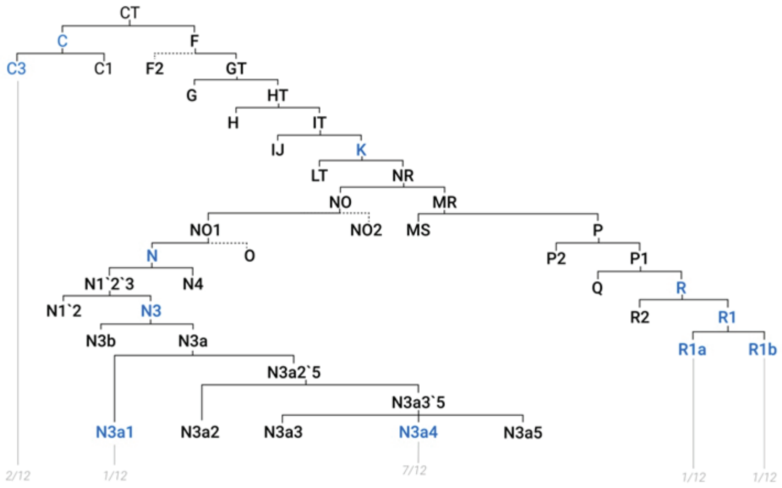

Location of samples from the village of Russkoye Ust'ye on the topology of Y-chromosome haplogroups according to Karmin, 2015 [13]

on the northern coast was based on industrial people, mainly people from the eastern regions of the Russian North and the Urals. According to E.A. Strogova, they were the first to reach the lower reaches of the Indigirka River, showing commercial interest in the traditional crafts of local residents, as well as in the collection of mammoth ivory [11].

In this work, for the first time, we have analyzed the Y-chromosome lines of men from Russkoye Ustye in order to compare the obtained data with the hypotheses of the origin of the Russkoye Ustye.

Materials and methods. The total population of the village of Russkoye Ustye, Allaikhovsky Ulus of the Republic of Sakha (Yakutia), according to the current archive of the administration was 148 people in 2012-2014 [6]. For research during expeditions in 2018-2019 we collected DNA samples from 12 unrelated men, native russkoustinians, aged 7 to 66 years (average age 42.4±17.4 years).

All DNA samples were tested for Y-chromosome markers C-M130 and K-M9 using real-time PCR. Then, using previously published primer sequences, PCR-RFLP analysis of SNP markers of haplogroups C-M216, R-M207, N-M231, and Q-M242 was performed [26; 23; 17]. Subsequently, in accordance with the defining marker, the following markers were hierarchically typed by PCR-RFLP: R1a-M420 [27], R1b-M343 (original sequence), C1-F3393 [21], C1b-F1370 [21], C2`4 -B477 (original sequence), C3b-P39 (original sequence), N2a1-P43 [19], N3-TAT/M46 (original sequence), N3a1-B211 (original sequence), N3a3-VL29 [20], N3a4-Z1936 [21], N3a5*-F4205 (original sequence), N3a5*-B202 [20]. The C3-M217 marker [25] was identified using Sanger sequencing. The original primer sequences were selected using FastPCR v.6.7.58 (trial) software.

The haplogroup nomenclature used is based on Karmin et al., 2015 [14], which provides the basic YCC 2002 (The Y Chromosome Consortium 2002) nomenclature with updated data from Jobling & Tyler-Smith, 2003 [21], Karafet et al., 2008 [23] and van Oven et al., 2014 [25].

Results and discussions. In the studied sample of Russkoye Ustye residents, five lines of the Y-chromosome N3a4-Z1936, N3a1-B211, R1a-M420, R1b-M343 and C3-M217 were identified, which belong to three haplogroups: N3 (8/12; 66.7%), R1 (2/12; 16.6%) and C3 (2/12; 16.6%) (Table 1).

