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Announcement of Population Data

Allele frequencies of 37 short tandem repeat loci in a Japanese population

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ABSTRACT

Allele frequencies for 37 STR autosomal loci (D1S1656, D2S1338, D2S1360, D2S441, D3S1358, D3S1744, D4S2366, D5S2500, D5S818, D6S474, D7S1517, D7S820, D8S1132, D8S1179, D10S1248, D10S2325, D12S391, D13S317, D16S539, D18S51, D19S433, D21S11, D21S2055, D22S1045, CSF1PO, F13A01, F13B, FESFPS, FGA, LPL, Penta C, Penta D, Penta E, SE33, TH01, TPOX, vWA) were obtained from a sample of 175 unrelated individuals in a Japanese population.

Population

Blood samples were collected from 175 autopsies performed during 2005–2009 at Kyoto University, Kyoto, Japan. All the samples were used with permission for research use from the ethical committee of the Graduate School of Medicine of Kyoto University.

Extraction

DNA was isolated using the QIAprep DNA Blood Kit (QIAGEN, Venlo, Netherlands) and stored at −20 °C until use.

Typing

Alleles on 37 STR loci (Table 1) were amplified from genomic DNA by using Applied Biosystems PCR systems (Veriti 96-well thermal cycler or GeneAmp PCR system 9700; Carlsbad, CA) and the 9600 Emulation mode, along with the following commercially available DNA typing kits: Life technologies AmpFLSTR Identifiler DNA amplification Kit (Identifiler; Carlsbad, CA), Promega PowerPlex ESX17, PowerPlex CS7 custom (Madison, WI), and QIAGEN HDplex kit; all assays were performed according to the manufacturer's protocols. All PCR products were run on the Applied Biosystems 310 Genetic analyzer, and analyzed with GeneMapper v4.0 software.

Analysis of data

Allele frequencies for each locus were analyzed with the web-based Genepop program [1], by using the Hardy–Weinberg exact test for each locus in the population (probability test with the default Markov chain parameters) and linkage disequilibrium test for each pair of loci in each population (log likelihood ratio statistic with default Markov chain parameters). PowerSTAT version 2.1 (Promega) was also used to calculate various forensic parameters, including power of discrimination (PD), polymorphism information content (PIC), power of exclusion (PE), and typical paternity index (TPI).

DNA sequencing

Variant allele fragments on D5S818, D19S433, F13B, and FGA, were independently amplified for sequence analysis according to previously reported methods [2–4]. PCR fragments were purified from agarose gels by using the Wizard PCR gel clean-up kit (Promega) and cloned into the pGEM-T easy vector (Promega) with Takara Ligation high ver.2 (Shiga, Japan) following the manufacturer's protocol. Positive clones were sequenced on a 310 genetic analyzer by using the Big Dye v3.1 sequence kit (Life technologies).

Results

All allele frequency data from the 37 loci are shown in Table 2.

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Table 1
Chromosomal distribution of the 37 STR loci.

Chromosome	Locus			
1	D1S1656	F13B		
2	D2S441	D2S1338	D2S1360	TPOX
3	D3S1358	D3S1744		
4	FGA	D4S2366		
5	D5S818	D5S2500	CSF1PO	
6	D6S474	F13A01	SE33	
7	D7S820	D7S1517		
8	D8S1132	D8S1179	LPL	
9	Penta C			
10	D10S1248	D10S2325		
11	TH01			
12	D12S391	vWA		
13	D13S317			
15	FESFPS	Penta E		
16	D16S539			
18	D18S51			
19	D19S433			
21	D21S11	D21S2055	Penta D	
22	D22S1045			

Other remarks

Several loci are covered by 2 or 3 typing kits. For such loci, we detected the same genotype from the same samples, with the exception of D19S433 in 4 samples because of a point mutation at the primer site [4,5]. In this study, we utilized the D19S433 population data from Identifiler because it is the most commonly used DNA typing kit in Japan.

The allele frequency data for D10S1248 and D22S1045 in the Japanese population have been previously reported by Asamura et al. [6]. On plotting the allele frequencies, they found that the most common alleles were seen at 14 for D10S1248 and 12 for D22S1045, respectively. In our study, we observed a similar allele distribution, but the most common allele was seen at 13 for D10S1248 and 15 for D22S1045. This difference is due to differences in nomenclature, since their study used a laboratory-made multiplex system [7,8]. Indeed the corrected allele frequencies were similar to ours. Therefore, we propose that allele frequency data should be generated with the commercial DNA typing kits used in this study to avoid future nomenclatural inconsistencies.

Table 2
Allele frequencies of 37 STR loci in a Japanese population.

	F13A01	Penta C	Penta E	TH01	Penta D	D5S818	D7S820	D10S2325
3.2	0.3314							
4	0.1114							
5	0.0200	0.0600	0.1086					
6	0.5314			0.1914	0.0057	0.0029	0.0029	0.0400
6.3								0.0029
7	0.0057			0.2829		0.0057		0.3000
8		0.0914	0.0029	0.0686	0.0200		0.1429	0.0229
9		0.3486	0.0143	0.4143	0.3343	0.0800	0.0714	0.1171
9.3				0.0343				
10		0.0514	0.0429	0.0086	0.2257	0.2143	0.2114	0.0457
11		0.3371	0.1171		0.1800	0.2829	0.2914	0.0914
12		0.0800	0.1486		0.1143	0.2486	0.2371	0.1543
13		0.0229	0.0314		0.0971	0.1486	0.0371	0.1057
14		0.0057	0.0486		0.0229	0.0143	0.0029	0.0629
15		0.0029	0.1000			0.0029	0.0029	0.0429
16			0.0829					0.0086
17			0.0686					0.0029
18			0.0600					0.0029
19			0.0686					
19.3			0.0029					
20			0.0400					
21			0.0286					
22			0.0229					
23			0.0057					
24			0.0057					
PD	0.7640	0.8923	0.9822	0.8511	0.9164	0.9191	0.9148	0.9567
PIC	0.5228	0.7052	0.9078	0.6564	0.7501	0.7496	0.7548	0.8272
PE	0.2774	0.5676	0.7204	0.5270	0.5171	0.5270	0.5885	0.6312
TPI	1.2153	2.3026	3.6458	2.0833	2.0349	2.0833	2.4306	2.7344
H	0.4114	0.2171	0.1371	0.2400	0.2457	0.2400	0.2057	0.1829
HWE	0.8212	0.5197	0.6184	0.4623	0.3482	0.8477	0.1099	0.5399
N	350	350	350	350	350	350	350	350

	F13B	LPL	D13S317	CSF1PO	TPOX	D16S539	FESFPS	D2S441
7	0.0029	0.0029	0.0029	0.0086				
8	0.0571		0.3029		0.4714	0.0029	0.0029	0.0029
9	0.2000	0.0029	0.1286	0.0486	0.1114	0.3771	0.0057	0.0057
9c	0.0029							
9.1								0.0143
10	0.7343	0.7171	0.1029	0.2657	0.0257	0.1914	0.0343	0.2400
11	0.0029	0.0943	0.2114	0.1971	0.3629	0.1943	0.3829	0.3686
11.3								0.0200
12		0.1829	0.1943	0.4086	0.0286	0.1457	0.3657	0.2143
13			0.0514	0.0571		0.0800	0.1914	0.0286
14			0.0057	0.0143		0.0086	0.0171	0.1029
15								0.0029

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