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# Gene Pool Similarities and Differences between Ukrainians and Russians of Slobzhanshchina Based on Y-Chromosome Data

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**Abstract**—Results from studying Y-chromosomal polymorphisms of Russian and Ukrainian populations are presented for Slobzhanshchina, which is a contemporary border region, inhabited in the 17th–18th centuries at the “Wild Field” boundary due to migrations of both the Russians from the north and Ukrainians from the west. In general, the Ukrainian and Russian populations of Slobzhanshchina are very close genetically; their set and frequency range of Y-chromosome haplogroups are typical for Eastern Europe. However, a detailed analysis of highly informative Y-chromosome markers showed that both nations retain the ethnic specificity of their gene pools after 3.5 centuries of coexistence in the same historical territory: the Ukrainian populations are similar to the rest of Ukraine, and Russian populations gravitate towards the south of European Russia. The persistent genetic differences may be due to the spatial characteristics of marriage migration and the predominant ethnic environment.

**Keywords:** Y-chromosome, haplogroup, gene pool, genetic differentiation, populations, Ukrainians, Russians, East Europe

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## INTRODUCTION

DNA-markers make it possible to study the population structure and to reconstruct its dynamics in the past. As applied to human populations, this is used to study the demographic history of individual regions or, on a larger scale, ethnogenetic processes. The Y-chromosome [1, 2], whose nonrecombining region is inherited as an integrated haplotype, is one of the most efficient instruments to track population migrations and other events in ethnic history. New haplotypes arise only as a result of the mutation process, and being transferred from generation to generation, form a “family tree” that reflects the order of their origin from each other and permits one to track the paternal line in the gene pool evolution.

This work presents the results from studying the SNP-polymorphism of the Y-chromosome among the population of Slobzhanshchina, which is a historical geographical area, including the northeast regions of Ukraine (almost the entire Kharkov oblast, the south of the Sumy oblast, and the north of the Lugansk oblast) as well as neighboring oblasts of Russia (the southern parts of the Kursk, Belgorod, and Voronezh oblasts). Slobzhanshchina was distinguished in the

17th–18th centuries as a border territory at the southern boundaries of the East-Slavic world, in the northern part of the Wild Field, which is an assembly of scantily populated Black Sea steppes devastated by Mongolian and Tatar forays. To protect the southern boundaries of the Russian state, a line of war fortifications was created in the late 16th–early 17th century: this was the Belgorod defense boundary, whose frontier fortresses were settled by migrants from the internal parts of Russia. The middle 17th century brought about the intense Ukrainian colonization of Slobzhanshchina, which took place at several stages and was formed mainly by natives of Right-Bank Ukraine [3, 4]. Thus, in the 17th century, Slobzhanshchina became a place of contact between two migration flows: the Russian flow from the north and Ukrainian flow from the west. The populations from which migrants came were relatively isolated from each other at least since the middle 13th century, which was the period of the Mongolian invasion into Russia. These migration flows partially overlapped in space; nevertheless, Ukrainian and Russian settlements in the newly developed territory were built separately, alternating with each other. This ethnic mosaic of

**Table 1.** Examined populations of Slobozhanshchina

Region	Ethnos	Y-chromosome	
		sample volume	data source
Ukraine, Sumy oblast, Nedrigailov region	Ukrainians	101	This study
Ukraine, Kharkov oblast, Valki region	Ukrainians	56	This study
Russia, Belgorod oblast, Graivoron and Krasnogvardeisk regions	Ukrainians	56	This study
Slobozhanshchina, Ukrainians (in total)		213	
Russia, Belgorod oblast, Yakovlevo, Prokhorovka, and Krasnoe regions	Russians	143	[6]
Russia, Kursk oblast, Pristen region	Russians	45	[6]
Russia, Voronezh oblast, Repyevo region	Russians	96	[6]
Slobozhanshchina, Russians (in total)		284	

Slobozhanshchina settlements retains its characteristic feature up to the present. Subsequently, until the late 20th century, the Ukrainian and Russian populations of Slobozhanshchina lived in the composition of the only state (first the Russian Empire and then the Soviet Union).

