1974, 1987, 1994a). Halkka *et al.* (1987) proposed an evolutionary hypothesis for the local chromosome races in Finland, based on the mechanism of whole-arm exchanges produced by reciprocal translocations between non-homologous bivalents. Karyotypic differences between the races are considered to originate mainly by a single reciprocal translocation event. The hypothesis was further revised by Halkka *et al.* (1994a), and a successive translocation cascade was proposed to reveal relationships between the chromosome races distributed in northern and eastern Europe and in Asia. The Novosibirsk race described in western Siberia was thought to be the most probable ancestor, from which the races known from



Fig. 1. G-banded karyotype of a male from Serov.

eastern Poland and Finland have evolved during the postglacial period. The authors concluded that only one hypothetical race, called the “Old-Northern” race, was needed to connect the North and East European karyotypic groups. This paper reveals that the hypothetical “Old-Northern” race of *Sorex araneus* is indeed found in the Ural Mts.

2. Material and methods

The shrews were collected from two sites on the eastern (i.e. Asiatic) side of the main ridge of the Ural Mts. in June 1995. The first trapping site was situated 50 km north of the city of Chelyabinsk, on the right bank of the Tetchya river (coordinates 55°59'N, 61°15'E). The other site was situated 10 km north of the city of Serov, on the right bank of the Kakva river (59°50'N, 60°22'E). The sample from the former site included 5 males and 2 females, that from the latter site 2 males and 3 females. Mitotic preparations were made by a standard method from bone marrow and spleen cells (Ford 1966). Slides were aged and G-banded using a modification of Seabright's technique (1971). A minimum of 5 complete banded spreads were scored for each individual. The standard nomenclature for the chromosomes of the common shrew (Searle *et al.* 1991) was applied in description of the karyotype. All the specimens examined were preserved as skulls and skins.

3. Results and discussion

All but one animal examined had a homozygous karyotype with all-metacentric autosomal constitution and XY_1Y_2 sex chromosomes. One male from Chelyabinsk was heterozygous for arm combination *jl* ($2N = 22$). The karyotypes of all shrews included the standard autosomal arm combinations *af*, *bc* and *tu*; the shrews were characterised by the metacentrics *go*, *hn*, *ip*, *jl*, *km* and *qr*. The representative karyotype of a homozygous male from Serov is shown in Fig. 1.

The observed autosomal arm constitution in shrews studied is different from any other karyotype of *Sorex araneus* reported in the literature (cf. Wójcik 1993 for a review). Therefore, the populations under study are described here as a new chromosome race, following the rules introduced by Hausser *et al.* (1994):

Serov race: XX/XY_1Y_2 *af*, *bc*, *go*, *hn*, *ip*, *jl*, *km*, *qr*, *tu*.

The type locality: The Kakva river, 10 km north of Serov, Ural Mts., Yekaterinburg region, Russia, 59°50'N–60°22'E.

Distribution: Known from two sites. The range presumably extends in the eastern slopes of the Urals, between the cities of Chelyabinsk and Serov.

The karyotype of this new race is apparently identical with that of the hypothetical “Old-Northern” race predicted by Halkka *et al.* (1994a). The known distribution of the Serov race fits well with the presumptive range of the “Old-Northern” race, which is hypothesized to connect phylogenetically the Finnish races and the Novosibirsk race (west Siberia). The finding of the Serov race completes the postulated translocation cascade (Halkka *et al.* 1994a) running from the Novosibirsk race in Siberia, through the Serov race in the northern Urals, to the Kuhmo (FIN-1) race in Finland and the Abisko (N) race in northern Sweden.

The other chromosome race that has been described from the Ural Mts. by Gabitova (1992) was found in Bashkiria, situated on the western (European) side of the southern Urals. This race has a karyotype rather different from that of the Serov race, but similar to the West European karyotypic group (autosomal arm combinations *gm*, *ho*, *in*, *kp*, *qr*). This karyotype can be related to the races of the West European group described

near Moscow (*gm, hi, kp, no, qr*; Ivanitskaya 1985) and in Chernogolovka in the Moscow region (*gm, hi, kr, no, pq*; Aniskin & Lukianova 1989) by another translocation cascade involving one reciprocal translocation in each step (*ho-in*, followed by *kp-qr*).

Migration routes of shrew populations (and/or of individual fusions or translocations) can thus be traced from western Siberia and northern Europe to western and central Europe, and from central Europe to eastern Europe back again. The Ural Mts. may represent a geographical contact zone between populations (and/or karyotypes) of different origin.

The translocation cascade hypothesis proposed by Halkka *et al.* (1987, 1994a) seems to be supported by the finding of the Serov race, as well as by frequent geographical contact of chromosome races differentiated by the presumptive single reciprocal whole-arm translocation between two metacentric. This mechanism of chromosomal change was also accepted as a molecular possibility in *Sorex araneus* (Garagna *et al.* 1991, Halkka *et al.* 1994b). An alternative hypothesis suggests successive spreading of fusions across primitively acrocentric populations, and fixation of two independent centric fusions, as a cause of differences observed between races (cf. Searle 1984, 1988, Hausser 1994, Taberlet *et al.* 1994). The two hypotheses are apparently not exclusive, and further data are needed to elucidate the actual importance of both mechanisms in karyotypic evolution of *Sorex araneus*.

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