Differentiation of Mitochondrial DNA and Y Chromosomes in Russian Populations

BORIS MALYARCHUK,[1] MIROSLAVA DERENKO,[1] TOMASZ GRZYBOWSKI,[2] ARINA LUNKINA,[1] JAKUB CZARNY,[2] SERGE RYCHKOV,[3] IRINA MOROZOVA,[3] GALINA DENISOVA,[1] AND DANUTA MIŚCICKA-ŚLIWKA[2]

Abstract The genetic composition of the Russian population was investigated by analyzing both mitochondrial DNA (mtDNA) and Y-chromosome loci polymorphisms that allow for the different components of a population gene pool to be studied, depending on the mode of DNA marker inheritance. mtDNA sequence variation was examined by using hypervariable segment I (HVSI) sequencing and restriction analysis of the haplogroup-specific sites in 325 individuals representing 5 Russian populations from the European part of Russia. The Y-chromosome variation was investigated in 338 individuals from 8 Russian populations (including 5 populations analyzed for mtDNA variation) using 12 binary markers. For both uniparental systems most of the observed haplogroups fell into major West Eurasian haplogroups (97.9% and 99.7% for mtDNA and Y-chromosome haplogroups, respectively). Multidimensional scaling analysis based on pairwise F_{ST} values between mtDNA HVSI sequences in Russians compared to other European populations revealed a considerable heterogeneity of Russian populations; populations from the southern and western parts of Russia are separated from eastern and northern populations. Meanwhile, the multidimensional scaling analysis based on Y-chromosome haplogroup F_{ST} values demonstrates that the Russian gene pool is close to central-eastern European populations, with a much higher similarity to the Baltic and Finno-Ugric male pools from northern European Russia. This discrepancy in the depth of penetration of mtDNA and Y-chromosome lineages characteristic for the most southwestern Russian populations into the east and north of eastern Europe appears to indicate that Russian colonization of the northeastern territories might have been accomplished mainly by males rather than by females.

The origin of Eastern Slavs (Russians, Ukrainians, and Belorussians) is a complex issue that has been debated by linguists, anthropologists, archeologists, and

[1]Genetics Laboratory, Institute of Biological Problems of the North, Far-East Branch of the Russian Academy of Sciences, Magadan 685000, Russia.
[2]Ludwik Rydygier Medical University, Forensic Medicine Institute, 85-094 Bydgoszcz, Poland.
[3]Vavilov Institute of General Genetics, Russian Academy of Sciences, Moscow 119991, Russia.

Human Biology, December 2004, v. 76, no. 6, pp. 877–900.

KEY WORDS: MTDNA, Y CHROMOSOME, PHYLOGEOGRAPHY, RUSSIAN POPULATIONS, POLES, UKRAINIANS, LATVIANS, LITHUANIANS, FINNS, ESTONIANS, FINNO-UGRIC-SPEAKING POPULATIONS, BALTIC-SPEAKING POPULATIONS, URALIC-SPEAKING POPULATIONS.

historians for more than 300 years. The Slavonic colonization of eastern Europe [which was most intensive in the 6th–7th centuries A.D. according to archeological data (Sedov 1995)] has entailed changes in the anthropological composition of Slavs because of their interpopulation contacts with Baltic tribes in the northwest, Finno-Ugric tribes in the north and east, and Iranian (or Iranic-speaking) tribes in the south of eastern Europe (Alekseeva and Alekseev 1989). Notwithstanding the vast factual material concerning ancient and modern Eastern Slavonic populations, accumulated by archeologists, anthropologists, and historians, many problems still remain unsolved, including the character of interactions between Slavs and autochthonous populations of eastern Europe.

Previous genetic studies of classical genetic markers (Rychkov et al. 1999) and anthropological data (Alekseeva 1973; Rychkov and Balanovska 1988) have shown geographic differences between Russian populations and have allowed researchers to recognize at least two groups of Russians. It has been suggested that the most western Russian populations appear to be descendants of the Slavs, whereas northern, eastern, and southern Russian populations are the result of admixture between Slavonic tribes and pre-Slavonic populations of eastern Europe (Rychkov and Balanovska 1988). In addition, principal components analyses performed on the basis of anthropological data revealed that modern Russians are represented by two regional groups of populations, southeastern and northwestern (Alekseeva 1999). Using computer cartography of anthropological and genetic data, Balanovsky and Balanovska (2002) recently identified a latitudinal (north–south) trend as the main geographic pattern of the Russian gene pool variation.

Although there are several examples of research on Russian populations using nuclear DNA (Limborska 1999; Spitsyn et al. 2001), Y-chromosome (Rosser et al. 2000; Wells et al. 2001), and mitochondrial DNA (mtDNA) variability (Orekhov et al. 1999; Malyarchuk et al. 2002), no detailed mtDNA and Y-chromosome studies have been performed to analyze the differentiation of regional populations of Russians. Previously, population samples of Russians were analyzed in different ways: Some studies covered only mtDNA hypervariable segment I (HVSI) sequences (Malyarchuk et al. 1995; Orekhov et al. 1999); other studies also included coding region RFLPs (Malyarchuk and Derenko 2001; Malyarchuk et al. 2002). As for the Y chromosome, a limited number of Russian population samples have been investigated but only in the framework of global Y-chromosome marker surveys in Europeans. These studies focused on placing Y-chromosome variation in Russians in a broader phylogeographic perspective (Karafet et al. 1999; Rosser et al. 2000; Wells et al. 2001). Given the large number of the Russian people and the complexity of their population history, it is necessary to perform a more detailed study of Russian populations inhabiting the European part of Russia (the East European, or Russian, plain), where the first stages of Russian ethnic history occurred. To obtain a better estimate of the level of genetic differentiation in Russian populations, we present here mtDNA and Y-chromosome data in Russian individuals (325 mtDNA and

338 Y-chromosome samples) originating from the indigenous geographic area of the Russian population.

Materials and Methods

Samples. For the mtDNA variation study, a sample of 325 Russian individuals (125 females and 200 males) from the following 5 populations of the European part of Russia was analyzed (sample sizes are given in parentheses): Tula (73), Kaluga (71), Vladimir (72), Yaroslavl (41), and Pskov (68) regions (Figure 1). All individuals were maternally unrelated, and their mothers had been born in the area considered for this study. For the Y-chromosome variation study, 338 Russian males from the same populations [Tula (44), Kaluga (42), Vladimir (51), Yaroslavl (23), and Pskov (40) regions] and three additional populations from the Belgorod (44), Orel (36), and Nizhniy Novgorod (58) regions were analyzed (Figure 1). All of these individuals were paternally unrelated and originated from the area considered for this study. Appropriate informed consent was obtained from all participants in this study. All samples were randomly taken mainly from towns of the corresponding administrative areas of Russia.

HVSI Sequencing and RFLP Analysis of mtDNA. Genomic DNA was extracted from whole blood by a standard phenol/chloroform method. Hypervariable segment I (HVSI) of the mtDNA noncoding control region was amplified and sequenced as described elsewhere (Malyarchuk et al. 2002). The nucleotide sequences of HVSI from position 15991 to 16400 were determined and compared with the Cambridge Reference Sequence (CRS) (Anderson et al. 1981; Andrews et al. 1999). Nucleotide positions showing point indels and transversions located between positions 16180 and 16193 were excluded from further analysis.

RFLP typing was performed using restriction endonuclease analysis of PCR-amplified mtDNA fragments; the same primer pairs and amplification conditions as described elsewhere by Torroni et al. (1996) and Finnilä et al. (2000) were used. The samples were typed for a restricted set of RFLPs (Table 1) that were diagnostic of all major Eurasian clusters, on the basis of the hierarchical mtDNA RFLP scheme (Macaulay et al. 1999; Richards et al. 2000; Yao et al. 2002). HVSI sequences, belonging to haplogroups N1a, N1b, U1, U3, U5, U7, M1, L1b, and L3b were identified on the basis of the HVSI motif classification (Richards et al. 2000; Salas et al. 2002; Yao et al. 2002).