The major goal of this work is to ascertain what are the genetic results of the coexistence of the Russian and Ukrainian gene pools in the Slobozhanshchina territory during more than the last 350 years. Data on the frequency ranges of Y-chromosome haplogroups in the Russian populations of Belgorod oblast were published in the work by Malyarchuk et al. [5]; data with a higher phylogenetic resolution and for another sample of the Russians in Belgorod oblast are presented by Balanovsky et al. [6]. Wozniak et al. [7] published data on the Y-chromosome STR-variation in the Russians of Belgorod oblast. The research by Lependina et al. [8] and Tsapkova [9] on the Y-chromosome polymorphism characterize both the Russian and the Ukrainian population of Belgorod oblast; moreover, the frequency ranges of several major haplogroups are presented for the Russians and Ukrainians, and the phylogenetic ratio of STR-haplotypes inside the major haplogroups is discussed. There are no literary data on Y-chromosome haplogroups in the Slobozhanshchina populations of Ukraine; the most related research on the East-Ukrainian populations are presented in [10]; however, the sample joins individuals of not only the Sumy and Kharkov oblasts but also other oblasts (the Poltava and Chernigov oblasts); moreover, the low level of phylogenetic resolution in this study does not make it possible to determine the frequency of haplogroup I-M170, which is very important for the region, and its variants.

This work has first studied the Slobozhanshchina populations in the context of interethnic comparison by haplogroups of Y-chromosome, which is the most efficient marker to distinguish close populations.

## MATERIALS AND METHODS

### *Studied Populations*

Expeditions were made among the Ukrainians of the Sumy, Kharkov, and Belgorod oblasts to gather biological material (Table 1). The sampling points in Ukraine were the urban-type village of Nedrigailov in the Sumy oblast and the city of Valki in the Kharkov oblast, which are regional centers. The village of Nedrigailov, which was at first settled by Ukrainian peasants, arose around a Polish hillfort in the 16th century and turned by 1632 into a large settlement, which passed to the Russian state after 1647 [11]. The sentry point of Valki appeared later, supposedly in 1641, and was settled almost at once by Ukrainian migrants from Right-Bank Ukraine [12]. In Belgorod oblast of the Russian Federation, a number of settlements were examined in the Graivoron and Krasnogvardeisk regions, which are historically formed living places of the Ukrainians, whose mass migration to the modern territory of Belgorod oblast started in the second half of the 16th century mainly from Right-Bank and Sloboda Ukraine [13]. The mentioned sample appeared in several earlier publications [8, 9, 14], but the frequency ranges of Y-chromosome haplogroups with a high phylogenetic resolution are published in this work for the first time (Table 2).

The data on the frequency ranges of Y-chromosome haplogroups in the Russian populations of Slobozhanshchina (Belgorod, Voronezh, and Kursk oblasts), which are used in this work, were published earlier [6]. To make a comparative analysis, the data on the Orel and Ryazan oblasts [6, 15] and the Ukrainian population of the Lvov and Khmel'nitsk oblasts were used [14].

### *Sampling and Preparation of DNA Collections*

Samples (venous blood, 13 mL) were collected based on regional hospitals and out-patients' clinics; donors were unrelated men, whose paternal and maternal forebears to the third generation belonged to

**Table 2.** Frequency ranges of major Y-chromosome haplogroups in Slobozhanshchina populations

Population	C (M130)	E1b (M35)	G (M201)	I* (M170)	I1 (M253)	I2a (P37.2)	J (M304)	K* (M9)	N1c (M178)	R1a (M198)	R1b (M269)
@Сумская	0.00	6.93	2.97	0.00	9.90	22.77	1.98	3.96	5.94	35.64	9.90
Kharkov	0.00	5.45	7.27	0.00	3.64	25.45	0.00	3.64	5.45	36.36	12.73
Belgorod	0.00	12.5	0.00	0.00	5.36	21.43	3.57	1.79	5.36	46.43	3.57
Slobozhanshchina, Ukrainians	0.00	8.30	3.41	0.00	6.30	23.22	1.85	3.13	5.58	39.48	8.73
Kursk	0.00	2.20	0.00	0.00	4.40	17.80	2.20	2.20	13.30	55.60	2.20
Voronezh	0.00	1.00	2.10	2.00	3.10	16.70	3.10	1.00	6.30	59.40	5.20
Belgorod	0.70	0.70	0.70	0.70	3.50	12.60	4.20	2.80	11.90	59.40	2.80
Slobozhanshchina, Russians	0.23	1.30	0.93	0.90	3.67	15.70	3.17	2.00	10.50	58.13	3.40