The topological position of the identified Russkoye Ustye lineages on the Y-chromosome phylogenetic tree is shown in Figure 1. Haplogroup designations correspond to the nomenclature proposed by Karmin et al., 2015 [14]

Haplogroup N3 (8/12; 66.7%) dominating in this sample is distributed throughout Northern Eurasia, from Japan to Scandinavia [20]. A more detailed analysis of the N3-lines of the russkoustinians showed that most (~58.4%) of the samples belong to the N3a4 subhaplogroup (Table 1), which was found mainly in North-Eastern Europe among northern Russians, Sami, Veps, Karelians, and Finns [20] and is not found in the gene pool of the neighboring peoples of Yakutia and Chukotka [16]. It should be noted that the N3a4 subhaplogroup and the N3a3 branch phylogenetically close to it are the most informative for the differentiation of the two so-called “poles” of the Russian gene pool, northern and southern Russians [3]. In the populations of northern Russians, the haplogroup N3a4 is associated with the ancient pre-Slavic (Finno-Ugric) component of the gene pool [3; 10].

One sample (8.3%) belongs to the N3a1 subhaplogroup, which is more typical for the Finno-Ugric populations of the Udmurts, Mari Komi-Zyryans and Komi-Permyaks [20], neighboring with the populations of northern Russians.

The Eurasian haplogroup R1 is found in more than half of men in Europe [15]. In the studied sample of Russkoye Ustye residents, haplogroup R1 is represented by two lines: R1a (~8.3%) and R1b (~8.3%), which are widespread in the Slavic populations of Eastern Europe (Russians, Ukrainians, Belarusians, Poles) [2; 3]. In the gene pool of the Yukaghirs, Evens, Evenks and Yakuts, these lines were found in small numbers and their origin is associated with the processes of miscegenation with Russians and, possibly, other Eastern European ethnic groups that have settled the territory of Yakutia since the time of joining the Russian Empire in the 17th century [16].

The frequency of the Asian haplogroup C3 among the russkoustinians was ~16.6%. This haplogroup is one of the most widespread in East Asia [24], including Siberia [16,19]. In Yakutia, haplogroup C3 occurs with high frequencies in the populations of Yukaghirs (46%), Evens (60%), and Evenks (54%) adjacent to the Russkoye Ustye people [16].

Thus, the frequency distribution of the Y-chromosome haplogroups in the studied sample of the Russkoye Ustye residents shows the dominance of lines characteristic of European populations (83.4%), of which more than half is the subhaplogroup N3a4. In the populations of the indigenous peoples of the northeast of Eurasia (Yukaghirs, Evens, Evenks, Yakuts, Dolgans, Chukchi, Eskimos), the N3a4 subhaplogroup was not found [16; 20]. The gene pool of the indigenous peoples of Yakutia and Chukotka is characterized by an insignificant

The frequency of haplogroups (%) of the Y-chromosome in residents of the village Russkoye Ustye

Haplogroup	C3		N3		R1
	C3-M217	N3a1-B211	N3a4-Z1936	R1a-M420	R1b-M343
n	1	7	1	1	2
%	8.3%	58.4%	8.3%	8.3%	16.7%

contribution of haplogroups of Western Eurasian origin (less than 10%) [16].

If we consider the distribution of haplogroups of the Russkoye Ustye people from the point of view of their origin, then we can assume that the dominance of the lines characteristic of the populations of the northeast of Europe most likely reflects the connection with the Russian North. It is known that the northern populations of Russians are characterized by similarities with the Finno-Ugric and Baltic peoples [3], while the central and southern populations of Russians are genetically closer to other Slavic populations [2; 22; 26]. The line N3a4 (58.7%), which dominates among the Russkoye Ustye people, is considered not typical for the Slavic populations in general, however, the highest frequencies of this subhaplogroup were found in the northern Russians of the Arkhangelsk and Vologda regions and much lower frequencies – among the Novgorodians [3].

Conclusions. As a result of the analysis of Y-chromosome lines, 83.4% of haplogroups (N3a4, N3a1, R1a, R1b), more characteristic of Western Eurasian populations, and 16.6% of East Eurasian lines (C3) were found in residents of the village of Russkoye Ustye. The paternal lines of the inhabitants of the village of Russkoye Ustye are represented mainly by Y-chromosome haplogroups, common in the populations of northeastern Europe. The dominant subhaplogroup is N3a4 (58.7%), which is absent in the gene pool of the neighboring peoples of Yakutia and Chukotka and occurs with high frequencies in the populations of the Russian North and among the Finnish-speaking peoples of Finland and Karelia. The results obtained are more in line with the Pomor hypothesis of the origin of the russkoustinians.

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