Analysis of Y-Chromosome Binary Polymorphism. Twelve binary markers [RPS4Y, SRY-8299, M89, 12f2, M9, M20, 92R7, SRY-10831, DYS199, Tat, LLY22g, and the *Alu* insertion polymorphism (YAP) at DYS287] defining the structure of the North Eurasian Y-chromosome variation (Underhill et al. 2001; Y Chromosome Consortium 2002) were analyzed in this study (Figure 2). The

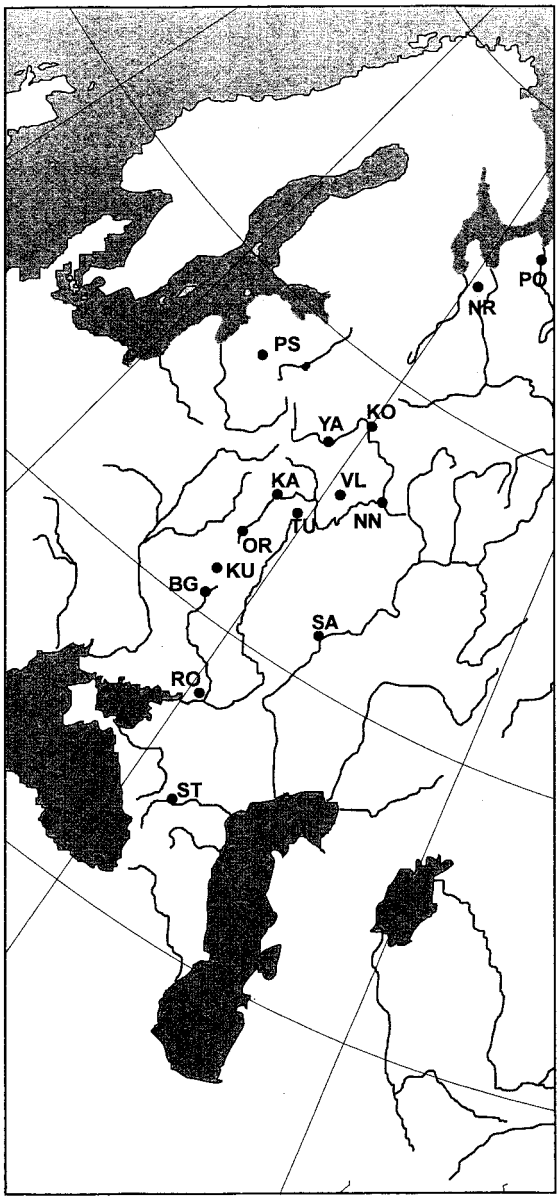

Figure 1. Geographic locations of Russian samples used in this study. Present data (regions): TU, Tula; KA, Kaluga; VL, Vladimir; YA, Yaroslavl; PS, Pskov; BG, Belgorod; NN, Nizhniy Novgorod. Previously published mtDNA data: ST, Stavropol region, OR, Orel region, and SA, Saratov region (Malyarchuk et al. 2002); KU, Kursk region, and KO, Kostroma region (Orekhov et al. 1999); and RO, Rostov region (Richards et al. 2000). Previously published Y-chromosome data (Wells et al. 2001): NR, Northern Russians; PO, Russian Pomors.

Table 1. RFLPs Analyzed to Identify Major Eurasian mtDNA Haplogroups

Haplogroup	*Characteristic Restriction Site(s)*
West Eurasian	
HV	−14766 *Mse*I
H	−14766 *Mse*I, −7025 *Alu*I
pre*V1	−14766 *Mse*I, −15904 *Mse*I, +4577 *Nla*III
pre*V2	−14766 *Mse*I, +15904 *Mse*I, +4577 *Nla*III
V	−14766 *Mse*I, +15904 *Mse*I, −4577 *Nla*III
U	+12308 *Hin*fI
K	+10394 *Dde*I, +12308 *Hin*fI, −9052 *Hae*II
U2	+12308 *Hin*fI, +15907*Rsa*I
U4	+12308 *Hin*fI, +4643*Rsa*I
U8	+12308 *Hin*fI, −7055*Alu*I
J	+10394 *Dde*I, −13704 *Bst*OI
T	+13366 *Bam*HI, +15606 *Alu*I
T1	+13366 *Bam*HI, +15606 *Alu*I, −12629*Ava*II
N1	−12498 *Nla*III
I	−4529 *Hae*II, +8249 *Ava*II, +10032 *Alu*I, +10394 *Dde*I, −12498 *Nla*III
W	+8249 *Ava*II, −8994 *Hae*III
X	−1715 *Dde*I, +14465 *Acc*I
East Eurasian	
M	+10394 *Dde*I, +10397 *Alu*I
C	+10394 *Dde*I, +10397 *Alu*I, −13259 *Hinc*II/+13262 *Alu*I
D	+10394 *Dde*I, +10397 *Alu*I, −5176 *Alu*I
E	+10394 *Dde*I, +10397 *Alu*I, −7598 *Hha*I
G	+10394 *Dde*I, +10397 *Alu*I, +4830 *Hae*II/+4831 *Hha*I
A	+ 663 *Hae*III
B	9-bp deletion
F1	−12406 *Hpa*I/*Hinc*II

RFLP markers are given relative to the revised version of the Cambridge Reference Sequence (Andrews et al. 1999) belonging to haplogroup H. Site gains and losses are indicated by a plus sign (+) or a minus sign (−).

binary markers were typed according to methods described elsewhere: M9 (Underhill et al. 1997) was typed according to the method of Hurles et al. (1998); YAP (Hammer 1994) was typed according to the method of Hammer and Horai (1995); SRY-10831 and SRY-8299 (Whitfield et al. 1995) were typed according to the methods of Kwok et al. (1996) and Santos et al. (1999), respectively; 92R7 (Mathias et al. 1994) was typed according to the method of Hurles et al. (1999); 12f2 (Casanova et al. 1985) was typed according to the method of Rosser et al. (2000); Tat was typed according to the method of Zerjal et al. (1997); LLY22g and M20 were typed according to the method of Underhill et al. (2000); RPS4Y-711 (Bergen et al. 1999) was typed according to the method of Kayser et al. (2000); DYS199 (Underhill et al. 1997) was typed according to the method of Santos et al. (1999); and M89 (Underhill et al. 2000) was typed according to the method of Ke et al. (2001).

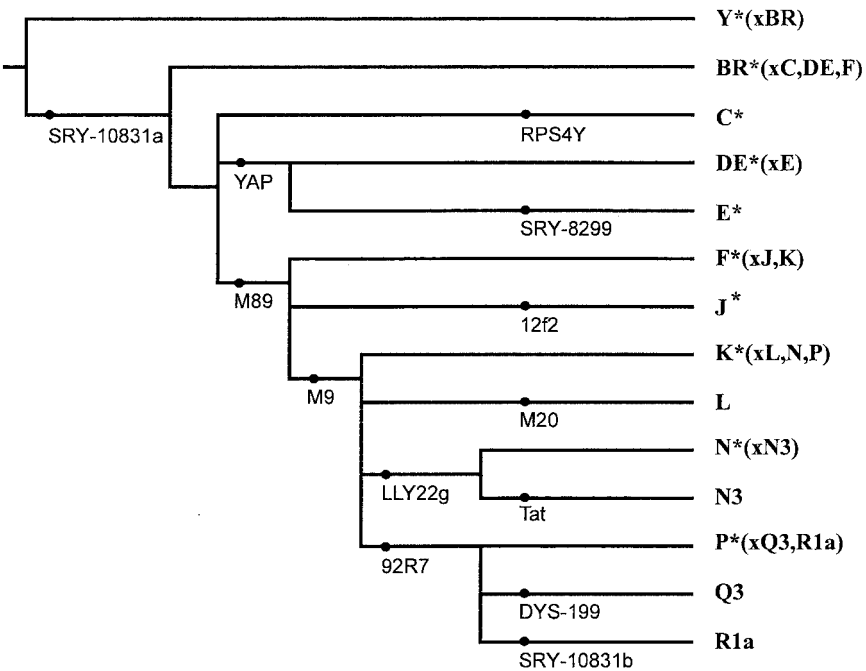

Figure 2. Maximum parsimony phylogeny of 12 Y-chromosome binary markers defining major haplogroups in North Eurasian populations. Haplogroup designation follows the nomenclature system recommended by the Y Chromosome Consortium (2002).

SNP variants at haplogroup-specific sites were determined using PCR RFLP assay, followed by an electrophoretic analysis of DNA fragments in 8% polyacrylamide gels and visualization through ethidium bromide staining. The Y-chromosome SNP haplogroup nomenclature used is that recommended by the Y Chromosome Consortium (2002).

Statistical Analysis. Genetic variation was analyzed using methods implemented in the Arlequin 1.1 software (Schneider et al. 1997). The statistical significance of F_{ST} values was estimated by permutation analysis using 10,000 permutations. Multidimensional scaling analysis of pairwise interpopulation F_{ST} values was performed by means of the software package Statistica (StatSoft Inc., Tulsa, Oklahoma).

mtDNA HVSI data from the following Russian populations were used for comparison (sample sizes are given in parentheses): the Stavropol (62), Orel (76), Saratov (63) regions (Malyarchuk et al. 2002); the Kursk (34) and Kostroma (55) regions (Orekhov et al. 1999); and the large Cossack village of Razdorskaya in

the Rostov region (25) (Richards et al. 2000). Additional samples from 9 populations across central and eastern Europe were also included in the comparative analysis. These populations were Adygei (50) from North Caucasus (Macaulay et al. 1999); Tatars (45) and Mari (60) from the Middle Volga region (Orekhov 2002); Austrians (101) (Parson et al. 1998); Finns (50), Estonians (47), and Karelians (83) (Sajantila et al. 1995); Poles (436) (Malyarchuk et al. 2002); and Lithuanians (120) (Kasperaviciute and Kucinskas 2002).