\* The data for the Russian populations of the Belgorod, Kursk, and Voronezh oblasts are given according to Balanovsky et al [6]. The frequency ranges of haplogroups are indicated in percentage.

the Ukrainian ethnos and lived in this region. Each donor filled a form about ethnic identity and birth-place of his forebears to the third generation and signed an informed agreement to the examination.

DNA were extracted from the donor blood by the method of phenol-chloroform extraction that makes it possible to obtain stable and long stored DNA collections. Then, DNA solutions were normalized to a concentration of 2 ng/ $\mu$ kL. The effective DNA concentration was determined by the PCR method in real time using a Quantifiler Human DNA Kit (Applied Biosystems) with an ABI 7900HT amplifier (Applied Biosystems).

#### Genotyping of Y-Chromosome Markers

DNA samples were genotyped using the following biallelic markers that determine Y-chromosome haplogroups: C-M130, E1b-M35, G-M201, I\*-M170, I1-M253, I2a-P37.2, J-M304, N1c-M178, R1a-M198, and R1b-M269. According to the classification of the International Y-Chromosome Consortium [16, 17], the major haplogroups are designated by Latin letters from A to T, and the names of branching subhaplogroups are supplemented with alternating numbers and small letters (for example, R1 and R2; R1a and R1b; R1a1a, etc.). A haplogroup is designated in the text with indicating a specific marker (for example, C-M130); markers are specified according to the ISOGG (International Society of Genetic Genealogy, <http://www.isogg.org/tree>). Genotyping was made by the PCR method in real time with an ABI 7900 amplifier (Applied Biosystems) using a TaqMan SNP-marker probe set (Applied Biosystems). At the first stage of genotyping, the samples were all tested for the presence of haplogroups, which are the most frequent for the region, and then selectively based on determining a probable haplogroup by the STR-haplotype. As a result, each DNA sample was related to specific

Y-chromosome haplogroup or a sub-branch within its limits.

#### Genetic Statistical Analysis

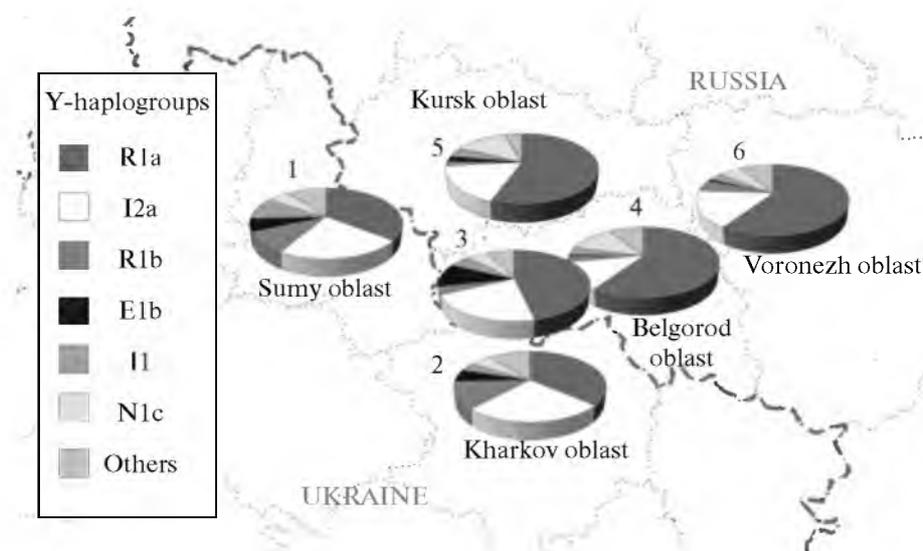
According to the results of genotyping, the frequency ranges of Y-chromosome haplogroups were calculated, and genetic distances  $d$  between the populations were estimated based on the frequency ranges [18]

