FOR THE RECORD

Allele Frequency Distributions for Nine STR Loci in the Japanese Population

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Populations: Individuals from Kyoto and Aomori regions of Japan

Specimens were collected from unrelated volunteer blood donors on absorbent cotton swatches or FTA™ bloodstain collection cards from two regions of Japan. The sample set consisted of 113 individuals from Kyoto region and 59 individuals from Aomori region. DNA was prepared by either organic extraction using standard procedures (1) or direct amplification of samples using the rapid FTA purification procedure according to manufacturer's instructions. Approximately one cm^2 bloodstain sample swatches were used which provided excess amount of DNA ($>$1 ng) for all amplification reactions. PCR amplification was performed using the AmpF*l*STR Profiler Plus™ PCR amplification kit (Perkin-Elmer, Foster City, CA) following established procedures (1) and the recommendations of the manufacturer. Fluorescent allele detection was carried out using the ABI Prism™ 310 Genetic Analyzer (Perkin-Elmer, Foster City, CA). All data sets were subject to independent review before compilation and testing using the GenePop program (2) and the DNA Type program written by Chakraborty and Zhong. The two populations sets (Kyoto and Aomori) were analyzed for Hardy-Weinberg equilibrium, linkage equilibrium and population differentiation tests. No deviation from Hardy-Weinberg or linkage equilibrium was noted which justified the amalgamation of the sample data into a single Japanese data set.

The complete data are available to any interested researcher upon request by accessing www.csfs.ca

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References

1. RCMP/Biology Section Methods Guide, 1998.
2. Raymond M, Rousset F. GENEPOP (version 1.2): Population genetics software for exact tests and ecumenicism. J Heredity 1995;86:248–9.

Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820
7								0.003	0.003
8							0.006	0.279	0.119
9			0.009				0.067	0.125	0.041
10			0.110			0.003	0.218	0.105	0.198
11			0.134			0.006	0.317	0.230	0.343
12			0.108			0.049	0.215	0.198	0.250
13	0.003		0.244			0.198	0.157	0.044	0.041
14	0.029	0.186	0.218			0.215	0.017	0.017	0.006
15	0.387	0.035	0.119			0.206	0.003		
16	0.299	0.169	0.047			0.122			
17	0.212	0.297	0.003	0.009		0.052			
18	0.067	0.206	0.035	0.003		0.047			
19	0.003	0.090	0.058			0.032			
20		0.015	0.096			0.026			
21		0.003	0.148			0.017			
21.2			0.003						
22			0.177			0.003			
23			0.256			0.015			
23.2			0.003						
24			0.116			0.003			
25			0.073			0.006			
26			0.026						
27			0.003						
28					0.047				
28.2					0.006				
29			0.003		0.215				
29.2					0.003				
30					0.363				
31					0.096				
31.2					0.064				
32					0.023				
32.2					0.125				
33					0.003				
33.2					0.049				
34					0.003				
34.2					0.003				
P(exact test)*	0.577	0.237	0.323	0.211	0.064	0.669	0.535	0.898	0.762

* P(exact test) based on 5000 dememorization steps, 1000 batches and 1000 iterations per batch using the GenePop program (2).