In a comparative analysis of Y-chromosome variation data, the Russian populations of northern Russia [Northern Russians (49) and Pomors (28) (Wells et al. 2001)] were also used. In addition, samples from nine central and eastern European populations (Rosser et al. 2000) were also analyzed: Mari (48) and Chuvash (17) from the Middle Volga region; Finns (57), Estonians (207), Lithuanians (38), Latvians (34), Ukrainians (27), Belorussians (41), and Poles (112).

Results

mtDNA and Y-Chromosome Haplogroups in Russians. The analysis of HVSI variation in combination with RFLP typing of the coding region haplogroup-diagnostic sites allowed detection of 188 different mtDNA haplotypes in a total sample of 325 Russian individuals (Table 2). It was found that these haplotypes are clustered, according to human mtDNA classification (Macaulay et al. 1999; Richards et al. 2000; Salas et al. 2002; Yao et al. 2002), into haplogroups H, pre-V, HV*, R1, U1, U2, U3, U4, U5, U7, U8, K, J, T*, T1, I, N1a, N1b, X, W, C, D, G, M1, L1b, and L3b.

Table 3 summarizes the frequencies of the mtDNA haplogroups and subgroups found in the Russian populations studied. Russians present relatively high means of pairwise nucleotide differences between HVSI sequences. This parameter ranges from 4.74 in the Yaroslavl sample to 5.46 in the Vladimir sample and is in accordance with diversity estimates found in European and Middle Eastern populations [from 2.95 in Basques to 7.08 in populations of the Middle East according to Comas et al. (1997)].

The majority (97.8%) of mtDNA haplotypes found in Russians fall into major West Eurasian haplogroups. The frequency of East Asian–specific haplotypes in Russians is very low (1.5% on average). All of them belong to macrohaplogroup M (C, D, G). A single haplotype found in Russians belongs to specific haplogroup M1, which is distributed mainly in East Africa (Somalia and Ethiopia) and the Red Sea region (Richards et al. 2003). However, the low frequencies of haplogroup M1 were observed in southern Europe and the Caucasus region (Richards et al. 2000), from where this haplogroup may have been introduced into the Russian population. An interesting finding of the present study is the occurrence of African-specific mtDNA lineages (L1b and L3b) in the Russian gene pool. Their frequency is very low (0.6%), but this estimate should be lowered to 0.3% to take into account the previous data on mtDNA

Table 2. mtDNA Haplotypes in Russians Obtained by Combining the Data on the HVSI Sequence and Haplogroup-Specific RFLPs

HVSI Variation (−16000 Relative to CRS Sequence Numbering)	*Haplo-group*	*Tula (n = 73)*	*Kaluga (n = 71)*	*Vladimir (n = 72)*	*Yaroslavl (n = 41)*	*Pskov (n = 68)*
Cambridge Reference Sequence (CRS)	H	11	6	7	3	3
70 93 311	H	1				
93 311	H		2			
93	H					1
126	H					1
129	H		1			
147	H		1			
162	H				1	3
51 162	H			1		
51 162 213 256	H	1				
162 311	H			2		
168	H					1
170	H	1				
176	H	1			1	
169 176	H					1
180	H		1			
183delA	H					1
189	H				1	
209	H	2				2
221	H	1		1		
222	H				1	
234	H	1				
86 239	H				1	
256 352	H			1		
261	H		2		1	
261 311	H		2		1	
261 335	H			1		
274	H					1
274 317	H			1		
241 274 287	H				1	
278 293 311	H				2	1
93 278 293 311	H		1			
134 278 293 311	H	1				
172 278 293 311	H		1			
224 278 293 311	H			1		
92 140 265 293 311	H	4	3			
286	H	1				1
235 291	H					1
249 291	H	1				
293	H	1				
296	H					1
300	H			1		
304	H	3	3			3
192 304	H	1				

Table 2. (Continued)

HVSI Variation (−16000 Relative to CRS Sequence Numbering)	*Haplo-group*	*Tula (n = 73)*	*Kaluga (n = 71)*	*Vladimir (n = 72)*	*Yaroslavl (n = 41)*	*Pskov (n = 68)*
209 304	H				1	
240 304	H	1				
258AT 304	H		1			
304 352	H		1			
304 390	H	1				
304 400	H	1		1	1	1
294CA 304	H					2
294 304	H	1			1	
271 294 304	H				1	
311	H	1				1
311 319	H				1	
320	H			1		
354	H	1		5		1
193 354	H	1				
189 356	H		1			1
188 189 356	H				1	
75 111 183AC 189 209 356	H	1				
183AC 189 193.1C 294 356	H			1		
80 189 356	H		1			
80 129 189 193.1C 356	H			1		
80 129 142 189 193.1C 193.2C 356	H					1
362	H	1			1	1
219 260 362	H	3				
153 298	V					1
153 298 319	V					1
169 298	V		1			
298	V	1	1			2
298	pre*V2				1	
298	pre*V1	1				
311	HV*				1	
113AC 172 311	HV*		1			
129 249 311	HV*				1	
249 261 311	HV*	1				
274 278 311	HV*		1			
278 311	HV*			1		
278 311	R1					1
69 126	J	1	1	1	1	3
63 69 126	J					1
69 126 163	J	1				
69 126 230	J	1				
69 92 126 261	J	1				
69 126 289AT	J					1
69 126 290	J					1
69 126 241	J			1		

Table 2. (Continued)

HVSI Variation (−16000 Relative to CRS Sequence Numbering)	*Haplo-group*	*Tula (n = 73)*	*Kaluga (n = 71)*	*Vladimir (n = 72)*	*Yaroslavl (n = 41)*	*Pskov (n = 68)*
69 126 145 231 261 399	J			1		
69 126 145 172 222 261	J		1	1		1
69 93 126 145 172 222 261	J		1		1	
69 126 145 172 222 260 261	J					1
69 126 193 278	J			2		
126 294 296 304	T*	1	1	2		
126 145 296 304	T*	2				
126 223 294 296 304	T*	1				
126 294 296 304 354	T*					1
126 294 296 304 362	T*		2			
126 294 304	T*		3	2		
126 172 294 304	T*	1		1		
78 126 294 296	T*				1	
126 182AC 183AC 189 294 296	T*					1
126 264 286 294 296 362	T*			1		
126 292 294 296 311 362	T*	1				
126 292 294 296	T*		1			
126 292 294	T*		1			
126 163 186 189 294	T1		1	5		
126 163 186 189 271 294	T1			2		
92 126 163 186 189 294	T1	1		1		
93 126 163 186 189 294	T1		1			1
126 163 186 189 294 302	T1					1
224 311	K		2	3	3	
224 311 368	K	2				
93 126 224 261 311	K		1			
180 189 224 233 311	K			1		
189 193.1C 270 311	K			1		
182AC 183AC 189 249	U1		1			
51 129GC 183AC 189 362	U2		1			
51 129GC 183AC 189 193.1C 362	U2			1		
51 129GC 182AC 183AC 189 311 362	U2					1
51 126 129GC 189 256 311 362	U2		1			
51 129GC 189 256	U2					1
343	U3	1	1	1		
168 189 343	U3	1				
Cambridge Reference Sequence	U4				1	
150 189 360	U4		2			
169 319	U4			1		
294	U4					1

Table 2. (Continued)

HVSI Variation (−16000 Relative to CRS Sequence Numbering)	*Haplo-group*	*Tula (n = 73)*	*Kaluga (n = 71)*	*Vladimir (n = 72)*	*Yaroslavl (n = 41)*	*Pskov (n = 68)*
357	U4				1	
356	U4	1	2			
223 356	U4		2			
134 356	U4	1		1		
154 356	U4					1
242CA 288 356 362	U4	1				
114CA 192 256 270 294	U5a	1	1	1		1
114CA 192 256 270 292 294	U5a					1
114CA 192 256 270 294 311	U5a		2		1	
192 256 270	U5a					2
192 256 269 270	U5a		1			
192 256 270 399	U5a					2
129 192 256 270 399	U5a		1			
93 172 192 256 270 399	U5a					1
192 218 256 270 278	U5a					1
192 222 256 270 399	U5a	1				
192 256 270 320 399	U5a					1
192 256 302 320 390 399	U5a				1	
192 256 270 291 399	U5a					1
93 192 256 270 291	U5a				1	
93 192 256 270 291 399	U5a				1	
92 192 209 256 291 399	U5a					1
92 145 189 192 256 270 399	U5a		1			
38 256 270 399	U5a			1		
256 270 399	U5a			1		
256 399	U5a					1
192 256 270 311	U5a			1		
234 240AC 270 362	U5a			1		
189 270	U5b		1			1
183AC 189 270	U5b	1				
189 264 325	U5b					1
144 189 270	U5b		1			
144 183AC 189 270	U5b	1				
318AT	U7			1		
342	U8					1
129 223 391	I			1		
86 129 223 391	I		1			
129 172 223 311 391	I	2		1	1	
129 172 223 266 311 391	I			2		
147CA 172 223 248 320 355	N1a			1		
172 223 248 320 355	N1a				1	
92 129 147CA 154 172 223 248 320 355	N1a	1				
145 176 223 390	N1b				1	
145 176CG 223 390	N1b	1		1		

