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A distinct chromosome race of the common shrew (*Sorex araneus* Linnaeus, 1758) within the Arctic Circle in European Russia

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Abstract. A unique arm chromosome combination detected in the common shrew karyotype from a Karelian locality within the Arctic Circle (Kandalaksha State Nature Reserve, European Russia) is interpreted as a new chromosome race - Poyakonda. According to the standard nomenclature of G-banded chromosomes of *Sorex araneus* the karyotype contains the species specific bi-armed autosomes *af*, *bc*, *jl*, *tu* and the typical complex sex chromosome system (two metacentrics XX in the female and one metacentric/two acrocentrics XY_1Y_2 in the male). A group of race specific chromosomes includes 4 metacentric combinations (*hn*, *ip*, *kq*, *mo*) and two acrocentric chromosomes (*g* and *r*). In all 5 shrew specimens examined the same homozygous autosome complement 2Na=20 was found. Data available from neighbouring regions in Russia and, in particular, from adjacent Fennoscandian countries reveal complex relationships between karyotypes of common shrews from the European North.

Key words: karyotype, chromosome race, common shrew, *Sorex araneus*, Northern Europe, European Russia.

Introduction

The common shrew (*Sorex araneus* Linnaeus, 1758) is a small insectivorous mammal found in northern Eurasia. Due to its extensive chromosomal variation resulting from multiple Robertsonian fusions and whole-arm reciprocal translocations (WARTs) the species has been the focus of evolutionary studies coordinated since 1987 by the International *Sorex araneus* Cytogenetics Committee, ISACC (Searle et al., 2007). In the course of regular field studies covering much of the huge species range - from Britain in the west to Baikal in the east – up to 70 chromosome races of *S. araneus* have incrementally been discovered and listed according to the proceedings of the ISACC meetings (Zima et al., 1996; Wójcik et al., 2003).

The racial diversity in the common shrew is in particular remarkable in regions and countries located within the northern limits of its distributional range in Europe. According to a geographically arranged list (Shchipanov et al., 2009), 6 chromosome races are recognized in the British Isles and 16 in Fennoscandia whose territories are best examined, and, in contrast, 8 races have so far been reported for northern European Russia, for latitudes above 60° N. The majority of chromosome races in

the western part of Europe are characterised by two metacentrics, *gm* and *hi*, that was considered the reason to distinguish the West Europe Karyotypic Group, or WEKG (Searle, 1984). In shrew karyotypes from northern Scandinavia and Finland, the metacentric *ip* is most frequent, thus characterising the races of the North Europe Karyotypic Group, or NEKG (Fredga, 1996b). Representatives of these two groups meet and hybridise in the central part of Sweden which suggested that the postglacial colonization routes of common shrew populations in western Scandinavia came in two directions – from the north and from the south (Fredga, 2007).

In races of European Russia, only a few karyotypes have both WEKG markers *gm* and *hi,* and not infrequently there is the alternative presence of either *gm* or *hi.* Also, races with the chromosome *ip* are present, some associated geographically with the Finnish races and thus extending the NEKG continuous range south from the Baltic coast to the middle of Belarus (Bulatova et al., 2000). Three NEKG races are present in the vicinity of the Urals and are separated from the main NEKG stock by various intermediate races in northern Russia (Orlov et al., 2007; Shchipanov et al., 2008). In contrast to the southern species border in Russia (Bystrakova et al., 2007), the very limits of the species range in the north are still not fully specified regarding chromosome races and karyotypic groups. In sum, one site of the Kanin chromosome race (a single specimen) was studied on the Kanin Peninsula, so far the most northern karyotypic description of the common shrew in Russia (Fredga, 1996a). A single finding concerns the Yagry race on an island in the North Dvina River delta in the White Sea (Orlov et al., 2007). Better described are the more central Russian races Kirillov, Petchora, Serov, Sok and Manturovo (Bystrakova et al., 2007; Shchipanov et al., 2008, 2009a). Here I describe the chromosomal characteristics of common shrews from close to the Kola Peninsula in Russia which may be interesting in view of the probable connection with Scandinavian chromosome races of the common shrew already well examined.

Material and methods

Karyotypes were studied in common shrews collected from the vicinity of the White Sea Biological Station of Moscow State University (WSBS, Kandalaksha State Nature Reserve, Karelia Republic, Russia, 66º33´N/33º06´E) in the beginning of July 2009. One immature and two adult males and one pregnant female were collected using special hand made live traps (Shchipanov et al., 2000).

Routine chromosome preparations were made on the four shrews following Ford and Hamerton (1956), with some modifications, and to one of 9 embryos in the pregnant female.

Meiotic chromosomes from the two adult males were prepared according to a centrifuge-free field procedure adapted from Williams et al. (1971).

A trypsin - Giemsa staining method of Král, Radjabli (1974) was used for identification of mitotic chromosomes. The racial status of each specimen was determined according to the standard nomenclature for the *S. araneus* karyotype (Searle et al., 1991).

