

FOR THE RECORD

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Allele Frequencies for the 15 Short Tandem Repeat Loci in Slovenian Population

POPULATION: We have analyzed the distribution of allele frequencies at fifteen autosomal short tandem repeats loci (D3S1358, TH01, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penta D, vWA, D8S1179, TPOX, FGA) in the representative sample of Slovenians. A total of 193 unrelated individuals (Caucasians) born in Slovenia have been sampled for the analysis.

KEYWORDS: forensic science, DNA typing, short tandem repeats, population genetics, representative sample, Slovenian population, PowerPlex 16 kit, D3S1358, TH01, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penta D, vWA, D8S1179, TPOX, FGA

All 193 tested individuals have been involved in legal proceedings concerning various forensic testing. Buccal swabs have been taken as the DNA source and Chelex procedure was used for DNA extraction (1). The PowerPlex 16 kit (Promega Corp., Madison, WI) has been used to simultaneously amplify by PCR 15 STR loci. The STR loci are: D3S1358, TH01, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penta D, vWA, D8S1179, TPOX and FGA. Similar amounts of DNA have been used in all PCR reactions. Amplification was carried out as described previously (2). The total volume of each reaction was 25 μ L. The PCR amplification has been carried out in PE Gene Amp PCR System Thermal Cycler (ABI, Foster City, CA) according to the manufacturer's recommendations. Electrophoresis of the amplification products was performed on an ABI PRISM 310 genetic analyzer (ABI, Foster City, CA). Raw data have been compiled and analyzed using the accessory software: ABI PRISM[®] Data Collection Software and Gene Scan[®]. Numerical allele designations of the profiles were obtained by processing with Powertyper16 Macro. Deviation from Hardy-Weinberg equilibrium, observed and expected heterozygosity (3) were calculated within Powermarker (4), power of discrimination and power of exclusion within Microsoft[®] Excel workbook template—PowerStats (5), tests of population differentiation within Arlequin ver. 2000 (6). All results are showed in Table 1.

We have compared Slovenian data with data obtained from geographically closer (neighboring) European populations. Bonferroni's correction was used before each comparative analysis ($p = 0.0125$). In comparison of Slovenian and southern Croatian data (7) no significant difference ($P < 0.0125$) is found at any

individual locus. The same statistical parameters are obtained in comparison with Bosnian and Herzegovinian data (8). Significant differences ($P < 0.0125$) are found only at D5S818 locus in comparative analysis of Slovenian and pooled Caucasian data.³ Joint result of this study presents continuation of our previous studies (9,10).

The entire data are available on <http://www.ingeb.ba/edat/str/slovenianstrbase.html>.

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TABLE 1—Slovenian allele frequencies for 15 autosomal loci ($N = 193$).

Allele	D3S1358	THO1	D21S11	D18S51	PENT.E	D5S818	D13S317	D7S820
5	0.0855
6	...	0.2461
7	...	0.1036	0.1321	0.0052	0.0026	0.0259
8	...	0.1192	...	0.0026	0.0078	0.0026	0.1218	0.1736
9	...	0.1865	0.0155	0.0415	0.0881	0.1295
9.3	...	0.3213
10	...	0.0233	...	0.0078	0.1269	0.0855	0.0518	0.2746
11	0.0078	0.0881	0.2927	0.3653	0.2021
12	0.1192	0.1865	0.4093	0.2591	0.1451
13	0.0026	0.1373	0.1036	0.1425	0.0881	0.0440
14	0.1399	0.1658	0.0622	0.0207	0.0233	0.0026
15	0.2409	0.1295	0.0518	0.0026
16	0.2202	0.1451	0.0415
17	0.2047	0.1036	0.0544
18	0.1788	0.0933	0.0207
19	0.0130	0.0337	0.0155
20	0.0337	0.0052
20.2
21	0.0130	0.0026
22	0.0078
22.2
23
23.2
24
25
26
27
28
26	0.0026
27	0.0365
28	0.1719
29	0.2109
30	0.1901
30.2	0.0703
31	0.0599
31.2	0.0964
32	0.0026
32.2	0.1172
33.2	0.0365
34.2	0.0052
H(ob)	0.8031	0.8083	0.8385	0.9119	0.8808	0.6788	0.7565	0.8187
H(ex)	0.7978	0.7757	0.8533	0.8774	0.8912	0.7150	0.7639	0.8111
P	0.8199	0.1072	0.1807	0.1301	0.6827	0.0226	0.0254	0.7481
PD	0.926	0.909	0.959	0.956	0.976	0.862	0.907	0.936
PE	0.605	0.615	0.672	0.774	0.756	0.346	0.521	0.634

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TABLE 1—Continued.

Allele	D16S539	CSF1P0	PENT.D	vWA	D8S1179	TPOX	FGA
5
6
7
8	0.0234	0.0052	0.0052	...	0.0052	0.6088	...
9	0.1042	0.0391	0.2448	...	0.0078	0.0907	...
9.3
10	0.0625	0.2578	0.1224	...	0.0648	0.0518	...
11	0.3021	0.3411	0.1510	...	0.0829	0.2409	...
12	0.3021	0.2786	0.1693	...	0.1606	0.0078	...
12.1	0.0026
13	0.1849	0.0677	0.2109	0.0104	0.3187
14	0.0208	0.0104	0.0677	0.1114	0.2306
15	0.0234	0.0544	0.1036
16	0.0026	0.1865	0.0259
17	0.3212
18	0.2409	0.0155
19	0.0648	0.0674
20	0.0104	0.1192
20.2	0.0026
21	0.1788
22	0.2358
22.2	0.0052
23	0.1347
23.2	0.0104
24	0.1244
24.2	0.0052
25	0.0725
26	0.0259
27	0.0026
28
26
27
28
29
30
30.2
31
31.2
32
32.2
33.2
H(ob)	0.7552	0.7448	0.8073	0.7876	0.7979	0.5699	0.8808
H(ex)	0.7655	0.7314	0.8218	0.7822	0.7949	0.5589	0.8516
P	0.5461	0.3950	0.0937	0.9542	0.7274	0.9942	0.2665
PD	0.909	0.877	0.937	0.919	0.928	0.755	0.881
PE	0.519	0.501	0.611	0.576	0.595	0.256	0.603

H(ob): observed heterozygosity; H(ex): expected heterozygosity; P: Deviation from Hardy-Weinberg equilibrium; PD: power of discrimination, PE: power of exclusion.