

FOR THE RECORD

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Genetic Polymorphisms of 15 STR Loci in a Japanese Population

POPULATION: A total of 650 unrelated Japanese individuals living in Tokyo area.

KEYWORDS: forensic science, DNA typing, short tandem repeats, population data, Tokyo Japanese, D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818, FGA

TABLE 1—Allele frequencies and statistical parameters for 15 STR loci in 650 Japanese individuals.

Allele	D8S1179	D21S11	D7S820	CSF1PO	D3S1385	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA
4						0.001*									
5						0.002									
6				0.001*		0.239								0.004*	
7			0.007	0.009		0.263	0.006					0.013		0.003	
8	0.001*		0.107	0.008		0.068	0.262	0.002				0.443		0.012	
9	0.007		0.066	0.081		0.375	0.133	0.331		0.001		0.126		0.072	
9.3						0.031									
10	0.156		0.231	0.233		0.021	0.121	0.205		0.014		0.037		0.209	
11	0.104		0.299	0.202			0.205	0.199		0.012		0.336	0.008	0.286	
11.2										0.001					
12	0.118		0.224	0.376	0.005		0.209	0.141		0.051	0.001*	0.039	0.052	0.249	
12.2										0.032					
13	0.214		0.054	0.089	0.002		0.053	0.109		0.251	0.001	0.006	0.193	0.147	
13.2										0.065			0.003*		
14	0.190		0.012	0.029	0.034		0.009	0.011		0.274	0.207		0.196	0.013	
14.2										0.089			0.002*		
15	0.128			0.002	0.408		0.002	0.001	0.001	0.072	0.037		0.166	0.005	
15.2										0.099					
16	0.074				0.295				0.009	0.009	0.179		0.159		
16.2										0.026					
17	0.008				0.189				0.102		0.265		0.082		0.005
17.2										0.001					
18					0.060				0.171		0.214		0.044		0.019
18.2										0.002					
19					0.005				0.202		0.077		0.026		0.055
19.2										0.001					
20					0.002				0.107		0.017		0.027		0.081
21									0.007		0.001		0.026		0.129
21.2															0.001
22									0.067		0.001		0.006		0.192
22.2															0.004
23									0.127				0.005		0.205
23.2															0.001

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Genetic polymorphisms of 15 short tandem repeat (STR) loci D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818 and FGA were determined in 650 unrelated healthy Japanese Tokyo individuals. DNA was extracted from

Table 1—Continued.

Allele	D8S1179	D21S11	D7S820	CSF1PO	D3S1385	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA
24		0.001*							0.102				0.003		0.161
24.2															0.003
25									0.061				0.002		0.101
25.2															0.002
26		0.004							0.031						0.035
26.2															0.001
27		0.002							0.009						0.003
28		0.058							0.004						0.001
28.2		0.005													
29		0.218													0.001*
29.2		0.002													
30		0.338													
30.2		0.011													
31		0.087													
31.2		0.072													
32		0.027													
32.2		0.112													
33		0.012													
33.2		0.042													
34		0.003*													
34.2		0.006													
Ho	0.843	0.806	0.785	0.752	0.695	0.648	0.810	0.777	0.869	0.823	0.802	0.672	0.858	0.786	0.858
He	0.847	0.808	0.788	0.754	0.706	0.738	0.812	0.778	0.873	0.831	0.803	0.673	0.859	0.787	0.859
PIC	0.840	0.806	0.769	0.735	0.670	0.717	0.802	0.762	0.868	0.827	0.790	0.665	0.856	0.765	0.857
PD	0.956	0.941	0.923	0.901	0.864	0.879	0.937	0.917	0.970	0.950	0.930	0.831	0.965	0.920	0.964
PE	0.649	0.587	0.557	0.512	0.442	0.463	0.586	0.536	0.699	0.630	0.569	0.401	0.666	0.551	0.659
<i>p</i>	0.959	0.998	0.871	0.899	0.903	0.996	0.999	0.887	0.997	0.889	0.530	0.518	0.998	0.751	0.914

*These alleles were not found in previous surveys of the Japanese population.

STR, short tandem repeat; Ho, observed heterozygosity; He, expected heterozygosity; PIC, polymorphic information content; PD, power of discrimination; PE, power of exclusion; *p*, exact test of Hardy–Weinberg equilibrium.

whole-blood specimens using the standard phenol/chloroform method and precipitated with ethanol. The multiplex PCR was performed using approximately 2 ng of genomic DNA in a total reaction volume of 25 μ L by the multiplex kit AmpF ℓ STR IdentifierTM (Applied Biosystems, Foster City, CA). The genotyping was carried out using the ABI PRISMTM 310 Genetic Analyzer and GeneScan software (Applied Biosystems). In order to confirm the variant alleles not included in the standard ladder markers, the samples were amplified again for the respective loci for sequence analysis.

The distributions of the observed allele frequencies for 15 STR loci are shown in Table 1. A total of 174 alleles and 673 genotypes were observed in these samples for 15 STR loci; the distributions of these observed genotypes were not significantly different from the expected distribution according to Hardy–Weinberg equilibrium. The combined power of discrimination (PD) and the combined power of exclusion (PE) for 15 STR loci were 0.9999999999999998 and 0.9999968, respectively.

Some variant alleles (eight of D8S1179, 24 and 34 of D21S11, six of CSF1PO, four of TH01, 12 of vWA, 13.2 and 14.2 of D18S51, six of D5S818, and 29 of FGA) were not reported in previous surveys of the Japanese population (Chiba, Okayama, Miyagi, Nagoya, Sendai) (1–5).

The complete data set is available to any interested researcher at <http://www.med.nihon-u.ac.jp/~legalmed/jtie/15-STR-JFS.doc>

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