$$d_{ij} = -\ln \frac{\sum_{a=1}^l p_{ai} p_{aj}}{\sqrt{\sum_{a=1}^l p_i^2 \sum_{a=1}^l p_j^2}},$$

where  $p_{ai}$  is the frequency range of a haplogroup  $a$  in a population  $i$ ;  $p_{aj}$  is the frequency range of the haplogroup  $a$  in a population  $j$ ;  $l$  is the total number of Y-chromosome haplogroups by which a comparison is made.

Genetic distances were calculated in the GDist program (the program was developed at the laboratory of human population genetics at the FSBI "Medical State Scientific Center" of the Russian Academy of Medical Sciences (MSSC RAMS)). The information on the frequency ranges of Y-chromosome haplogroups from the Y-base developed at the laboratory of human population genetics at the FSBI "MSSC" RAMS under the direction of O.P. Balanovskii based on literary data was used to calculate distances. The frequency ranges were used for the following haplogroups: E1b-M35, G-M201, I1-M253, I2a-P37.2, J-M304, N1c-M178, R1b-M269; others were taken in total. The genetic distance matrices were used to build genetic distance maps in the GeneGeo program [19].

The cluster analysis was made based on the obtained genetic distance matrix by the Word method



**Fig. 1.** Frequency distribution of Y-chromosome haplogroups in the Slobzhanshchina populations: (1) Ukrainians of the Sumy oblast, (2) Ukrainians of the Kharkov oblast, (3) Ukrainians of Belgorod oblast, (4) Russians of Belgorod oblast, (5) Russians of the Kursk oblast, and (6) Russians of the Voronezh oblast.

of minimum intracluster variance using the Statistica 6.0 software package. The data on the frequency ranges were used for the following haplogroups: E1b-M35, I1-M253, I2a-P37.2, N1c-M178, R1a-M198, and R1b-M269; others were taken in total.

The intra- and interethnic gene pool differentiation (AMOVA) was estimated using the Arlequin 3.1 software package.

The migration coefficient  $m$  was calculated by the formula

$$m = 1 - \sqrt[t]{\frac{p_t - p_m}{p_0 - p_m}},$$

where  $t$  is the number of migration generations,  $p_0$  is the frequency of an allele in an initial population,  $p_t$  is the frequency of the allele in the same population in  $t$  migration populations, and  $p_m$  is the frequency of the allele in a population of migrants.

## RESULTS AND DISCUSSION

### *Y-Chromosome Haplogroups in the Slobzhanshchina Populations*

Both the Ukrainians and Russians in the studied region had a similar character of major (highly frequent) Y-chromosome haplogroups (Table 2). Haplogroup R1a-M198 was the most frequent; haplogroup I2a-P37 was somewhat less frequent, and N1c-M178, R1b-M269, I1-M253, and E1b-M35 also occurred with significant frequencies. This spectrum of Y-chromosome haplogroups and character of their frequency distribution are typical for the populations of East Europe, except for its northern regions [20, 21].

### *Intra- and Interethnic Differentiation of the Slobzhanshchina Populations*

Despite the general picture of Y-chromosome polymorphism being similar, the Ukrainians and Russians somewhat differed from each other in the frequency ranges of major haplogroups (Table 2, Fig. 1). Thus, the most frequent haplogroup R1a-M198, which is typical for East Europe [22], occurred in approximately 60% of the Russians, meanwhile its frequency in the Ukrainians proved to be less than 40% (the statistical significance of distinctions is  $p < 0.001$ ). In comparison with the Ukrainians, the Russians had a twice-greater frequency of haplogroup N1c-M178 ( $p = 0.0497$ ), which is characteristic of the Finno-Ugric, Baltic, and North-Russian populations in the Baltic Ural region [6, 23–26]. Meanwhile, in comparison with the Russians, the Ukrainians proved to have higher frequencies of haplogroups I2a-P37 (by a factor of 1.3,  $p = 0.0374$ ) and E1b-M35 (by a factor of more than 6,  $p = 0.0002$ ), which reach the greatest frequencies in the European space in the Balkans [27, 28]. In addition, haplogroup R1b-M269, which has a frequency maximum in West Europe, occurred more often in the Ukrainians (by a factor of more than 2.5,  $p = 0.0087$ ) [29].

