

Japanese population data on six STR loci

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Loci: F13A01, F13B, LPL, TH01, TPOX and vWF

Population and sample size: 531 unrelated Japanese individuals living in Gifu Prefecture (central region of Japan). Number of individuals analyzed for each locus: 140 (F13A01), 357 (F13B), 276 (LPL), 531 (TH01), 314 (TPOX) and 362 (vWF)

Methods: PCR amplification for the six STR loci was performed using the *GenePrint*TM STR System (Promega). The amplified products were electrophoretically separated in 4% denaturing polyacrylamide gels (300 mm long and 1 mm thick) according to the *GenePrint*TM Technical Manual and visualized by silver staining [1]. Alleles were determined by comparison with the allelic ladders included in the kits. The chance of exclusion (CE) was calculated using the computer program described by Ohno et al. [2]. The power of discrimination, heterozygosity, and polymorphism information content were calculated as described by Fisher [3], Nei and Roychoudhury [4], and Botstein et al. [5], respectively.

Results:

Allele frequencies

F13A01		F13B		LPL	
Allele	Frequency	Allele	Frequency	Allele	Frequency
3.2	0.332	7	0.003	7	0.004
4	0.093	8	0.064	9	0.002
5	0.043	9	0.203	10	0.707
6	0.525	10	0.725	11	0.100
7	0.004	11	0.004	12	0.185
12	0.004			13	0.004
TH01		TPOX		vWF	
Allele	Frequency	Allele	Frequency	Allele	Frequency
6	0.243	8	0.463	13	0.004
7	0.289	9	0.111	14	0.181
8	0.049	10	0.037	15	0.039
9	0.377	11	0.344	16	0.196
9.3	0.031	12	0.040	17	0.275
10	0.011	14	0.005	18	0.214
				19	0.076
				20	0.015

Statistical evaluations

Loci	CE	PD	h	PIC
F13A01	0.34	0.77	0.61	0.53
F13B	0.22	0.62	0.43	0.38
LPL	0.24	0.66	0.46	0.41
TH01	0.46	0.86	0.71	0.66
TPOX	0.39	0.82	0.65	0.59
vWF	0.60	0.93	0.80	0.77
Combined	0.95	0.99994		

CE: chance of exclusion, PD: power of discrimination, h: Heterozygosity, PIC: polymorphism information content

Comments: Conventional χ^2 test between observed and expected genotype frequencies showed all loci conformed to Hardy-Weinberg equilibrium. The results of this study demonstrate that TH01, TPOX and vWF are more useful for forensic investigations in the Japanese population than the other 3 loci.

References

1. Budowle B, Chakraborty R, Giusti AM, Eisenberg AJ, Allen RC (1991) Analysis of the VNTR locus D1S80 by the PCR followed by high-resolution PAGE. *Am J Hum Genet* 48: 137-144
2. Ohno Y, Sebetan IM, Akaishi S (1982) A simple method for calculating the probability of excluding paternity with any number of codominant alleles. *Forensic Sci Int* 19: 93-98
3. Fisher RA (1951) Standard calculations for evaluating a blood group system. *Heredity* 5: 95-102
4. Nei M, Roychoudhury AK (1974) Sampling variances of heterozygosity and genetic distance. *Genetics* 76: 379-390
5. Botstein D, White RL, Skolnick M, Davis RW (1980) Construction of a genetic linkage map in man using restriction fragment length polymorphisms. *Am J Hum Genet* 32: 314-331