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Announcement of population data

Allele distribution data of nine short tandem repeat loci for Turkish population: D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820

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Abstract

Allele and genotype frequencies for the nine loci D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317 and D7S820 were determined for 310 unrelated Turkish individuals.

Keywords: Forensic science; Short tandem repeat; Population data; Allele frequencies; Turkish; CODIS

Population: Our donors were sampled from different regions of Turkey. Whole blood samples from 310 unrelated Turkish Caucasians were drawn into EDTA vacutainer tubes, also bloodstains were prepared on sterilized cotton cloth, and air dried.

Extraction: The DNA was extracted by the salting out method according to the procedure described by Miller et al. [1], and Chelex extraction was done for blood stain [2].

PCR: Amplification was performed by strictly following the manufacturer's recommended protocol, and using the commercially available AmpFISTR Profiler Plus Kit (PE Applied Biosystem, USA).

Typing: The Gene Scan 2.1 and Genotyper 2.0 (Applied Biosystems, USA) software used for sizing and typing.

Results: See Table 1.

Analysis of data: The statistical tests for Hardy-Weinberg equilibrium (HWE) by the exact test [3] were performed using the HWE-analysis program. Heterozygosity rate, power of exclusion, power of discrimination, polymorphism information content, matching probability were carried out as described previously [4].

Other remarks: Additional information on Turkish population samples can be found in [5-9]. No significant difference was found with the results of previous studies in same population [6,9].

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Table 1
Allele frequencies at nine STR loci in the AmpFeSTR Profiler Kit in the Turkish population (310 individuals)^a

Allele	D3S1358	HumvWA	HumFGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820
6	-	-	-	-	-	-	-	-	0.002
7	-	-	-	-	-	-	0.002	-	0.026
8	-	-	-	0.023	-	-	0.006	0.108	0.210
9	-	-	-	0.019	-	-	0.056	0.102	0.098
10	-	-	-	0.061	-	0.005	0.100	0.065	0.227
11	-	-	-	0.060	-	0.019	0.276	0.263	0.216
12	0.002	-	-	0.111	-	0.140	0.352	0.339	0.187
13	0.003	0.003	-	0.258	-	0.111	0.192	0.108	0.031
13.2	-	-	-	-	-	0.002	-	-	-
14	0.071	0.068	-	0.247	-	0.215	0.011	0.016	0.003
15	0.273	0.097	-	0.171	-	0.135	0.005	-	-
16	0.239	0.240	-	0.042	-	0.121	-	-	-
17	0.247	0.266	-	0.008	-	0.098	-	-	-
18	0.152	0.223	0.002	-	-	0.077	-	-	-
19	0.015	0.085	0.079	-	-	0.044	-	-	-
20	-	0.016	0.102	-	-	0.015	-	-	-
21	-	0.002	0.179	-	-	0.005	-	-	-
21.2	-	-	0.006	-	-	-	-	-	-
22	-	-	0.165	-	-	0.013	-	-	-
22.2	-	-	0.002	-	-	-	-	-	-
23	-	-	0.158	-	-	-	-	-	-
23.2	-	-	0.002	-	-	-	-	-	-
24	-	-	0.163	-	-	-	-	-	-
25	-	-	0.084	-	0.005	-	-	-	-
26	-	-	0.053	-	0.005	-	-	-	-
27	-	-	0.005	-	0.013	-	-	-	-
28	-	-	-	-	0.145	-	-	-	-
29	-	-	0.002	-	0.248	-	-	-	-
29.2	-	-	-	-	0.002	-	-	-	-
30	-	-	-	-	0.216	-	-	-	-
30.2	-	-	-	-	0.026	-	-	-	-
31	-	-	-	-	0.055	-	-	-	-
31.2	-	-	-	-	0.095	-	-	-	-
32	-	-	-	-	0.013	-	-	-	-
32.2	-	-	-	-	0.119	-	-	-	-
33	-	-	-	-	0.003	-	-	-	-
33.2	-	-	-	-	0.050	-	-	-	-
34	-	-	-	-	-	-	-	-	-
34.2	-	-	-	-	0.003	-	-	-	-
35	-	-	-	-	-	-	-	-	-
36	-	-	-	-	0.002	-	-	-	-
HR	0.771	0.803	0.874	0.835	0.845	0.855	0.755	0.726	0.835
PD	0.914	0.927	0.964	0.943	0.953	0.966	0.895	0.924	0.935
X ²	21.990	47.698	57.727	51.119	72.751	112.949	19.370	19.029	19.751
PIC	0.74	0.77	0.85	0.80	0.82	0.86	0.71	0.75	0.78
PE	0.546	0.605	0.743	0.666	0.685	0.704	0.518	0.469	0.666

¹ HR: heterozygosity rate; PD: power of discrimination; PIC: polymorphism information content; PE: power of exclusion

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