The quantitative estimate of interethnic distinctions is given in Table 3. According to the results from analyzing the molecular variability (AMOVA), the level of interethnic variability ( $F_{ST} = 0.0345$ ) was four times higher than the level of intraethnic variability ( $F_{ST} = 0.0087$ ); however, it turned out to be low in the absolute value. For comparison, the index of intraethnic variability for a number of European ethnoses is approximately 0.07–0.17 [5, 6, 26]. Therefore, on the one hand, the AMOVA confirms the interethnic dis-

tinctions, but, on the other hand, the latter prove to be relatively low.

As for the intraethnic differentiation, it was absent, i.e., the Slobozhanshchina populations proved to be very homogenous inside ethnic groups, which is visually illustrated by circular diagrams in Fig. 1. Attention is drawn by the high similarity of frequency distributions in three Russian populations (4, 5, 6). As for the Ukrainian populations, a high similarity is observed between two of them (the Sumy (1) and Kharkov (2) populations) with significant distinctions of Belgorod population (3), in which the frequencies of several haplogroups are intermediate between the Ukrainians and Russians. It is evident that it is just its peculiarity, which increases the estimates of intraethnic heterogeneity for the Ukrainian population group.

It is necessary to note that the Ukrainians living in Belgorod oblast of Russia are at the periphery of the major ethnic area. They are predominantly surrounded by the Russians, which contributes to international marriage and may be the most evident cause of intermediate gene pool characteristics. The distinction in frequencies most greatly touches the most widespread haplogroup (R1-M198). Its frequency among the Ukrainians of Belgorod oblast is higher than in the populations of Sloboda Ukraine but lower than in the Russian populations of Slobozhanshchina. If it is assumed that there was a flow of genes from the Russian populations into the Ukrainian ones, and that the change in generations takes place for 25 years (14 generations have changed for 350 years), the migration coefficient proves to be 0.041, i.e., the flow of R1a-Y-chromosomes from the Russians to the Ukrainians averaged approximately 4% for one generation.

Belgorod Ukrainians did not differ from the Kharkov and Sumy Ukrainians in the frequency ranges of haplogroups I2a-P37.2, I1-M253, and N1c, but haplogroup E1b-M35 is noticeably more frequent in them than in all surrounding populations (Fig. 1). The high frequencies of E1b-M35 cannot be explained by the influence of the Russian ethnic environment, in which this haplogroup is rare. It is possible that the effects of genetic drift manifested themselves with respect to the mentioned haplogroup.

One more interesting peculiarity is that haplogroup G-M201 is extraordinarily frequent (in terms of the studied region) in the Ukrainians of the Kharkov oblast (Table 2). The major propagation area of G-M201 is related to West Asia and the Caucasus [30], and this group is among minor ones in the studied region; its frequency usually is not more than a few percent. In this connection, it seems interesting to study in more detail the population in the city of Valki, since the Muravsky trail, which was one of the main foray ways of the Crimean and Nogay Tatars in the 16th–17th centuries, went just through the territory of the modern Valki region.

**Table 3.** Results from analyzing molecular variability (AMOVA) for the Ukrainians and Russians of Slobozhanshchina

Index	$N_{\text{pop}}$	$N$	$N_{\text{hg}}$	$d$	AMOVA ( $F_{\text{st}} \times 10^2$ )
Ukrainians	3	71	11	0.036	1.161
Russians	3	95	11	0.009	0.544
Interethnic level					3.45
Intraethnic level					0.87
Intrapopulation level					95.68

\*  $N_{\text{pop}}$  is the number of populations in a group,  $N_{\text{hg}}$  is the average size of a population sample,  $n$  is the number of analyzed haplogroups,  $d$  is the average pairwise genetic distance between populations, and  $F_{\text{st}}$  is the normalized dispersion of haplogroup frequencies.

