

Igor S. Veselinović, M.D., M.Sc.; Dragana M. Zgonjanin, M.Sc.; Milan A. Simić, M.D., Ph.D.; Goran B. Stojiljković, M.D., Ph.D.; and Miloš M. Tasić, M.D., Ph.D.

Serbian Population Data at the CODIS Core STR Loci

POPULATION: Two hundred healthy unrelated adult persons from Serbia.

KEYWORDS: forensic science, population genetics, DNA typing, CSF1PO, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, D21S11, FGA, TH01, TPOX, vWA

Blood samples from 200 healthy adult donors were collected on FTA-papers and air-dried. DNA was extracted using Chelex 100 method (1). Quantitation was performed using the Quantifiler™ Human DNA Quantification Kit (Applied Biosystems, Foster City, CA) on the ABI PRISM 7000 Sequence Detection System (Applied Biosystems). PCR amplification of approximately 1 ng of DNA template was carried out on the GeneAmp PCR System 2700 (Applied Biosystem) using the AmpF/STR Identifiler PCR Amplification Kit, according to the manufacturer's recommendation (2).

Electrophoresis, detection of PCR products, and genotyping were performed on the ABI PRISM 310 Genetic Analyzer (Applied Biosystems) using the ABI PRISM 310 Data Collection Software and Genotyper 3.7 Software (Applied Biosystems).

Allele frequencies were estimated using standard counting procedures. Data were analyzed by the PowerStats software (Promega, Madison, WI) (3) (Table 1). The genotype distribution was tested for Hardy–Weinberg equilibrium by the chi-square test, and no significant deviation from Hardy–Weinberg equilibrium was observed.

The complete dataset is available to any interested researcher upon request to corresponding author Dr. Igor S. Veselinović at agnus@eunet.yu.

References

1. Walsh BS, Petzger DA, Higuchi R. Chelex 100 as a medium for simple extraction of DNA for PCR-based typing from forensic material. *Biotechniques* 1991;10:506–10.
2. Applied Biosystems. AmpFISTR™ Identifiler™ PCR amplification kit user's manual. Foster City, CA: Applied Biosystems, 2001.
3. <http://www.promega.com> (accessed September 12, 2005).

Additional information and reprint requests:

Igor S. Veselinović, M.D., M.Sc.
Institute of Forensic Medicine
Hajduk-Veljkova 1-7
Novi Sad 21000
Serbia
E-mail: agnus@eunet.yu

TABLE 1—Observed allele frequencies and statistical parameters at the 13 CODIS STR loci in a Serbian population sample (n = 200).

Allele	CSF1PO	D3S1358	D5S818	D7S820	D8S1179	D13S317	D16S539	D18S51	D21S11	FGA	TH01	TPOX	VWA
5	—	—	—	—	—	—	—	—	—	—	0.0025	—	—
6	—	—	—	—	—	—	—	—	—	—	0.2625	—	—
7	—	—	0.0025	0.0050	—	—	—	—	—	—	0.1225	0.0050	—
8	0.0025	—	0.0050	0.1500	0.0050	0.1550	0.0125	—	—	—	0.0925	0.5800	—
9	0.0400	—	0.0425	0.2025	0.0075	0.0725	0.0950	0.0025	—	—	0.2100	0.1075	—
9.3	—	—	—	—	—	—	—	—	—	—	0.2950	—	—
10	0.2625	—	0.0550	0.2675	0.0375	0.0600	0.0700	0.0075	—	—	0.0150	0.0550	—
11	0.3050	—	0.3550	0.2225	0.0800	0.3175	0.2650	0.0175	—	—	—	0.2325	—
12	0.3375	—	0.3675	0.1300	0.1600	0.2600	0.3475	0.1275	—	—	—	0.0200	—
13	0.0475	—	0.1625	0.0150	0.3100	0.0750	0.1725	0.1425	—	—	—	—	0.0075
14	0.0050	0.0900	0.0050	0.0050	0.2350	0.0600	0.0300	0.1525	—	—	—	—	0.1325
15	—	0.2600	0.0050	0.0025	0.1500	—	0.0050	0.1425	—	—	—	—	0.1150
16	—	0.3075	—	—	0.0150	—	0.0025	0.1600	—	0.0025	—	—	0.1725
17	—	0.2025	—	—	—	—	—	0.0900	—	—	—	—	0.2675
18	—	0.1300	—	—	—	—	—	0.0875	—	0.0150	—	—	0.2125
19	—	0.0100	—	—	—	—	—	0.0225	—	0.0550	—	—	0.0825
20	—	—	—	—	—	—	—	0.0275	—	0.1200	—	—	0.0100
21	—	—	—	—	—	—	—	0.0075	—	0.1900	—	—	—
22	—	—	—	—	—	—	—	0.0075	—	0.2100	—	—	—
22.2	—	—	—	—	—	—	—	—	—	0.0025	—	—	—
23	—	—	—	—	—	—	—	—	—	0.1600	—	—	—
23.2	—	—	—	—	—	—	—	—	—	0.0050	—	—	—
24	—	—	—	—	—	—	—	0.0025	—	0.1425	—	—	—
25	—	—	—	—	—	—	—	—	—	0.0650	—	—	—
25.2	—	—	—	—	—	—	—	—	—	0.0025	—	—	—
26	—	—	—	—	—	—	—	0.0025	0.0050	0.0250	—	—	—
27	—	—	—	—	—	—	—	—	0.0500	0.0050	—	—	—
28	—	—	—	—	—	—	—	—	0.1275	—	—	—	—
29	—	—	—	—	—	—	—	—	0.2300	—	—	—	—
30	—	—	—	—	—	—	—	—	0.2350	—	—	—	—
30.2	—	—	—	—	—	—	—	—	0.0425	—	—	—	—
31	—	—	—	—	—	—	—	—	0.0600	—	—	—	—
31.2	—	—	—	—	—	—	—	—	0.1175	—	—	—	—
32	—	—	—	—	—	—	—	—	0.0125	—	—	—	—
32.2	—	—	—	—	—	—	—	—	0.0875	—	—	—	—
33	—	—	—	—	—	—	—	—	0.0025	—	—	—	—
33.2	—	—	—	—	—	—	—	—	0.0025	—	—	—	—
34.2	—	—	—	—	—	—	—	—	0.0025	—	—	—	—
Hobs	0.760	0.760	0.740	0.745	0.770	0.785	0.760	0.900	0.850	0.875	0.735	0.665	0.855
PM	0.142	0.087	0.149	0.070	0.075	0.080	0.092	0.034	0.047	0.045	0.085	0.218	0.063
PD	0.858	0.913	0.851	0.930	0.925	0.920	0.908	0.966	0.953	0.955	0.915	0.782	0.937
PIC	0.67	0.74	0.66	0.77	0.76	0.76	0.73	0.86	0.83	0.83	0.74	0.55	0.79
PE	0.527	0.527	0.493	0.501	0.545	0.572	0.527	0.795	0.695	0.745	0.484	0.376	0.705
TPI	2.08	2.08	1.92	1.96	2.17	2.33	2.08	5.00	3.33	4.00	1.89	1.49	3.45

Hobs, observed heterozygosity; PM, probability of match; PD, power of discrimination; PIC, polymorphism information content; PE, power of exclusion; TPI, typical paternity index.