Table 2. (Continued)

HVSI Variation (−16000 Relative to CRS Sequence Numbering)	*Haplo-group*	*Tula (n = 73)*	*Kaluga (n = 71)*	*Vladimir (n = 72)*	*Yaroslavl (n = 41)*	*Pskov (n = 68)*
223 292	W			1		
192 223 292 325	W			1		2
93 223 292 295	W			1		
189 223 266 278	X		1			
183AC 189 193.1C 223 278	X				1	
182AC 183AC 189 193.1C 223 278	X				1	
183AC 189 193.1C 223 255 278	X				1	
183AC 189 223 255 278	X		1			
223 287 298 327	C		1			
93 129 223 298 327	C		1			
223 245 362	D				1	
223 278 362	G2a					1
183AC 189 249 311	M1			1		
126 175 189 223 264 270 278 311 400	L1b	1				
124 223 278 294 362	L3b		1			

The nucleotide positions in HVSI sequences correspond to transitions; transversions are further specified. Haplogroup names are according to the recommended mtDNA classification (Macaulay et al. 1999; Richards et al. 2000). The presence of insertions or deletions is referred to by "." or "del," respectively, following the nucleotide position.

variability in Russian populations (Orekhov et al. 1999; Malyarchuk et al. 2002). These results indicate that the appearance of African mtDNAs among Russians was probably casual.

Table 4 reports the frequencies of the Y-chromosome haplogroups found in Russian samples. The pattern of Y-chromosome haplogroup distributions in Russians is typical for northeastern European populations (Rosser et al. 2000). The principal diagnostic haplogroups for Russians are haplogroups R1a and N3, which occur in the studied populations at a total frequency of 50–72%. The remaining Y-chromosome haplogroups represent mostly paraphyletic groups distributed with similar frequencies in European populations.

It should be noted that the frequency of paragroup P* [or haplogroup 1 according to Rosser et al.'s (2000) nomenclature] in Russians (2.3–19%) reflects the known pattern of distribution, with a high incidence of P* in western European populations (especially those of Celtic origin) and a lower frequency in the east (Zerjal et al. 2001). Haplogroups E* and J* were found only in the most southwestern Belgorod population at frequencies of 6.8% and 13.6%, respectively. These haplogroups probably are associated with the contributions of Neolithic farmers to the European gene pool, because both haplogroups E* and J*

Table 3. mtDNA Haplogroup Distributions (Percentage, with Number of Individuals in Parentheses) in Russian populations

Haplogroup	*Tula* ($n = 73$)	*Kaluga* ($n = 71$)	*Vladimir* ($n = 72$)	*Yaroslavl* ($n = 41$)	*Pskov* ($n = 68$)
H	58.9 (43)	38.0 (27)	34.7 (25)	48.8 (20)	42.6 (29)
V	1.4 (1)	2.8 (2)	0	0	5.9 (4)
pre*V	1.4 (1)	0	0	2.4 (1)	0
HV*	1.4 (1)	2.8 (2)	1.4 (1)	4.9 (2)	0
R1	0	0	0	0	1.5 (1)
J	5.5 (4)	4.2 (3)	8.3 (6)	4.9 (2)	11.8 (8)
T*	8.2 (6)	11.3 (8)	8.3 (6)	2.4 (1)	2.9 (2)
T1	1.4 (1)	2.8 (2)	11.1 (8)	0	2.9 (2)
K	2.7 (2)	4.2 (3)	6.9 (5)	7.3 (3)	0
U1	0	1.4 (1)	0	0	0
U2	0	2.8 (2)	1.4 (1)	0	2.9 (2)
U3	2.7 (2)	1.4 (1)	1.4 (1)	0	0
U4	4.1 (3)	8.5 (6)	2.8 (2)	4.9 (2)	2.9 (2)
U5a	2.7 (2)	8.5 (6)	6.9 (5)	9.8 (4)	17.6 (12)
U5b	2.7 (2)	2.8 (2)	0	0	2.9 (2)
U7	0	0	1.4 (1)	0	0
U8	0	0	0	0	1.5 (1)
I	2.7 (2)	1.4 (1)	5.6 (4)	2.4 (1)	0
N1a	1.4 (1)	0	1.4 (1)	2.4 (1)	0
N1b	1.4 (1)	0	1.4 (1)	2.4 (1)	0
W	0	0	4.2 (3)	0	2.9 (2)
X	0	2.8 (2)	1.4 (1)	4.9 (2)	0
C	0	2.8 (2)	0	0	0
D	0	0	0	2.4 (1)	0
G2a	0	0	0	0	1.5 (1)
M1	0	0	1.4 (1)	0	0
L1b	1.4 (1)	0	0	0	0
L3b	0	1.4 (1)	0	0	0

show the highest frequencies in Anatolia and southern Europe (Rosser et al. 2000; Semino et al. 2000; Underhill et al. 2001). Thus the lack of haplogroups E* and J* in most Russian populations studied suggests a minor genetic effect from southern European populations. A single haplotype revealed in Russians from the Belgorod population belongs to the East Asian–specific haplogroup C*, which is widespread in Central Asia (Zerjal et al. 2002). Therefore Y-chromosome variation data allow us to speculate that East Eurasian male gene flow in Russian populations was insignificant (0.3%).

In general, the data indicate that the Russian male gene pool preserves the main peculiarity of Y-chromosome diversity in central-eastern European populations. In the first instance, it is the high frequency of haplogroup R1a that is rare in western Europe but widely present in eastern and central Europe, being found at a frequency of 50–60% in Poles, Hungarians, Ukrainians, and Belorussians

Table 4. Y-Chromosome Haplogroup Distributions (Percentage, with Number of Individuals in Parentheses) in Russian Populations

Haplo-group	*Tula* (*n* = 44)	*Kaluga* (*n* = 42)	*Vladimir* (*n* = 51)	*Yaroslavl* (*n* = 23)	*Pskov* (*n* = 40)	*Belgorod* (*n* = 44)	*Orel* (*n* = 36)	*Nizhniy Novgorod* (*n* = 58)
P*	6.8 (3)	9.5 (4)	5.9 (3)	13.0 (3)	2.5 (1)	2.3 (1)	13.9 (5)	19.0 (11)
R1a	50.0 (22)	50.0 (21)	56.9 (29)	60.9 (14)	35.0 (14)	45.5 (20)	52.8 (19)	36.2 (21)
N*	0	0	2.0 (1)	0	0	0	0	0
N3	11.4 (5)	4.8 (2)	11.8 (6)	8.7 (2)	35.0 (14)	6.8 (3)	19.4 (7)	13.8 (8)
BR*	2.3 (1)	7.1 (3)	2.0 (1)	0	5.0 (2)	0	0	10.3 (6)
F*	29.5 (13)	26.2 (11)	21.6 (11)	4.4 (1)	20.0 (8)	18.2 (8)	13.9 (5)	20.7 (12)
K*	0	2.4 (1)	0	14.0 (3)	2.5 (1)	4.5 (2)	0	0
E*	0	0	0	0	0	6.8 (3)	0	0
J*	0	0	0	0	0	13.6 (6)	0	0
C*	0	0	0	0	0	2.3 (1)	0	0

(Rosser et al. 2000; Semino et al. 2000; Wells et al. 2001; Behar et al. 2003). Analysis of the haplogroup R1a distribution in Russian populations reveals a relatively homogeneous pattern, with a population frequency of 50–60%, except for the most northwestern Pskov population and the most eastern Nizhniy Novgorod population from the Volga region, where this haplogroup is observed with a lower frequency of about 35%.

It is noteworthy that among the Russian populations studied, the Pskov population shows the highest frequency (35%) of haplogroup N3, which is characteristic of all Uralic- and Baltic-speaking populations north and east of the Baltic Sea (Rosser et al. 2000; Zerjal et al. 2001). This haplogroup is considered a signature of Uralic Finno-Ugric-speaking tribes migrating to northern Europe about 5,000 years ago (Passarino et al. 2002). The presence of haplogroup N3 in Russians suggests that some admixture between Slavonic and Finno-Ugric and/or Baltic tribes occurred during the colonization of the East European plain by Slavs in the early Middle Ages and later. In addition, the distribution pattern of haplogroup N3 in other Slavonic-speaking populations suggests that proto-Slavs probably did not carry this lineage at a substantial frequency (Barac et al. 2003).