#### *Russian and Ukrainian Slobozhanshchina Populations against the Genetic Background of Surrounding Regions*

The comparison of the Ukrainian and Russian Slobozhanshchina populations would be incomplete without correlation with neighboring regions, in particular, with other populations of Russia and populations of Right-Bank Ukraine. This correlation will make it possible to answer the question whether the modern frontier regions have remained genetically similar to the territories from which migrants initially came or if they are some transitional variant. It is not improbable either that the interethnic distinctions revealed in Slobozhanshchina will prove to be insignificant against the surrounding genetic background, and it will be possible to relate all the studied populations to some only genetic continuum, which may be Ukrainian, Russian, or common East-Slavic.

For these purposes, we have analyzed the data in several ways, having added the information on other populations from the Y-base ([www.genofond.ru](http://www.genofond.ru)) to our own results. Figure 2 presents the results of the cluster analysis, which reflect the mutual location of the South-Russian, West-Ukrainian, and East-Ukrainian populations depending on their genetic similarity in Y-chromosome polymorphism. The dendrogram has two well-marked clusters (Ukrainian and South-Russian). The Russians proved to be more homogenous in Y-chromosome markers than the Ukrainians: the average genetic distance between the indicated Russian populations was  $d = 0.016$ , meanwhile it was a factor of 1.5 greater between the Ukrainian populations ( $d = 0.025$ ). However, the “interethnic” genetic distances (between the Ukrainians and Russians) were several times higher than the “intraethnic” distances (on average,  $d = 0.062$ ), which resulted in distinguishing ethnically specific clusters.

In order to reveal the regions that are genetically close to the studied populations on the scale of entire Europe, we built genetic distance maps (Fig. 3). The maps show that the regions genetically close to the

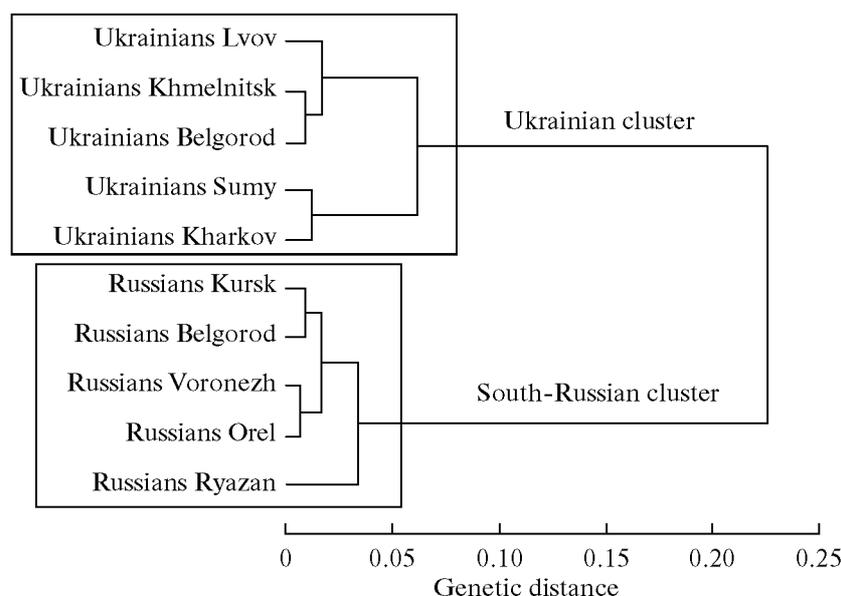


Fig. 2. Dendrogram of genetic ratios according to Y-chromosome markers for the Ukrainian and South-Russian populations.

Slobozhanshchina Russians and Ukrainians have different patterns. Other Ukrainian populations of Central and Western Ukraine, as well as populations of the Lower Don and Belarusian Polesye, prove to be the closest to the Slobozhanshchina Ukrainians ( $d < 0.03$ ). The Russian populations of Slobozhanshchina are similar to the southern and central Russian populations and to the central and northern Belarusians and Poles ( $d < 0.03$ ).

