FOR THE RECORD

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Allele Frequencies for D1S80 (pMCT118) Locus in Some East European Populations

POPULATION: Russians ($n = 57$), Byelorussians ($n = 166$), Ukrainians ($n = 138$), Mordovians ($n = 87$), Tartars ($n = 46$), Bashkirs ($n = 250$), Komi ($n = 44$), and Mari ($n = 33$).

KEYWORDS: forensic science, DNA typing, population genetics, D1S80, pMCT118, minisatellite, Russia, Ukraine, Belarus

The Byelorussian populations are from three regions of the Republic of Belarus (Grodno, Bobruisk, and Mjadel areas); the Russians are from the Kholmogory town of the Russian Federation (Arkhangelsk district); and the Ukrainian populations are from the Kiev and L'vov areas of Ukraine. The Mordva-Moksha (Staro-Shaiginsk and Romodanovsk areas of Mordva Republic), the Bashkirs (Ilishevsky, Abzelilovsky, Sterlibashevsky, Arkhangelsky, and Beloretsky districts of Bashkir Republic), the Komi-Zyrjan (Sysolsky district of Komi Republic), the Tartar (Almetyevsk town of Tartar Republic), and the Mari (Zvenigovsk area of Mari Republic) populations present distinct ethnic groups of the region between the Volga River and the Ural Mountains in Russia. Eastern Slavonic populations (Russians, Byelorussians, Ukrainians) are Caucasoids; other populations were considered as admixture populations with different levels of a Mongoloid component.

Blood samples were collected in EDTA vacutainer tubes from healthy unrelated volunteers belonging to a native ethnic group of the regions studied. DNA was isolated by phenol-chloroform extraction (1). The PCR amplification was performed using a Perkin Elmer Cetus thermal cycler. DNA samples (100–200 ng of total genomic DNA for one reaction) were amplified with 20 μL of master mix containing: D1S80 primer pair (2) (each at 5 pM), 1X PCR Buffer (containing 10 mM Tris-HCl pH 8.3, 50 mM KCl, 1.5 mM MgCl$_2$), 200 μM of dNTP, and 1U native Taq polymerase™ (all reagents from MBI Fermentas). Optimized cycling conditions were: 94°C for 2 min, 30 cycles at 92°C for 30 s, 65°C for 30 s, 72°C for 45 s, and 72°C at 5 min. The amplified products were detected by vertical polyacrylamide gel (25 cm long; 6%T, 2.5%C, and TBE buffer pH 9.0) electrophoresis at constant voltage (700V) till the xylene cyanol tracking dye migrated to the end of the gel. Allele designation was achieved by coelectrophoresis of the PCR products with the AmpliFLP D1S80™ Perkin-Elmer allelic ladder. The PCR products were visualized with manual silver staining (3). Data were analyzed with POPGENE software (4).

A total of 27 different alleles (121 distant genotypes) were found in 16 populations (Table 1). All populations studied showed no significant departures from HWE proportions. Locus diversity ranged from 0.69–0.95. D1S80 appears to have an ethnic affiliation in a comparison of East European ethnic groups. The most frequent alleles in East Slavonic populations were allele 24 ($>$29%), followed by allele 18 ($>$18%). An inversion in the magnitude of two most frequent alleles can be noted in some mixed populations, where allele 18 exists at the highest frequency (up to 33%).

The complete data set is available upon request at email: dav@img.ras.ru

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TABLE 1—*D1S80 allele frequencies and other population characteristics in some East European populations.*

Allele	Russians	Ukrainians		Byelorussians			Mordvinians (Moksha)		Komi (Zyrjans)	Tartars	Bashkirs					Mari
	Kholmogory	Lviv	Kiev	Grodno	Khoiniki	Mjadel	Staro-Shaiginsky	Romodanovsky	Sysolsky	Almetievsk	Ilishevsky	Abzeliiovsky	Steribashevsky	Arkhangelsky	Beloretzky	Zvenigovsky
16		0,008						0,012	0,034	0,011	0,017	0,038	0,023		0,042	
17			0,007	0,011							0,009				0,017	
18	**0,280**	**0,284**	**0,204**	**0,273**	**0,182**	**0,224**	**0,136**	**0,197**	**0,295**	**0,314**	**0,220**	**0,313**	**0,333**	**0,316**	**0,292**	**0,333**
19											0,009				0,017	
20	0,017	0,030	0,021	0,023	0,018	0,030				0,033	0,017			0,031		
21	0,009	0,015	0,028		0,018	0,008	0,023	0,035	0,011				0,024		0,033	0,015
22	0,042	0,037	0,078	0,034	0,091	0,052	0,034	0,047	0,057	0,054	0,025	0,063	0,083	0,041	0,067	0,046
23	0,017	0,008	0,014		0,009				0,023	0,022	0,025			0,010		
24	**0,390**	**0,291**	**0,366**	**0,318**	**0,418**	**0,388**	**0,399**	**0,360**	**0,204**	**0,250**	**0,280**	**0,300**	**0,202**	**0,195**	**0,133**	**0,197**
25	0,017	0,060	0,056	0,046	0,055	0,082	0,102	0,035	0,080	0,022	0,068	0,025	0,060	0,051	0,025	
26	0,025	0,008	0,014	0,023	0,009	0,045	0,011	0,012						0,012		0,015
27			0,021			0,008				0,022			0,025			
28	0,068	0,082	0,063	0,057	0,082	0,052	0,080	0,081	0,114	0,033	0,119	0,075	0,071	0,051	0,116	0,061
29	0,009	0,015	0,042	0,046	0,018	0,008	0,057	0,070	0,023	0,065	0,042	0,037	0,060	0,071	0,033	0,015
30	0,034	0,015				0,015	0,011	0,058		0,011		0,009	0,025	0,082	0,042	
31	0,059	0,105	0,063	0,068	0,055	0,090	0,102	0,081	0,102	0,108	0,076	0,012	0,060	0,122	0,083	0,167
32				0,011			0,011		0,011	0,011						
33	0,017	0,008		0,011	0,009							0,012				
34	0,008			0,023												
35		0,008														
36	0,008	0,022	0,007	0,011	0,018		0,023			0,011	0,051	0,025	0,036	0,020	0,075	0,136
37		0,008	0,007	0,034	0,009		0,011	0,012	0,046	0,022	0,017	0,038	0,024	0,010	0,025	0,015
38										0,011						
39											0,009	0,012				
40			0,007								0,009					
41				0,011									0,012			
>41					0,009											
Chromosome number	118	134	142	88	110	134	88	86	88	92	118	80	84	98	120	66
Number of distinct alleles	15	17	16	16	15	12	13	12	12	16	17	14	13	13	14	10
Number of distinct genotypes	25	31	30	24	25	26	25	20	25	25	34	23	24	28	29	17
Observed homozygosity	0,75	0,78	0,69	0,91	0,78	0,75	0,73	0,86	0,82	0,78	0,92	0,88	0,81	0,84	0,95	0,76
Expected heterozygosity	0,76	0,82	0,81	0,82	0,78	0,78	0,79	0,81	0,83	0,82	0,84	0,80	0,82	0,83	0,86	0,80
Likelihood ratio test for HWE																
G-squared	60,1	71,5	86,0	66,5	42,7	38,8	43,3	51,9	46,2	61,0	63,0	41,8	50,0	38,2	90,5	30,8
Probability	1,000	1,000	0,992	1,000	1,000	0,997	1,000	0,897	0,969	1,000	1,000	1,000	0,994	0,998	0,496	0,946
Degree of freedom	105	136	120	120	105	66	78	66	66	120	136	91	78	66	91	45

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