Differentiation of mtDNA and Y-Chromosome in Russian Populations. In order to study differentiation of Russian populations, we performed an analysis of molecular variance (AMOVA) separately on the level of mtDNA haplogroups and HVSI sequences. Analysis of between-population differentiation based on the frequencies of the mtDNA haplogroups revealed that 1.4% of the variation was due to differences among populations ($F_{ST} = 1.4\%$, $p = 0.007$). Significant pairwise F_{ST} differences ($p < 0.05$) were found only between the Tula population and samples from Kaluga, Vladimir, and Pskov. In addition, the Vladimir and Pskov populations differed at a significant level. One should note, however, that

the level of between-population differentiation was considerably lower when additional data on the mtDNA haplogroup frequencies in the Stavropol, Orel, and Saratov populations were taken into account ($F_{ST} = 0.6\%$, $p = 0.048$).

The AMOVA results of the mtDNA HVSI sequence data show that when the five Russian populations studied here were treated as a single group, 99.28% of the total variance was within populations ($F_{ST} = 0.72\%$, $p = 0.009$). Similar results were obtained ($F_{ST} = 0.42\%$, $p = 0.005$) when six additional Russian samples from the Stavropol, Orel, Saratov, Kostroma, Kursk, and Rostov regions were taken into account. Therefore the AMOVA results indicate the low but statistically significant level of mtDNA differentiation in Russian populations.

To further investigate genetic relationships between Russian populations, we used additional published data on the mtDNA HVSI variability in eastern and central European populations. These were the North Caucasus population of Adygei, Finno-Ugric-speaking Mari and Turkic-speaking Tatars from the Middle Volga region, North European Finno-Ugric populations of the Finns, Estonians, and Karelians, and the Baltic-speaking population of Lithuanians. Austrians and Poles were chosen because of their geographic location relative to the putative Central European homeland of the Slavs in the early Middle Ages. The AMOVA results showed that there is a low but statistically significant level of differentiation between the European populations analyzed ($F_{ST} = 0.41\%$, $p = 0$).

The multidimensional scaling analysis performed on the basis of pairwise F_{ST} values (Table 5) revealed that Russian populations do not cluster together (Figure 3). It is noteworthy that all southern and western Russian populations (Stavropol, Saratov, Rostov, Kursk, Orel, and Kaluga) as well as Poles, Austrians, Lithuanians, and Estonians are separated from other, mostly northern and eastern Russian populations (such as Tula, Vladimir, Yaroslavl, Kostroma, and Pskov), which are clustered together with Finns, Karelians, Mari, Tatars, and Adygei. In the latter group of populations, Kostroma and Pskov Russians cluster more with Finno-Ugric-speaking Karelians and Mari than they do with the other Russian populations. The Tula, Vladimir, and Yaroslavl populations are close together but separated from the remaining Russian populations. In general, the results of the multidimensional scaling analysis of the mtDNA data indicate that, despite the low values of between-population differentiation, Russian populations appear to be heterogeneous.

The AMOVA results of Y-chromosome binary data in eight Russian populations (i.e., based on the haplogroup frequencies) indicate that the highest fraction of variability was due to within-population differences (97.53%), but a substantial fraction was due to differences among populations (2.47%, $p = 0.0057$). However, significant pairwise F_{ST} differences ($p < 0.05$) were found only between the Pskov population and the rest of the Russian populations, with the exception of the Nizhniy Novgorod and Orel populations. In addition, the Nizniy Novgorod sample differs significantly from the Vladimir, Belgorod, and Yaroslavl populations. Similar results ($F_{ST} = 3.09\%$, $p = 0$) were obtained

Table 5. Matrix of F_{ST} Values Derived from mtDNA HVSI Sequences in European Populations[a]

	ST	*OR*	*SA*	*KO*	*KU*	*RO*	*EST*	*FIN*	*KAR*	*ADY*	*KA*	*PS*	*TU*	*VL*	*YA*	*POL*	*AUS*	*LIT*	*MAR*
OR	0.002																		
SA	0.008	−0.002																	
KO	0.012[b]	0.000	−0.001																
KU	−0.001	0.001	0.009	0.008															
RO	−0.009	−0.005	−0.008	0.003	−0.006														
EST	−0.001	−0.001	0.001	0.000	−0.003	−0.003													
FIN	−0.002	0.009[b]	0.015[b]	0.012[b]	−0.002	0.003	−0.002												
KAR	0.004	0.006	0.009	0.005	0.005	0.009	−0.006	0.001											
ADY	0.006	0.012[b]	0.016[b]	0.019[b]	0.003	0.000	0.007	0.016[b]	0.020[b]										
KA	0.004	−0.002	0.003	0.005	0.001	−0.007	−0.001	0.011[b]	0.013[b]	0.007									
PS	0.005	0.002	0.003	0.009	0.005	0.003	0.004	0.014[b]	0.009[b]	0.011[b]	0.010[b]								
TU	0.010[b]	0.002	0.005	0.010[b]	0.003	−0.001	0.005	0.013[b]	0.015[b]	0.013[b]	0.002	0.014[b]							
VL	0.007	0.003	0.003	−0.001	0.004	0.002	0.002	0.014[b]	0.014[b]	0.017[b]	0.001	0.014[b]	0.010[b]						
YA	−0.003	0.004	0.015[b]	0.019[b]	−0.001	−0.005	0.006	0.009	0.017[b]	0.007	−0.002	0.010	0.000	0.008					
POL	0.003	−0.001	0.002	0.003	−0.001	−0.004	−0.003	0.004	0.005[b]	0.011[b]	0.001	0.008[b]	0.001	0.007[b]	0.004				
AUS	0.003	−0.005	0.002	0.002	0.001	−0.003	−0.001	0.008[b]	0.009[b]	0.009	0.001	0.006	0.004	0.003	0.002	0.001			
LIT	0.002	0.001	0.007[b]	0.002	−0.001	0.003	−0.005	0.002	0.001	0.012[b]	0.006	0.008[b]	0.007[b]	0.007[b]	0.004	0.002	−0.001		
MAR	0.016[b]	0.006	0.006	0.022[b]	0.011	0.013	0.019*	0.025[b]	0.016[b]	0.030[b]	0.020[b]	0.001	0.018[b]	0.028[b]	0.023[b]	0.014[b]	0.012[b]	0.015[b]	
TAT	0.011[b]	0.010[b]	0.009	0.014[b]	0.000	−0.006	0.005	0.014[b]	0.016[b]	0.017[b]	0.011[b]	0.023[b]	0.011[b]	0.011[b]	0.009	0.009[b]	0.009[b]	0.010[b]	0.024[b]

a. ST, Stavropol region; OR, Orel region; SA, Saratov region; KO, Kostroma region; KU, Kursk region; RO, Rostov region; EST, Estonians; FIN, Finns; KAR, Karelians; ADY, Adygei; KA, Kaluga; PS, Pskov; TU, Tula; VL, Vladimir; YA, Yaroslavl; POL, Poles; AUS, Austrians; LIT, Lithuanians; MAR, Mari; TAT, Tatars.

b. Significant differences ($p < 0.05$).

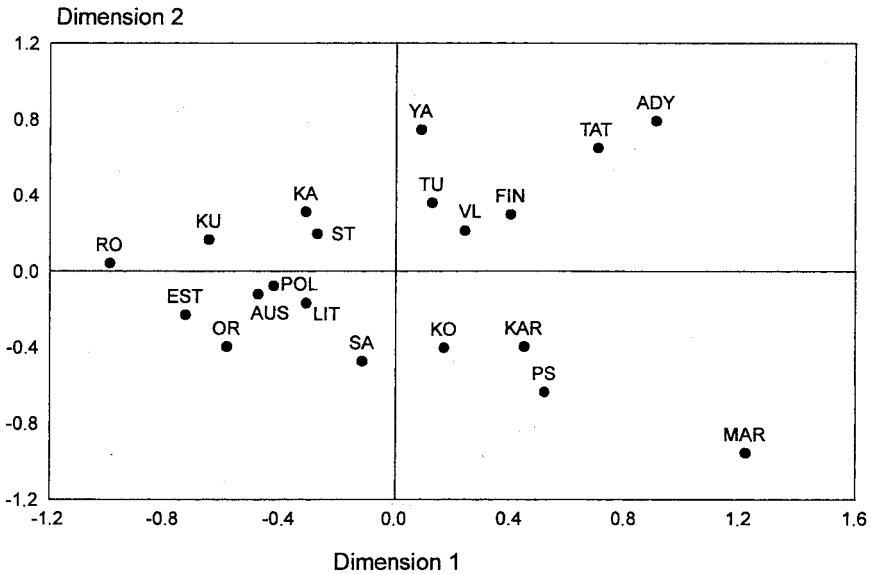

Figure 3. Two-dimensional multidimensional scaling plot of European populations based on pairwise F_{ST} values derived from mtDNA HVSI sequences. The multidimensional scaling stress value equals 0.0064. Russian populations designated as in Figure 1. POL, Poles (Malyarchuk et al. 2002); AUS, Austrians (Parson et al. 1998); LIT, Lithuanians (Kasperaviciute and Kucinskas 2002); EST, Estonians, FIN, Finns, and KAR, Karelians (Sajantila et al. 1995); TAT, Tatars, and MAR, Mari (Orekhov 2002); ADY, Adygei (Macaulay et al. 1999).

when two additional Russian samples from the north of European Russia (Northern Russians and Pomors) were included in analysis. The Russian Pomors sample was found to be distinct from all the Russian populations except for Pskov, Northern Russians, and Orel. Meanwhile, the Northern Russian sample differs significantly only from the Nizhniy Novgorod and Yaroslavl samples.