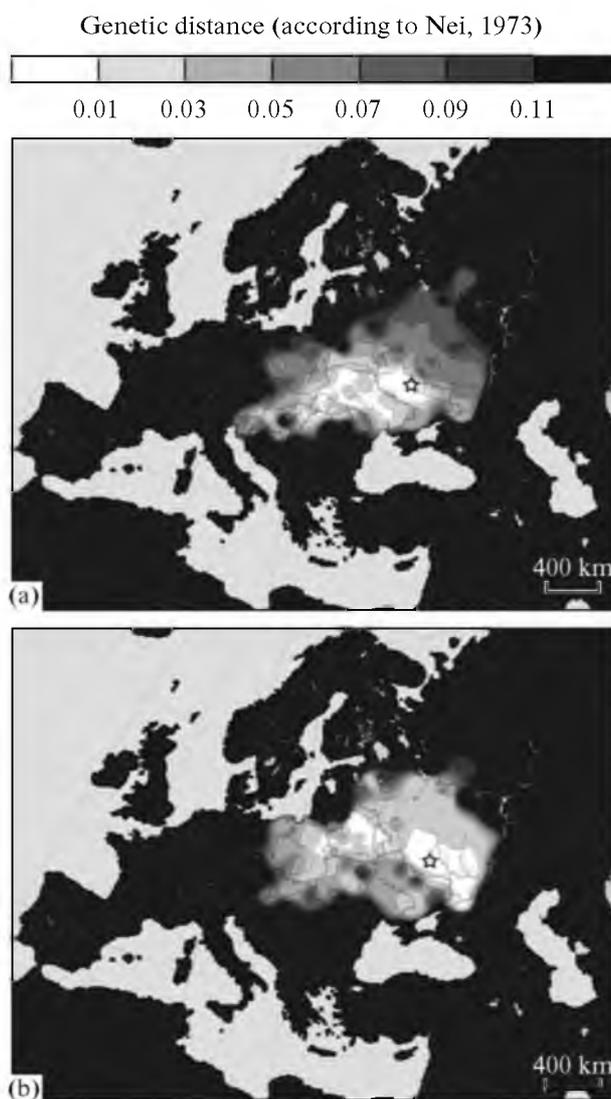
The results of the performed study indicate the genetic distinctions in Y-chromosome markers between the Ukrainians and Russians within the Slobozhanshchina historical region. Despite the geographic proximity and historically caused close cooperation, both peoples retain the ethnic specificity of their gene pools two centuries later: the Ukrainians gravitate towards the remaining part of Ukraine, and the Russians are drawn towards the south of European Russia. This result was partially reported about in the works [9, 31], according to which the population in the south of Central Russia has minimal genetic distances from the “Middle-Russian” population and is genetically distant from the “Middle-Ukrainian” population.

Nevertheless, the Russian and Ukrainian populations prove to be very genetically close on the scale of the entirety of Europe. Both genetic distance maps have almost coincident shapes of light clouds, into which three East-Slavic peoples get (the Russians (except for the genetically specific Northern Russians [6]), Ukrainians, Belarusians as well as representatives of West Slavs (the Poles and Slovaks) ( $d < 0.1$ ).

#### *Genetic and Geographical Properties of the Region*

The obtained results have something in common with the results of genetic and demographic research

