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Population data for 15 STR loci D3S1358, TH01, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penat D, vWA, D8S1179, TPOX and FGA in Japanese

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Abstract. Fifteen short tandem repeat (STR) loci D3S1358, TH01, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penta D, vWA, D8S1179, TPOX and FGA were analyzed in 164 unrelated Japanese using the PowerPlex® 16 System kit. The genotype frequency distribution of each locus did not deviate from the Hardy–Weinberg equilibrium. Penta E was the best STR for forensic purpose. The combined power of discrimination (PD) was 0.999999999999999978.

Keywords: Short tandem repeats; Multiplex PCR; Population data; Japanese

1. Introduction

The development of multiplex PCR techniques has made it possible to analyze a number of short tandem repeat (STR) loci simultaneously. In this paper, we report population data for the allele frequency distributions and statistical parameters of the 15 STR loci (D3S1358, TH01, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penta D, vWA, D8S1179, TPOX and FGA) in Japanese.

2. Materials and methods

Blood samples were obtained from 164 unrelated healthy Japanese individuals living in a central region of Japan. DNA was extracted by the phenol–chloroform method and quantified by UV spectroscopy. PCR amplification of the 15 loci was performed using the

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Table 1
Allele frequencies and forensic parameters for 15 STR loci in Japanese

Allele	D3S1358	TH01	D21S11	D18S51	Penta E	D5S818	D13S317	D7S820	D16S539	CSF1PO	Penta D	vWA	D8S179	TPOX	FGA
5					0.1098										
6		0.2225									0.0031			0.0031	
7		0.2439				0.0061	0.0091			0.0031	0.0031				
8		0.0396			0.0092	0.0031	0.2957	0.1281		0.0031	0.0213			0.4329	
9		0.4543			0.0031	0.0762	0.1220	0.0427	0.3445	0.0305	0.3293		0.0031	0.1189	
9.3		0.0305													
10		0.0092			0.0396	0.2073	0.0945	0.2012	0.2043	0.2531	0.2317		0.1372	0.0152	
11				0.0031	0.1372	0.2348	0.2073	0.3323	0.1860	0.1890	0.1860		0.1281	0.3933	
12	0.0031			0.0396	0.1463	0.2409	0.1982	0.2470	0.1829	0.3933	0.1189		0.1067	0.0335	
13				0.2134	0.0274	0.1646	0.0640	0.0457	0.0671	0.1128	0.0793		0.2226		
14	0.0335			0.1951	0.0457	0.0671	0.0091	0.0031	0.0122	0.0122	0.0274	0.2378	0.2195	0.0031	
15	0.3476			0.2195	0.1250				0.0031	0.0031		0.0183	0.1067		
16	0.3110			0.1098	0.0579							0.2043	0.0701		
17	0.2287			0.0732	0.0976							0.2713	0.0061		
18	0.0671			0.0610	0.0793							0.2012			0.0396
19	0.0091			0.0305	0.0518							0.0488			0.0518
20				0.0244	0.0335							0.0152			0.1128
21				0.0183	0.0092							0.0031			0.1494
22				0.0031	0.0183										0.2043
22.2															0.0031
23				0.0031	0.0061										0.1921
23.2															0.0061
24				0.0061	0.0031										0.1159
24.2															0.0061
25															0.0610
26															0.0427
27															0.0091
28			0.0366												0.0061
28.2			0.0092												
29			0.2287												
29.2			0.0031												
30			0.3476												
31			0.1006												
31.2			0.0640												
32			0.0183												
32.2			0.1494												
33.2			0.0396												
34.2			0.0031												
ET	0.5637	0.0710	0.5047	0.8050	0.1890	0.9677	0.7927	0.0623	0.0687	0.3860	0.1430	0.8173	0.5177	0.4243	0.3837
H-obs	0.6951	0.7805	0.7988	0.8476	0.8659	0.8293	0.7683	0.6890	0.7805	0.7134	0.7683	0.8232	0.8415	0.6402	0.8659
H-exp	0.7301	0.6820	0.7870	0.8436	0.9042	0.8064	0.8022	0.7678	0.7647	0.7317	0.7817	0.7847	0.8407	0.6424	0.8629
PD	0.8760	0.8273	0.9209	0.9521	0.9782	0.9331	0.9328	0.9110	0.8993	0.8842	0.9195	0.9112	0.9506	0.8099	0.9629
PIC	0.6753	0.6295	0.7596	0.8252	0.8632	0.7780	0.7745	0.7317	0.7290	0.6892	0.7501	0.7503	0.8462	0.5738	0.8481
MEC	0.4788	0.4300	0.5980	0.6903	0.8063	0.6148	0.6124	0.5528	0.5503	0.5006	0.5797	0.5745	0.6778	0.3714	0.7240

PowerPlex® 16 System kit (Promega) according to the manufacturer's recommended protocol [1]. Amplified products were separated by denaturing capillary electrophoresis in an ABI PRISM 310 Genetic Analyzer (Applied Biosystems). The results were analyzed using GeneScan Analysis 3.1 software (Applied Biosystems) and genotyping was performed using Genotyper 2.5 software (Applied Biosystems). Possible divergence from the Hardy–Weinberg equilibrium was determined using the exact test (ET) [2]. Some statistical parameters of forensic interest such as observed and expected heterozygosities (H-obs and H-exp) [3], power of discrimination (PD) [4], polymorphic information content (PIC) [5] and mean exclusion chance (MEC) [6] were calculated.

3. Results and discussion

Allele frequencies and forensic parameters for the 15 STR loci in Japanese are shown in Table 1. The genotype frequency distribution of each locus did not deviate from the Hardy–Weinberg equilibrium expectations based on the exact test (the data were shuffled 3000 times). Penta E gave the highest power of discrimination (0.9782), the highest polymorphic information content (0.8632) and the highest mean exclusion chance (0.8063). The combined power of discrimination was 0.999999999999999978 and the combined mean exclusion chance was 0.9999989.

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