To provide the broader context for the study of the subdivision of Russian populations based on the Y-chromosome SNP F_{ST} distances, we considered additional European populations in the analysis: Slavonic-speaking Poles, Ukrainians, and Belorussians; Baltic-speaking Latvians and Lithuanians; Finno-Ugric-speaking Finns, Estonians, and Mari; and Turkic-speaking Chuvash [all the data are from Rosser et al.'s (2000) study]. The AMOVA results show a significant level of differentiation between the European populations analyzed ($F_{ST} = 7.04\%$, $p = 0$). The multidimensional scaling analysis based on Y-chromosome haplogroup F_{ST} values (Table 6) revealed that the strongest division was between Pskov and Pomor Russians together with all Finno-Ugric and Baltic-speaking populations, on the one hand, and the remaining Russian populations clustered together

Table 6. Matrix of F_{ST} Values Derived from Y-Chromosome Haplogroup Frequencies in European Populations[a]

	PS	*YA*	*VL*	*KA*	*TU*	*OR*	*BG*	*NN*	*NR*	*PO*	*FIN*	*EST*	*LAT*	*LIT*	*BEL*	*UKR*	*MAR*	*CHU*
YA	0.103[b]																	
VL	0.054[b]	0.018																
KA	0.064[b]	0.051	−0.005															
TU	0.038	0.050	−0.012	−0.020														
OR	0.032	−0.001	−0.005	0.022	0.009													
BG	0.055[b]	0.027	0.013	0.016	0.013	0.018												
NN	0.031	0.075[b]	0.030[b]	0.006	0.005	0.021	0.035[b]											
NR	0.002	0.079[b]	0.011	0.007	0.007	0.024	0.022	0.013										
PO	−0.022	0.117[b]	0.082[b]	0.108[b]	0.075[b]	0.045	0.078[b]	0.066[b]	0.028									
FIN	0.077[b]	0.325[b]	0.272[b]	0.282[b]	0.246[b]	0.225[b]	0.245[b]	0.191[b]	0.173[b]	0.055[b]								
EST	0.001	0.106[b]	0.091[b]	0.091[b]	0.082[b]	0. 051[b]	0.077[b]	0.055[b]	0.048[b]	−0.005	0.057[b]							
LAT	−0.001	0.049	0.042[b]	0.068[b]	0.045[b]	−0.006	0.048[b]	0.028	0.032	−0.003	0.126[b]	0.004						
LIT	−0.003	0.139[b]	0.112[b]	0.143[b]	0.108[b]	0.060[b]	0.109[b]	0.087[b]	0.063[b]	−0.025	0.048[b]	− 0.001	−0.001					
BEL	0.063[b]	0.078[b]	0.026	−0.008	−0.001	0.044[b]	0.011	0.002	0.013	0.106[b]	0.253[b]	0.093[b]	0.074[b]	0.140[b]				
UKR	0.039	0.171[b]	0.074[b]	0.029	0.024	0.095[b]	0.065[b]	0.014	0.006	0.086[b]	0.191[b]	0.084[b]	0.093[b]	0.125[b]	0.006			
MAR	0.033	0.102[b]	0.104[b]	0.129[b]	0.106[b]	0.053[b]	0.079[b]	0.077[b]	0.082[b]	0.022	0.106[b]	0.010	0.011	0.021	0.117[b]	0.130[b]		
CHU	0.023	0.103[b]	0.097[b]	0.068	0.065[b]	0.069[b]	0.037	0.017	0.038	0.043	0.132[b]	0.016	0.039	0.069[b]	0.027	0.029	0.044	
POL	0.096[b]	0.007	0.006	0.013	0.017	0.002	0.020[b]	0.033[b]	0.056[b]	0.126[b]	0.300[b]	0.112[b]	0.054[b]	0.146[b]	0.033[b]	0.110[b]	0.113[b]	0.099[b]

a. PS, Pskov; YA, Yaroslavl; VL, Vladimir; KA, Kaluga; TU, Tula; OR, Orel region; BG, Belgorod; NN, Nizhniy Novogorod; NR, Northern Russians; PO, Russian Pomors; FIN, Finns; EST, Estonians; LAT, Latvians; LIT, Lithuanians; BEL, Belorussians; UKR, Ukrainians; MAR, Mari; CHU, Chuvash; POL, Poles.

b. Significant differences ($p < 0.05$).

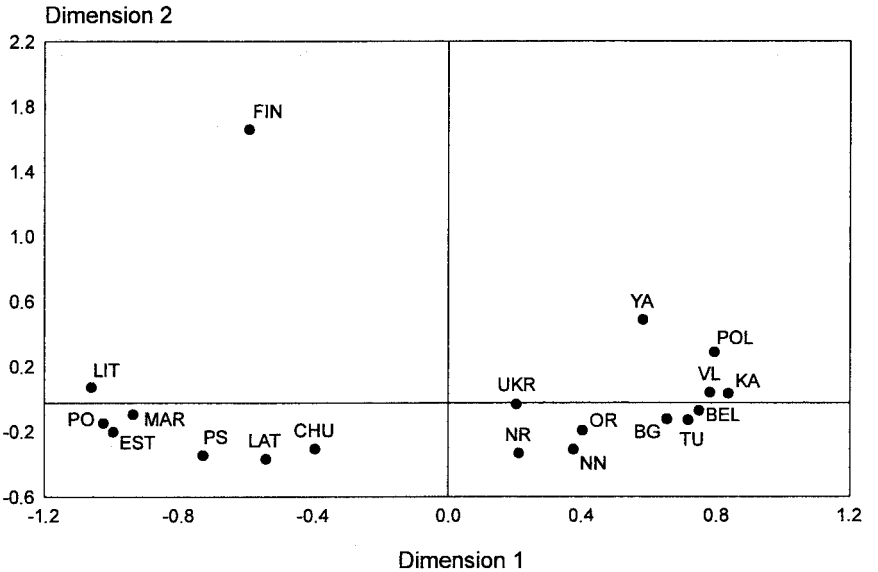

Figure 4. Two-dimensional multidimensional scaling plot of European populations based on pairwise F_{ST} values derived from Y-chromosome haplogroup frequencies. The stress value of the multidimensional scaling plot is 0.0001. Russian populations designated as in Figure 1. Data for other populations from Rosser et al. (2000): POL, Poles; UKR, Ukrainians; BEL, Belorussians; LIT, Lithuanians; LAT, Latvians; EST, Estonians; FIN, Finns; MAR, Mari; CHU, Chuvash.

with other Slavonic-speaking groups, on the other hand (Figure 4). As for Baltic-speaking populations, it is well known that the Latvians and Lithuanians show genetic similarity with Finno-Ugric populations based on the increased frequency of haplogroup N3 (Rosser et al. 2000; Zerjal et al. 2001). Similarly, clustering of northern Pskov and Pomor Russian populations with Finno-Ugric and Baltic ones may be explained by increased frequency of haplogroup N3 found in these populations.

In general, Y-chromosome and mtDNA variation data indicate that the differentiation of the geographically distinct Russian populations appears to be more prominent in the male than in the female lineages (F_{ST} values are 3.09% and 0.42%, respectively). Such a pattern has been found before in many human populations and is usually explained by patrilocal residence (Seielstad et al. 1998; Oota et al. 2001; Kayser et al. 2003). Thus the discordance between mtDNA and Y-chromosome variation in Russian populations may be a consequence of cultural features, such as patrilocality and the patrilineal social system that Russians practiced in the past, especially before the peasant reforms of the first half of the 20th century (Alekseev and Pershits 1999). In modern times, however, these features are preserved as a community tradition only in some rural localities of

Russians in the north of eastern Europe (Alekseev and Pershits 1999). However, we cannot exclude other reasons (e.g., sex-specific migration or genetic drift in isolated populations) to explain why both genetic loci, Y chromosomes and mtDNA, can provide different pictures. Therefore the problem of contrasting patterns for Y-chromosome and mtDNA differentiation in Russian populations needs to be studied in more detail.