in the studied region, according to which rather high indices of marriage association by nationality persist in the rural area [32], i.e., intraethnic marriages are contracted more often than is expected in the complete absence of ethnic endogamy. It is probable that this marriage structure is due to the mosaic ethnic specificity of settlement of the region in the 17th–18th centuries, when the Russians and Ukrainians “grew roots” in different villages. Meanwhile, the spatial and geographical characteristics of marriage migrations indicate that, when choosing a marriage partner, preference is given to the persons who originate from the same locality. For example, this trend was described for Ukrainian villages in the Kharkov oblast [33]. It was shown that approximately 90% of all marriages were contracted between natives of one region (in the late 20th century, approximately 50%) [34, 35] and the average marriage distance (the distance between birthplaces of spouses) did not surpass several tens of kilometers in the south of Central Russia in the early and middle 20th century [36, 37]. It is logical to suppose that the structure of nationality marriages can be affected by the prevalent ethnic environment: in the places where the population proved to be ethnically homogenous (or almost homogenous), small marriage distances will keep this state of affairs in the future. According to the results of censuses, the ethnic structure of the population is abruptly changing along almost the entire Ukrainian-Russian boundary: in the Kursk, Belgorod, and Voronezh oblasts of the Russian Federation, 94.4–96.5% of the population are Russians [<http://www.perepis-2010.ru>]; in the Kharkov and Sumy oblasts, 70.7–88.8% of the population are Ukrainians (Ukrainians account for 81.3–91.4% of the rural population) [<http://www.ukrcensus.gov.ua>].



**Fig. 3.** Maps of genetic distances from the Ukrainians and Russians of Slobozhanshchina (based on the data on the frequency ranges of Y-chromosome haplogroups). The maps were built based on the calculated genetic distances from reference populations of (a) Slobozhanshchina Ukrainians (the Sumy, Kharkov, and Belgorod oblasts taken together) and (b) Slobozhanshchina Russians (Belgorod, Voronezh, and Kursk oblasts taken together) to more than 500 populations of Europe, Ural, Caucasus, Near East, and Northern Africa. The reference populations are marked with asterisks. Light and dark colors correspond to genetically close and distant regions.

Where Ukrainian and Russian villages are neighboring, there are genetic properties that can be attributed to the results of mixed marriages. In the research by Lependina [38], the regions of Belgorod oblast with the Ukrainian and Russian population, which were studied as regards the polymorphism of 12 autosome loci, were joined into clusters according to geographic proximity rather than nationality; meanwhile, genetic distances were strongly correlated with geographic distances ( $r = 0.77$ ). According to the results of the mentioned work, the gene pool characteristics in the Ukrainians who settle the regions of Belgorod oblast of the Russian Federation were intermediate between the

Ukrainians and Russians in Y-chromosome polymorphism.

Consequently, genetic distinctions between the Ukrainians and Russians may be largely due to the spatial characteristics of marriage migration and prevalent ethnic environment.

## CONCLUSIONS

The Ukrainian and Russian populations of Slobozhanshchina prove to be very similar in the set and frequency distribution of Y-chromosome haplogroups and completely fit into the East-European genetic space. The closest regions ( $d < 0.03$ ) defined by

the genetic distance maps (Fig. 3) cover the territory of Ukraine, the south and center of European Russia, as well as Belarus, Poland, and Slovakia. However, despite this high basic similarity of the Ukrainian and Russian gene pools in Slobzhanshchina, the use of Y-chromosome polymorphism has also permitted us to reveal the distinctions between such a close kinship and neighborhood of ethnic groups. According to the results of the cluster analysis (Fig. 2) and in the genetic distance maps (Fig. 3), the Ukrainian populations of Slobzhanshchina gravitate towards the remaining part of Ukraine, and the Russian populations are drawn towards the south of European Russia. This regularity in the genetic differentiation of gene pools has been confirmed by the results from analyzing the interpopulation variability by the AMOVA method (Table 3). Significant distinctions involve the frequencies of important haplogroups that determine the genetic landscape of the territory, such as R1a-M198, 12a-P37, R1b-M269, N1c-M178, and E1b-M35 (Table 2).

The persistent distinctions in Y-chromosome gene pools between the Slobzhanshchina Ukrainians and Russians may be due, despite their being neighboring for more than 150 years, to the trend of marriage contraction in their own locality against the background of the historically formed mosaic ethnic structure of settlements.

Both the Ukrainians and Russians of Slobzhanshchina proved to be genetically homogenous within their ethnoses (Table 3, Fig. 1). This primarily speaks for significant migration flows leading to “leveling” of gene pools. Against the background of the Russian populations, the Ukrainian populations looked somewhat less homogenous, probably, thanks to the Belgorod population, which probably took the gene flows from the Russian ethnic environment.

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