Results

All 5 individuals had karyotypes typical for the common shrew. The diploid number differs between specimens of different sex according to the specific sex chromosome constitution - XX in females and XY_1Y_2 in males (Fig. 1). The three large biarmed pairs include two pairs of autosomes (*af, bc*) and the X-chromosome (*de*). Six smaller metacentric pairs are present in chromosomal spreads including *jl* and *tu* which are universal over the species range, and 4 metacentrics of race specific

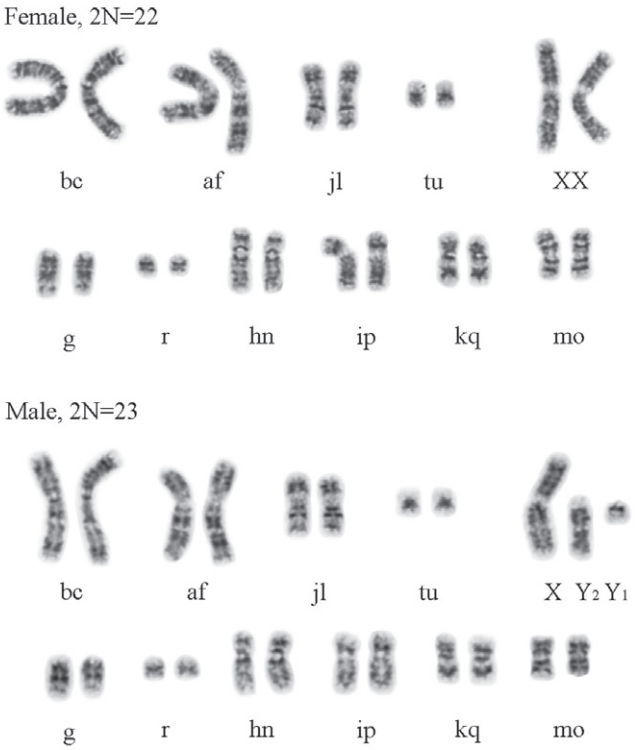

Fig. 1. G-banded karyotypes of a female (2N=22) and male (2N=23) *S. araneus* belonging to the new chromosome race, Poyakonda.

value (*hn, ip, kq, mo*). Additionally, two acrocentrics corresponding to Y_1 (*s*) and Y_2 (*d*) were observed and two pairs of acrocentric autosomes defined as *g* and *r* in G-banded karyograms. Thus, the autosome number (2Na) for this complement is 20.

Meiotic I divisions were visible in preparations made from both adult males. The haploid number in all spreads observed corresponds to the karyotypic status of specimens, i.e. N=11. Among 11 separate configurations there was the sex trivalent (XY_1Y_2), two large bivalents (*af, bc*) and 8 medium to small configurations representing the six metacentrics and two acrocentrics mentioned above. Configurations involving the two acrocentric autosomes (*g, r*) were connected by only one terminal chiasma, thus showing a reduction of chiasma frequency per bivalent in comparison with other (metacentric) configurations with 2-3 chiasmata in each (Fig. 2).

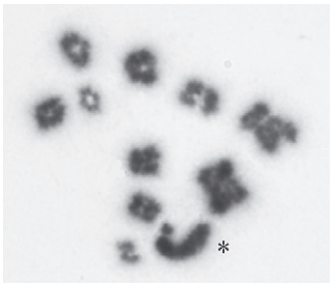

Fig. 2. Diakinesis/M I spread showing 10 autosomal bivalents and the sex trivalent XY_1Y_2 (star) in a male shrew with the karyotype of the new race.

Table 1. Summary of chromosome races of Sorex araneus from northern European Russia and Fennoscandia. Only the type sites for each race and the most recent karyotype descriptions are indicated. The list is organised on the basis of geographical and proposed chromosomal relationships.

Country, region	Coordinates of type locality	Race (Symbol)	Chromosome diagnosis	2Na	Reference
Russia (Karelia), Poyakonda	66º33'N/ 33º06'E	**Poyakonda** (Py) *New race*	*g, hn, ip, kq, mo, r*	20	This paper
Sweden, Ammarnäs	65º58'N/ 16º13'E	**Ammarnäs** (Am)	*g, m, hn, ip, k/q, o, r*	23-25	Fredga, 2007
Sweden, Abisko	68º22'N/ 18º50'E	**Abisko** (Ai)	*g/m, hn, ip, k/q, o/r*	20-22	Fredga, 2007
Sweden, Hattsjö	63º36'N/ 18º58'E	**Hattsjö** (Ha)	*g/m, h/n, i/p, k/q, o, r*	20-24	Fredga, 2007
Finland, Savukoski	67º28'N/ 27º16'E	**Savukoski** (Sa)	*g/o, hn, ip, k/q, m, r*	21-24	Zima et al., 1996
Finland, Kuhmo	63º55'N/ 30º13'E	**Kuhmo** (Ku)	*g/o, hn, i/p, k/q, m/r*	20-23	Zima et al., 1996
Finland, Ilomantsi	62º45'N/ 30º59'E	**Ilomantsi** (Il)	*g/o, hn, i/p, k/r, m/q*	20-23	Zima et al., 1996
Russia, Kanin Peninsula	68º20'N/ 45º13'E	**Kanin** (Ka)	*gp, hi, kq, mn, or*	18	Fredga, 1996a
Russia, Island Yagry	64º35'N/ 40º00'E	**Yagry** (Ya)	*go, hi, kq, mp, nr*	18	Orlov et al., 2007
Russia, Kirillov	59º50'N/ 38º25'E	**Kirillov** (Kr)	*g/m, hi, k/q, no, pr*	18	Orlov et al., 2007