Discussion

Y-chromosome variation data obtained in the present study demonstrate that the Russian gene pool appears to be close to central-eastern European populations. The data show a high frequency of haplogroups R1a and N3. The high incidence of R1a haplotypes in Eastern Slavs and in Baltic and some Finno-Ugric populations of eastern Europe is a well-established fact (Rosser et al. 2000; Wells et al. 2001; Zerjal et al. 2001), but little is known about the spread of haplogroup N3 in different Russian populations. Our data indicate that this haplogroup is unevenly distributed in Russian populations, with frequencies ranging from 4.8% to 35%. It is noteworthy that in most of the populations studied (with the exception of the Pskov sample) the frequency of haplogroup N3 does not exceed 20%. An important feature distinguishing Russians from their eastern European neighbors is almost complete absence of paragroup N*, which is ancestral to haplogroup N3. In Europe the highest frequencies of paragroup N* (up to 42.5%) were detected in Volga Finno-Ugric populations: Udmurts and Mari (Rosser et al. 2000; Khusnutdinova et al. 2002). Therefore Y-chromosome data suggest that the Russian male gene pool is characterized by its own structural features, although genetic influences on Russians from Uralic- or Baltic-speaking populations are also highlighted. The latter is clearly defined in the most northern Russian populations, such as Pskov Russians and Pomors. A possible explanation for this phenomenon includes replacement of an earlier Uralic or Baltic language in populations of the north of eastern Europe by the present Russian language, occurring with a low input of Slavonic mtDNA and Y-chromosome haplotypes. The high frequency of haplogroup N3 in Pskov and Pomor Russians (and probably in other northern Russian populations) is striking and should be investigated further using Y-chromosome STR analysis and a comparison with published N3-associated Y-chromosome STR haplotype data in Finno-Ugric and Baltic populations. These data should be studied with respect to the hypothesis that the genetic history of N3 Y chromosomes in Baltic-speaking populations is distinct from that of the Uralic speakers and "that there were two distinct early migrations of haplogroup 16 into Europe" (Zerjal et al. 2001). To test this and other hypotheses concerning the recent historical interactions between eastern European populations, more populations need to be studied for more genetic markers.

The present study demonstrates that Russian populations contain relatively high levels of mtDNA sequence diversity (in the means of pairwise nucleotide

differences), but the level of F_{ST}-based between-population differentiation is low. However, the results of the multidimensional scaling analysis performed on the basis of pairwise F_{ST} values for mtDNA HVSI sequences suggest that the Russian populations can be differentiated into subregions. The multidimensional scaling analysis revealed that Russian populations analyzed in combination with other central and eastern European populations do not cluster together and that populations from the southern and western parts of Russia (such as Stavropol, Rostov, Kursk, Orel, Kaluga, and Saratov) are separated from eastern and northern populations (Vladimir, Tula, Yaroslavl, Kostroma, and Pskov). Interestingly, southwestern Russian populations demonstrate genetic similarities with a set of central and northern European populations of different linguistic affiliation [Slavonic, Baltic, Germanic, and even Finno-Ugric (Estonians)], whereas northeastern Russian populations cluster together with eastern and northern European populations speaking not only Finno-Ugric languages but also Turkic (Tatars) and North Caucasus (Adygei) ones.

The multidimensional scaling analysis performed on the basis of pairwise F_{ST} values for Y-chromosome haplogroup data shows a somewhat different picture (for mtDNA sequences) of population differentiation in Russia. The most important subdivision was found only between northern populations of Pskov and Pomor Russians and the rest of the Russian populations studied. Historically, this observed discrepancy in the depth of penetration of mtDNA and Y-chromosome lineages characteristic for the most southwestern Russian populations into the east and north of eastern Europe may indicate [in accordance with anthropological data (Rychkov and Balanovska 1988)] that only the most western Russian populations appear to be descendants of the Slavs, whereas northern and eastern Russian populations seem to be the result of an admixture between Slavonic tribes and pre-Slavonic populations of eastern Europe. In addition, the data allow one to assume the possibility that Slavonic male lineages penetrated the original eastern European populations further than mtDNA lineages. One should note, however, that this scenario should be tested with additional mtDNA and Y-chromosome data in multiple Russian-, Finno-Ugric-, and Turkic-speaking populations of eastern Europe, which are poorly characterized genetically.

In addition, to estimate the degree of population replacement in eastern Europe associated with the Slavonic colonization starting in the early Middle Ages [6th–7th centuries A.D. according to archeological data (Sedov 1995)], it would be important to perform analyses of multiple samples from small urban areas, because such an approach seems to be informative in genetic history studies (Capelli et al. 2003).

Acknowledgments We would like to thank two anonymous reviewers for their useful comments. This research was supported by the Russian Fund for Basic Research through grants 00-06-80448 and 03-04-48162 (awarded to B. Malyarchuk), the Polish State Committee for Scientific Research through grant 3P04C 04823 (2002–2005) (awarded to

T. Grzybowski), the Far-East Branch of the Russian Academy of Sciences through grant 03-3-A-06-047 (awarded to M. Derenko), and the Russian State Program "Frontiers in Genetics" through grants "Data Base of Population Gene Pool" and "Preservation and Genetic Monitoring of Population Gene Pool" (awarded to S. Rychkov).

Received 22 September 2003; revision received 21 May 2004.

Literature Cited

Alekseev, V.P., and A.I. Pershits. 1999. *History of Primeval Society*. Moscow: Vysshaya shkola (in Russian).

Alekseeva, T.I. 1973. *Ethnogenesis of Eastern Slavs*. Moscow: Moscow State University (in Russian).

Alekseeva, T.I. 1999. Ethnogenesis and ethnic history of Eastern Slavs. In *Eastern Slavs: Anthropology and Ethnic History,* T.I. Alekseeva, ed. Moscow: Nauchny Mir, 307–316 (in Russian).

Alekseeva, T.I., and V.P. Alekseev. 1989. Anthropological view of the origin of Slavs. *Priroda* 881:60–69 (in Russian).

Anderson, S., A.T. Bankier, B.G. Barrel et al. 1981. Sequence and organization of the human mitochondrial genome. *Nature* 290:457–465.

Andrews, R.M., I. Kubacka, P.F. Chinnery et al. 1999. Reanalysis and revision of the Cambridge Reference Sequence for human mitochondrial DNA. *Nature Genet*. 23:147.

Balanovsky, O.P., and E.V. Balanovska. 2002. The gene pool of Eastern European populations: Computer cartography of anthropological, classical genetic, and DNA data. In *The First Workshop on Information Technologies Application to Problems of Biodiversity and Dynamics of Ecosystem in North Eurasia (WITA 2001): Selected Papers,* V.K. Shumny, N.A. Kolchanov, and A.M. Fedotav, eds. Novosibirsk: Institute of Cytology and Genetics, 255–258.

Barać, L., M. Peričić, I. Martinovic Klaric et al. 2003. Y-chromosomal heritage of Croatian population and its island isolates. *Eur. J. Hum. Genet.* 11:535–542.

Behar, D.M., M.G. Thomas, K. Skorecki et al. 2003. Multiple origins of Ashkenazi Levites: Y-chromosome evidence for both Near Eastern and European ancestries. *Am. J. Hum. Genet.* 73:768–779.

Bergen, A.W., C.-Y. Wang, J. Tsai et al. 1999. An Asian–Native American paternal lineage identified by RPS4Y resequencing and by microsatellite haplotyping. *Ann. Hum. Genet.* 63:63–80.

Capelli, C., N. Redhead, J.K. Abernethy et al. 2003. A Y-chromosome census of the British Isles. *Curr. Biol.* 13:979–984.

Casanova, M., P. Leroy, C. Boucekkine et al. 1985. A human Y-linked DNA polymorphism and its potential for estimating genetic and evolutionary distance. *Science* 230:1,403–1,406.

Comas, D., F. Calafell, E. Mateu et al. 1997. Mitochondrial DNA variation and the origin of the Europeans. *Hum. Genet.* 99:443–449.

Finnilä, S., I.E. Hassinen, L. Ala-Kokko et al. 2000. Phylogenetic network of the mtDNA haplogroup U in northern Finland based on sequence analysis of the complete coding region by conformation-sensitive gel electrophoresis. *Am. J. Hum. Genet.* 66:1,017–1,026.

Hammer, M.F. 1994. A recent insertion of an *Alu* element on the Y chromosome is a useful marker for human population studies. *Mol. Biol. Evol.* 11:749–761.

Hammer, M.F., and S. Horai. 1995. Y-chromosomal DNA variation and the peopling of Japan. *Am. J. Hum. Genet.* 56:951–962.

Hurles, M.E., C. Irven, J. Nicholson et al. 1998. European Y-chromosomal lineages in Polynesia: A contrast to the population structure revealed by mtDNA. *Am. J. Hum. Genet.* 63:1,793–1,806.

Hurles, M.E., R. Veitia, E. Arroyo et al. 1999. Recent male-mediated gene flow over a linguistic

barrier in Iberia, suggested by analysis of a Y-chromosomal DNA polymorphism. *Am. J. Hum. Genet*. 65:1,437–1,448.

