

FOR THE RECORD

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Population Data of the 25 STR Loci in Koreans

POPULATION: Koreans

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Unrelated 500 Korean blood samples were obtained from Korean Red Cross National Blood Center. From these, genomic DNA was extracted as described (1). Allelic distribution was studied for 25 STR loci using AmpF/STR[®] Identifiler[™] PCR Amplification Kit (Applied Biosystems) and three Quadruplex amplification systems. Three quadruplex amplification systems have been developed in our laboratory (2) and registered as Korean Patent (3). These systems covers 12 STR loci as following:

Quadruplex 1: D5S818, D13S317, D19S253, D3S2406
Quadruplex 2: D2S1371, D8S1477, D12S391, D20S470
Quadruplex 3: D6S1043, D9S925, D7S821, D4S2368

With Identifiler system, PCR amplification was carried out according to manufacturer's user manual (4) and analyzed by ABI Prism 3100 Avant Genetic Analyzer (Applied Biosystems). For the three quadruplex system, amplification was performed as described (2,3) and analyzed by silver stained denaturing PAGE. All allelic nomenclature was designated by actual repeat number determined by sequencing analysis. Two loci (D5S818 and D13S317) were overlapped at both Identifiler and Quadruplex 1. Though the flanking primer sequences and sizes of resulting PCR products are different between two systems, all the genotype data for two loci were identical to each other.

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Allelic distribution data are summarized in Table 1. Some statistical values were calculated and evaluated for usefulness as identification marker (5). As shown Table 1, 25 STR loci were proved to be good marker systems for the identification and paternity test in Korean population. These systems could be used not only in criminal DNA database but also in paternity DNA database for missing child which should need even more STR markers than criminal database.

References

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TABLE 1—Allele frequencies of 25 STR loci in Korean.

Allele	D5S818	D13S317	D19S253	D3S2406	D2S1371	D8S1477	D12S391	D20S470	D6S1043	D9S925	D7S821	D4S2368	D8S1179
5	...	0.001
6
7	0.006	0.001	0.160	0.001
8	0.003	0.262	0.056	0.018	0.018	...
9	0.091	0.130	0.014	...	0.015	0.034	0.046	0.005
10	0.195	0.143	0.039	...	0.005	0.096	0.031	0.187	0.096
11	0.332	0.225	0.145	...	0.120	0.042	0.095	...	0.002	0.379	0.101
12	0.212	0.186	0.311	...	0.233	0.003	...	0.062	0.106	...	0.011	0.279	0.143
13	0.152	0.039	0.208	...	0.248	0.020	...	0.106	0.145	0.002	0.089	0.085	0.257
14	0.008	0.013	0.061	...	0.238	0.189	...	0.155	0.152	0.171	0.071	0.007	0.176
15	0.001	...	0.006	...	0.123	0.329	0.031	0.133	0.018	0.185	0.178	...	0.145
16	0.020	0.163	...	0.165	0.020	0.329	0.247	...	0.065
17	0.189	0.102	0.093	0.050	0.203	0.258	...	0.011
18	0.063	0.253	0.058	0.195	0.103	0.116	...	0.001
19	0.034	0.190	0.034	0.147	0.007	0.021
20	0.006	0.168	0.001	0.030	...	0.007
21	0.006	0.128	...	0.009
22	0.077	...	0.002
23	0.034
24	0.017
25
26
27
28	0.012
29	0.049
30	0.077
31	0.026
32	0.041
33	0.075
34	0.082
35	0.065
36	0.082
37	0.125
38	0.118
39	0.106
40	0.061
41	0.036
42	0.024
43	0.012
44	0.005
45	0.005
MP	0.083	0.065	0.066	0.014	0.075	0.079	0.049	0.025	0.031	0.084	0.060	0.112	0.049
PD	0.917	0.935	0.934	0.986	0.925	0.921	0.951	0.975	0.969	0.916	0.940	0.888	0.951
PIC	0.740	0.780	0.780	0.910	0.770	0.760	0.820	0.880	0.886	0.757	0.800	0.701	0.820
PE	0.483	0.595	0.649	0.756	0.606	0.664	0.666	0.703	0.390	0.264	0.388	0.199	0.708
H	0.734	0.798	0.827	0.881	0.804	0.834	0.835	0.854	0.845	0.781	0.845	0.735	0.857

Allele	D21S11	D7S820	CSF1PO	D3S1358	TH01	D16S539	D2S1338	D19S433	VWA	TPOX	D18S51	FGA
5
6	0.156
7	...	0.003	0.001	...	0.256
8	...	0.150	0.001	...	0.041	0.005	0.437
9	...	0.057	0.038	...	0.499	0.288	0.134
9.3	0.042
10	...	0.172	0.252	...	0.005	0.142	...	0.002	...	0.041
11	...	0.345	0.234	...	0.001	0.262	0.353	0.008	...
11.2	0.002
12	...	0.234	0.395	0.007	...	0.209	...	0.034	...	0.032	0.039	...
12.2	0.005
13	...	0.033	0.063	0.001	...	0.087	...	0.284	0.002	0.003	0.235	...
13.2	0.046
14	...	0.005	0.016	0.039	...	0.007	...	0.286	0.207	...	0.218	...
14.2	0.113
15	0.002	0.402	0.053	0.037	...	0.167	...
15.2	0.137
16	0.309	0.007	0.007	0.192	...	0.112	...
16.2	0.031
17	0.186	0.091	...	0.284	...	0.060	0.002
18	0.053	0.135	...	0.157	...	0.061	0.014
19	0.003	0.202	...	0.093	...	0.038	0.059
20	0.096	...	0.022	...	0.025	0.054

TABLE 1—Continued.

Allele	D21S11	D7S820	CSF1PO	D3S1358	TH01	D16S539	D2S1338	D19S433	VWA	TPOX	D18S51	FGA
20.2	0.001
21	0.024	...	0.006	...	0.015	0.131
21.2	0.002
22	0.034	0.012	0.147
22.2	0.003
23	0.185	0.005	0.249
23.2	0.004
24	0.132	0.003	0.194
24.2	0.003
25	0.070	0.001	0.087
25.2	0.003
26	0.001	0.017	0.039
27	0.005	0.004
28	0.046	0.004
28.2	0.010
29	0.215	0.002
30	0.349
30.2	0.004
31	0.125
31.2	0.064
32	0.020
32.2	0.120
33	0.006
33.2	0.036
34	0.001
34.2	0.004
MP	0.067	0.090	0.130	0.135	0.169	0.086	0.037	0.070	0.066	0.173	0.044	0.041
PD	0.933	0.910	0.870	0.865	0.831	0.914	0.963	0.930	0.934	0.827	0.956	0.959
PIC	0.770	0.730	0.670	0.650	0.610	0.740	0.850	0.770	0.780	0.600	0.830	0.830
PE	0.562	0.549	0.477	0.414	0.368	0.485	0.678	0.641	0.617	0.344	0.727	0.648
H	0.780	0.772	0.731	0.691	0.659	0.736	0.841	0.822	0.810	0.642	0.866	0.826

MP: matching probability, PD: power of discrimination, PIC: polymorphism information content, PE: power of exclusion, H: observed heterozygosity (5).