



Population data for nine STR loci FGA, vWA, D3S1358, CSF1PO, TPOX, TH01, D7S820, D13S317 and D5S818 in Japanese

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Abstract

Nine AmpF/STR Profiler loci were analyzed in 197 Japanese individuals living in Saitama and allele frequencies collated using an ABI 310 genetic analyzer. The combined power of discrimination for the nine STR loci was 0.999999990. The results showed that the AmpF/STR Kit is very useful for personal identification and paternity testing in the Japanese population.

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1. Introduction

Analysis of short tandem repeat (STR) polymorphisms is one of most widely used techniques in human identification and paternity analysis [1]. The AmpF/STR Profiler PCR Amplification Kit co-amplifies the repeat regions of the following nine STR loci (D3S1358 [2], vWA [3], FGA [4], TH01 [5], TPOX [6], CSF1PO [7], D5S818 [8], D13S317 [8] and D7S820 [9]) plus sex determination (X–Y Amelogenin).

In the present study, we analyzed these nine AmpF/STR Profiler loci to obtain allele frequency data for a Japanese population living in Saitama.

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Table 1

Allele frequencies distribution of the nine STR loci in a Japanese population; allele frequency (%), $n = 194$

Locus	TH01	TPOX	CSF1PO	D5S818	D13S317	D7S820	D3S1358	vWA	FGA
Allele 6	20.9	0.3	–	–	–	–	–	–	–
Allele 7	23.2	0.0	0.5	0.5	0.5	0.0	–	–	–
Allele 8	4.6	41.8	0.5	0.5	30.4	13.1	–	–	–
Allele 9	46.9	12.6	3.6	8.8	10.3	4.9	–	–	–
Allele 9.3	3.6	–	–	–	–	–	–	–	–
Allele 10	0.8	1.8	24.2	24.5	10.6	20.4	–	–	–
Allele 11	–	39.9	18.6	25.8	21.1	33.2	–	–	–
Allele 12	–	3.6	40.7	22.7	20.4	23.7	0.3	–	–
Allele 13	–	–	10.3	16.5	5.7	4.1	0.0	0.0	–
Allele 14	–	–	1.3	0.8	1.0	0.5	3.1	22.4	–
Allele 15	–	–	0.3	–	–	0.0	33.8	1.5	–
Allele 16	–	–	–	–	–	–	32.2	20.1	–
Allele 17	–	–	–	–	–	–	22.7	27.6	–
Allele 18	–	–	–	–	–	–	7.2	20.9	3.6
Allele 19	–	–	–	–	–	–	0.8	5.7	5.4
Allele 20	–	–	–	–	–	–	–	1.5	10.8
Allele 21	–	–	–	–	–	–	–	0.3	14.9
Allele 22	–	–	–	–	–	–	–	–	21.1
Allele 23	–	–	–	–	–	–	–	–	20.6
Allele 23.2	–	–	–	–	–	–	–	–	0.3
Allele 24	–	–	–	–	–	–	–	–	11.1
Allele 24.2	–	–	–	–	–	–	–	–	0.5
Allele 25	–	–	–	–	–	–	–	–	6.4
Allele 26	–	–	–	–	–	–	–	–	3.9
Allele 26.2	–	–	–	–	–	–	–	–	0.0
Allele 27	–	–	–	–	–	–	–	–	0.8
Allele 28	–	–	–	–	–	–	–	–	0.5
Allele 29	–	–	–	–	–	–	–	–	0.0
Allele 30	–	–	–	–	–	–	–	–	0.0

 n = number of studied chromosomes.

Table 2

Statistical parameters for the nine STR loci in Japanese

	EX ($P=$)	LR ($P=$)	H.obs	H.exp	PD	PIC
FGA	0.856	0.808	0.872	0.858±0.025	0.965	0.842
vWA	0.664	0.621	0.825	0.787±0.029	0.913	0.755
D3S1358	0.583	0.639	0.701	0.724±0.032	0.878	0.675
CSF1PO	0.555	0.607	0.753	0.729±0.032	0.879	0.687
TPOX	0.392	0.267	0.660	0.649±0.034	0.808	0.582
TH01	0.110	0.088	0.753	0.679±0.034	0.834	0.629
D7S820	0.074	0.119	0.696	0.771±0.030	0.916	0.736
D13S317	0.649	0.587	0.789	0.797±0.029	0.929	0.769
D5S818	0.859	0.832	0.825	0.786±0.029	0.916	0.752

2. Materials and methods

Blood samples were obtained from 194 unrelated Japanese individuals living in a central part of Japan, Saitama prefecture. DNA was extracted using the kit: DRLab. PCR amplification was performed with AmpF/STR Profiler PCR Amplification Kit (Perkin Elmer, USA) according to the manufacturer's protocol [10]. Genotyping of FGA, vWA, D3S1358, CSF1PO, TPOX, TH01, D7S820, D13S317 and D5S818 were performed by capillary electrophoresis using the ABI Prism™ 310 Genetic Analyzer (Perkin Elmer) in a 47 cm, 50 mm i.d. capillary, filled with Performance Optimized Polymer 4 (POP 4, Perkin Elmer) at 15 kV for 24 min at 60 °C. Allelic ladders were used as a reference for allele designation using Gene Scan™ Analysis Software ver. 2.5.

3. Results and discussion

Thirteen alleles were identified for FGA, eight alleles for vWA, seven alleles for D3S1358, nine alleles for CSF1PO, six alleles for TPOX, seven alleles for TH01, seven alleles for D7S820, eight alleles for D13S317 and eight alleles for D5S818. The distribution of the nine STR allele frequencies is shown in Table 1 for the 197 Japanese subjects. No significant deviations from Hardy–Weinberg equilibrium were detected in any loci.

The statistical parameters (exact test: EX, likelihood ratio test: LR, heterozygosity observed: H.obs, heterozygosity expected: H.exp, power of discrimination: PD, polymorphism information content: PIC) for nine STR loci are shown in Table 2. The combined power of discrimination for the nine STR loci was 0.9999999990. The results showed that the AmpF/STR Kit is very useful for personal identification and paternity testing in the Japanese population.

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