Karafet, T.M., S.L. Zegura, O. Posukh et al. 1999. Ancestral Asian source(s) of New World Y-chromosome founder haplotypes. *Am. J. Hum. Genet*. 64:817–831.

Kasperaviciute, D., and V. Kucinskas. 2002. Variability of the human mitochondrial DNA control region sequences in the Lithuanian population. *J. Appl. Genet*. 43:255–260.

Kayser, M., S. Brauer, G. Weiss et al. 2000. Melanesian origin of Polynesian Y chromosomes. *Curr. Biol*. 10:1,237–1,246.

Kayser, M., S. Brauer, G. Weiss et al. 2003. Reduced Y-chromosome, but not mitochondrial DNA, diversity in human populations from West New Guinea. *Am. J. Hum. Genet*. 72:281–302.

Ke, Y., B. Su, X. Song et al. 2001. African origin of modern humans in east Asia: A tale of 12,000 Y chromosomes. *Science* 292:1,151–1,152.

Khusnutdinova, E., T. Victorova, M. Bermisheva et al. 2002. Evolution of Volga-Ural people gene pool on the data of mitochondrial DNA and Y chromosomal polymorphisms. In *The First Workshop on Information Technologies Application to Problems of Biodiversity and Dynamics of Ecosystem in North Eurasia (WITA'2001): Selected Papers,* V.K. Shumny, N.A. Kolchanov, and A.M. Fedotav, eds. Novosibirsk: Institute of Cytology and Genetics, 266–271.

Kwok, C., C. Tyler-Smith, B.B. Medonca et al. 1996. Mutation analysis of 2 kb 5′ to SRY in XY females and XX intersex subjects. *J. Med. Genet*. 33:465–468.

Limborska, S.A. 1999. Human molecular genetics: Medical genetic and population studies. *Mol. Biol. (Moscow)* 33:63–73 (in Russian).

Macaulay, V., M. Richards, E. Hickey et al. 1999. The emerging tree of West Eurasian mtDNAs: A synthesis of control-region sequences and RFLPs. *Am. J. Hum. Genet*. 64:232–249.

Malyarchuk, B.A., and M.V. Derenko. 2001. Mitochondrial DNA variability in Russians and Ukrainians: Implication to the origin of the Eastern Slavs. *Ann. Hum. Genet*. 65:63–78.

Malyarchuk, B.A., M.V. Derenko, and L.L. Solovenchuk. 1995. Types of mitochondrial DNA control region in eastern Slavs. *Rus. J. Genet*. 31:723–727.

Malyarchuk, B.A., T. Grzybowski, M.V. Derenko et al. 2002. Mitochondrial DNA variability in Poles and Russians. *Ann. Hum. Genet*. 66:261–283.

Mathias, N., M. Bayes, and C. Tyler-Smith. 1994. Highly informative compound haplotypes for the human Y chromosome. *Hum. Mol. Genet*. 3:115–123.

Oota, H., W. Settheetham-Ishida, D. Tiwawech et al. 2001. Human mtDNA and Y-chromosome variation is correlated with matrilocal versus patrilocal residence. *Nat. Genet*. 29:20–21.

Orekhov, V.A. 2002. *Characteristics of mtDNA Types in Three Ethnic Groups of the European Part of Russia*. Ph.D. thesis, Vavilov Institute of General Genetics, Moscow (in Russian).

Orekhov, V., A. Poltoraus, L.A. Zhivotovsky et al. 1999. Mitochondrial DNA sequence diversity in Russians. *FEBS Lett*. 445:197–201.

Parson, W., T.J. Parsons, R. Scheithauer et al. 1998. Population data for 101 Austrian Caucasian mitochondrial DNA d-loop sequences: Application of mtDNA sequence analysis to a forensic case. *Int. J. Legal Med*. 111:124–132.

Passarino, G., G.L. Cavalleri, A.A. Lin et al. 2002. Different genetic components in the Norwegian population revealed by the analysis of mtDNA and Y-chromosome polymorphisms. *Eur. J. Hum. Genet*. 10:521–529.

Richards, M.B., V.A. Macaulay, E. Hickey et al. 2000. Tracing European founder lineages in the Near Eastern mtDNA pool. *Am. J. Hum. Genet*. 67:1,251–1,276.

Richards, M., C. Rengo, F. Cruciani et al. 2003. Extensive female-mediated gene flow from sub-Saharan Africa into Near Eastern Arab populations. *Am. J. Hum. Genet*. 72:1,058–1,064.

Rosser, Z.H., T. Zerjal, M. Hurles et al. 2000. Y-chromosomal diversity in Europe is clinal and influenced primarily by geography rather than by language. *Am. J. Hum. Genet*. 67:1,526–1,543.

Rychkov, Yu.G., and E.V. Balanovska. 1988. Synthetic cartographic analysis in anthropology: A reflection of the chronicle of Slavonic tribes in the anthropological geography of the modern Russian population. *Vopr. Anthropol*. 80:3–37 (in Russian).

Rychkov, Yu.G., E.V. Balanovska, S.D. Nurbaev et al. 1999. Historical genogeography of Eastern Europe. In *Eastern Slavs: Anthropology and Ethnic History,* T.I. Alekseeva, ed. Moscow: Nauchny Mir, 109–135 (in Russian).

Sajantila, A., P. Lahermo, T. Anttinen et al. 1995. Genes and languages in Europe: An analysis of mitochondrial lineages. *Genome Res.* 5:42–52.

Salas, A., M. Richards, T. De la Fe et al. 2002. The making of the African mtDNA landscape. *Am. J. Hum. Genet.* 71:1,082–1,111.

Santos, F.R., A. Pandya, C. Tyler-Smith et al. 1999. The central Siberian origin for native American Y chromosomes. *Am. J. Hum. Genet.* 64:619–628.

Schneider, S., J.M. Kueffer, D. Roessli et al. 1997. *Arlequin, ver. 1.1: A Software for Population Genetic Data Analysis*. Geneva: Genetics and Biometry Laboratory, University of Geneva.

Sedov, V.V. 1995. *The Slavs in the Early Middle Ages*. Moscow: Archaeological Fund (in Russian).

Seielstad, M., E. Minch, and L.L. Cavalli-Sforza. 1998. Genetic evidence for a higher female migration rate in humans. *Nat. Genet.* 20:278–280.

Semino, O., G. Passarino, P.J. Oefner et al. 2000. The genetic legacy of Paleolithic *Homo sapiens sapiens* in extant Europeans: A Y-chromosome perspective. *Science* 290:1,155–1,159.

Spitsyn, V.A., W. Kuchheuser, S.V. Makarov et al. 2001. The Russian gene pool: Frequencies of genetic markers. *Genetika* 37:386–401 (in Russian).

Torroni, A., K. Huoponen, P. Francalacci et al. 1996. Classification of European mtDNAs from an analysis of three European populations. *Genetics* 144:1,835–1,850.

Underhill, P.A., L. Jin, A.A. Lin et al. 1997. Detection of numerous Y-chromosome biallelic polymorphisms by denaturing high-performance liquid chromatography. *Genome Res.* 7:996–1,005.

Underhill, P.A., G. Passarino, A.A. Lin et al.. 2001. The phylogeography of Y-chromosome binary haplotypes and the origins of modern human populations. *Ann. Hum. Genet.* 65:43–62.

Underhill, P.A., P. Shen, A.A. Lin et al. 2000. Y-chromosome sequence variation and the history of human populations. *Nat. Genet.* 26:358–361.

Wells, R.S., N. Yuldasheva, R. Ruzibakiev et al. 2001. The Eurasian heartland: A continental perspective on Y-chromosome diversity. *Proc. Natl. Acad. Sci. USA* 98:10,244–10,249.

Whitfield, L.S., J.E. Sulston, and P.N. Goodfellow. 1995. Sequence variation of the human Y chromosome. *Nature* 378:379–380.

Yao, Y.-G., Q.-P. Kong, H.-J. Bandelt et al. 2002. Phylogeographic differentiation of mitochondrial DNA in Han Chinese. *Am. J. Hum. Genet.* 70:635–651.

Y Chromosome Consortium. 2002. A nomenclature system for the tree of human Y-chromosomal binary haplogroups. *Genome Res.* 12:339–348.

Zerjal, T., L. Beckman, G. Beckman et al. 2001. Geographical, linguistic, and cultural influences on genetic diversity: Y-chromosomal distribution in Northern European populations. *Mol. Biol. Evol.* 18:1,077–1,087.

Zerjal, T., B. Dashnyam, A. Pandya et al. 1997. Genetic relationships of Asians and Northern Europeans, revealed by Y-chromosomal DNA analysis. *Am. J. Hum. Genet.* 60:1,174–1,183.

Zerjal, T., R.S. Wells, N. Yuldasheva et al. 2002. A genetic landscape reshaped by recent events: Y-chromosomal insights into Central Asia. *Am. J. Hum. Genet.* 71:466–482.