Discussion

The karyotype that I describe was found on the southern (Karelian) shore of the Kandalaksha Gulf of the White Sea (Fig. 3). Shrew populations distributed by the northern shore of Kandalaksha Gulf in the whole area of the Kola Peninsula remain still not studied, whereas races from territories to the west and south-west (Fennoscandia), east and south-east (Russia) are known. The available data from the literature on 9 chromosome races of the common shrew from these adjacent territories are presented in Fig. 3 and Table 1.

It is notable that three fused arm combinations found in the karyotype that I describe (*hn, ip, kq*) are common with 5 other races distributed westwards in the countries of northern

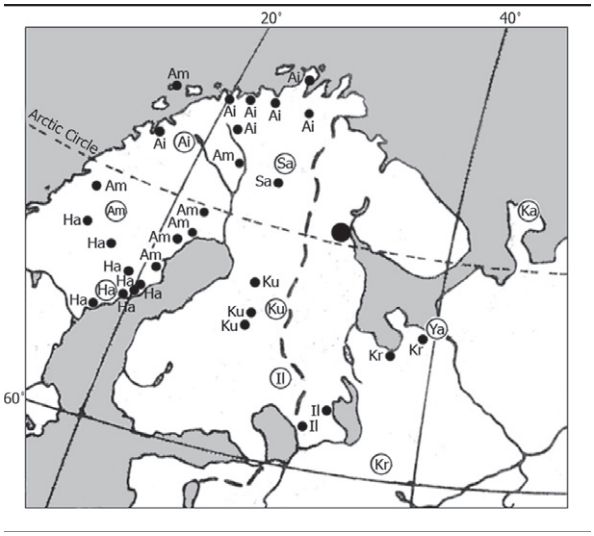

Fig. 3. A geographic presentation of the type sites (bi-letter symbol in circle) and nearest findings (small closed circles) of chromosome races of *S. araneus* in Northern Europe: Kanin (Ka), Yagry (Ya), Kirillov (Kr), Ilomantsi (Il), Kuhmo (Ku), Savukoski (Sa), Abisko (Ai), Ammarnäs (Am), Hattsjö (Ha). The location of the new Arctic race, Poyakonda, is indicated by a large closed circle. The data from the literature are mapped according to recent reviews of Fredga (2007) for Fennoscandia and Orlov et al. (2007) for Russian sampling localities. The bold dashed line designates the Russian border.

Europe - 2 in Finland (Savukoski, Kuhmo) and 3 in Sweden and Norway (Abisko, Ammarnäs, Hattsjö). At the same time, the condition of 4 other arms – *g*, *m*, *o*, and *r* - is race specific. In a detailed consideration of material from northern Fennoscandia, Fredga (2007) describes how the Ammarnäs race always has *g*, *m*, *o*, and *r* unfused, the Abisko race often has *o* and *r* fused and in two races – Abisko and Hattsjö – the fused combination between *g* and *m* occurs. Two neighbouring Finnish races are characterised by alternative polymorphic arm combinations *g/o – m/r*. In the new karyotype that I describe one more possible alternative combination - fused arms *mo* and *g* and *r* unfused – is realised (Table 1). This unique combination of chromosomes indicates clearly the racial distinctness of this new karyotype. This race can be titled "Poyakonda" following the name of the nearest settlement and railway station. It is yet another race at the extremes of the European north in addition to the 3 races of northern Fennoscandia already known (Abisko, Ammarnäs, Savukoski) and the Russian Kanin race also distributed above the Arctic Circle (see Fig. 3). Needless to say, the question of the distributional range of the new race remains open, especially in the top territories to the north including the Kola Peninsula. Close karyological relationship between this race and 5 other races of the NEKG is evident from the comparison of their chromosomal formulae (Table 1). Further studies are needed to identify contact zones with Finnish races in the west (Savukoski, Kuhmo) or in the south (Ilomantsi) and possibly the Russian Kirillov race (see Fig. 3).

Below, the description of the new race is given according to the rules of ISACC:

Poyakonda race (Py). XX/XY_1Y_2, *af, bc, g, hn, ip, jl, kq, mo, r, tu.*

Description: First description

Type locality: Poyakonda railway station vic., southern bank of the Gulf of Kandalaksha, White Sea Biological Station of Moscow State University, Kandalaksha State Nature Reserve, Karelia Republic, Russia, 66º33´N/33º06´E.

Distribution: type locality only.

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