

FOR THE RECORD

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Population Genetics for the CODIS Core STR Loci in the Population of Northeastern Poland

POPULATION: 842 unrelated individuals from Podlasie (Northeastern Poland).

KEYWORDS: forensic science, DNA typing, population genetics, CODIS, Poland

In 1997 the FBI announced the selection of 13 STRs loci to constitute the core of the United States national database—CODIS, which has been widely adopted by forensic DNA analysts in the United States (1). Polish-worldwide population today is estimated at almost 60 million. According to the last U.S. Census taken in year 2000, in the United States of America live about 9,053,660 Poles/Polish-Americans. The largest population of Poles is recorded in the state of New York, Illinois, Michigan, and Pennsylvania (2). The aim of this study was to provide a 13 STRs database for a population sample of Poland for the use as a highly discriminatory system of genetic markers in forensic community. DNA was extracted from the blood specimens of 842 unrelated adult individuals using Chelex-100 and proteinase K (3). Two commercially available kits AmpF ℓ STR Profiler and AmpF ℓ STR SGM Plus (Applied Biosystems, US) were used to amplify the 13 STR loci included in the CODIS STR standardization project: D3S1358, vWA, D8S1179, D21S11, D18S51, TH01, FGA, TPOX, CSF1PO, D5S818, D13S317, D7S820, D16S539. Genotyping was performed in a 310 ABI Prism Genetic Analyzer. Hardy-Weinberg equilibrium was tested using the Fisher's exact test by the GDA software (4). The forensic efficiency parameters were

calculated using the PowerStats software (www.promega.com/techserv/apps).

All 13 loci met Hardy-Weinberg equilibrium based on the exact test. The combined values of the matching probability and the power of exclusion are 2.30×10^{-15} and 99.9999, respectively. The complete dataset is available at <http://www.amb.edu.pl/wydzialy/lekarski/data-zms.rtf>.

References

1. Baechtel FS, Monson KL, Forsen GE, Budowie B, Kearney JJ. Tracking the violent criminal offender through DNA typing profiles—a national database system concept. *EXS* 1991;58:356–60.
2. <http://www.census.gov>
3. Wiegand P, Bajanowski T, Brinkmann B. PCR typing of debris from fingernails. *Int J Legal Med* 1993;106:81–4.
4. Lewis PO, Zaykin D. Genetic data analysis: computer program for the analysis of allelic data. Version 1.0 (d16c). Free program distributed by the authors over the internet from <http://lewis.eeb.uconn.edu/lewishome/software.html>

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TABLE 1—Allele frequencies and forensic efficiency parameters for the CODIS core STR loci in the population of Podlasie, Northeastern Poland.

Allele	D3S1358	vWA	FGA	TH01	TPOX	CSF1PO	D5S818	D13S317	D7S820	D16S539	D21S11	D18S51	D8S1179
5				0.002									
6				0.247									
7				0.120	0.002				0.028				
8				0.123	0.550	0.008	0.005	0.133	0.179	0.008			0.005
9				0.199	0.074	0.030	0.056	0.060	0.146	0.069		0.002	0.012
9.3				0.298									
10				0.010	0.078	0.266	0.077	0.050	0.280	0.030		0.010	0.057
11				0.002	0.266	0.330	0.338	0.364	0.194	0.303		0.008	0.099
12					0.030	0.284	0.356	0.256	0.144	0.348		0.094	0.153
13	0.002	0.008				0.071	0.142	0.090	0.025	0.194		0.106	0.310
14	0.148	0.128				0.010	0.025	0.040	0.003	0.045		0.145	0.224
15	0.227	0.109					0.002	0.005		0.002		0.173	0.103
16	0.229	0.180										0.158	0.030
17	0.199	0.266										0.121	0.002
18	0.182	0.222	0.017									0.086	
19	0.010	0.072	0.086									0.040	
20	0.003	0.012	0.168									0.034	
21		0.002	0.152									0.013	
22			0.197									0.007	
22.2			0.003									...	
23			0.138									...	
23.2			0.003									...	
24			0.135									0.002	
25			0.059										
26			0.034										
27			0.007								0.034		
28											0.167		
29											0.146		
30											0.239		
30.2											0.057		
31											0.072		
31.2											0.099		
32											0.032		
32.2											0.076		
33.2											0.069		
34.2											0.008		
Ho	0.78	0.83	0.85	0.75	0.61	0.74	0.73	0.78	0.83	0.73	0.84	0.89	0.78
He	0.80	0.81	0.86	0.78	0.61	0.74	0.73	0.77	0.81	0.74	0.86	0.88	0.80
Exact Test	0.260	0.743	0.218	0.052	0.949	0.472	0.334	0.656	0.179	0.788	0.664	0.624	0.348
MP	0.071	0.064	0.037	0.083	0.203	0.121	0.118	0.097	0.070	0.106	0.036	0.031	0.069
PD	0.929	0.936	0.963	0.917	0.797	0.879	0.882	0.903	0.930	0.894	0.964	0.969	0.931
PIC	0.77	0.79	0.84	0.75	0.56	0.69	0.69	0.74	0.78	0.70	0.85	0.87	0.78
PE	0.558	0.666	0.685	0.511	0.309	0.486	0.468	0.560	0.653	0.466	0.666	0.773	0.565
TPI	2.25	3.03	3.23	2.01	1.30	1.89	1.82	2.26	2.91	1.81	3.03	4.50	2.28

Ho: observed heterozygosity; He: expected heterozygosity; MP: matching probability; PD: power of discrimination; PIC: polymorphism information content; PE: power of exclusion; TPI: typical paternity index.