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SHORT COMMUNICATION

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Allele frequencies of eight STRs in Japanese and Chinese

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Abstract Allele frequencies for the eight STR loci Hum-CSF1P0, F13A01, F13B, FES/FPS, LPL, TH01, TPOX and VWA were investigated in Japanese and Chinese populations. No significant deviations from Hardy-Weinberg equilibrium could be found for all loci. In the Japanese population VWA, CSF1PO, TH01, FES/FPS and TPOX were found to be useful for forensic applications and in the Chinese population, VWA, CSF1PO, TH01 and TPOX were found to be useful. Allele distributions were similar between both populations except for FES/FPS.

Key words STR · Population data · Japanese · Chinese

Introduction

We report on a study of the eight STR loci Hum-CSF1PO [1, 2], F13A01 [3], F13B [4], FES/FPS [1, 2, 5], LPL [1, 6], TH01 [7–9], TPOX [10] and VWA [11] in Japanese and Chinese populations.

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Materials and methods

About 120 unrelated Japanese (Sendai, Northeast region of Japan) and about 90 unrelated Chinese (Shenyang, Northeast region of China) were analysed. The amplification of eight STR loci was performed using the Gene Print STR system (Promega Corporation, Madison, Wis., USA).

The χ^2-test between observed and expected genotype frequencies was carried out to test for deviations from Hardy-Weinberg equilibrium. The power of discrimination (PD) [12], expected heterozygosity (H–exp) [13], standard error (SE) [8], polymorphic information content (PIC) [14] and mean exclusion chance (MEC) [15] were calculated. Examination for population sample homogeneity was also done by the χ^2-test of $2 \times C$ contingency table.

Results and discussion

Allele frequencies for the eight loci in the both populations are shown in Table 1 and no significant deviations from Hardy-Weinberg equilibrium could be found for all loci in both populations.

In the comparison of allele frequency distribution in the Japanese population of this study and the results reported by Nagai et al. [16], Kozma et al. [17], no significant differences were observed and in the comparison with the results by Lee et al. [18] no significant differences were observed.

In the comparison of allele frequency distributions between the Japanese and Chinese populations by the χ^2-test of $2 \times C$ contingency table, no significant differences ($P > 0.01$) were observed except for FES/FPS (Table 2), χ^2-value was calculated to be 17.11 (df = 5, $P < 0.005$).

Statistical parameters for the eight loci, observed heterozygosity (H-obs), H-exp, PD, PIC and MEC in the both populations are shown in Table 2.

The forensic efficiency values of VWA, CSF1PO, TH01, FES/FPS and TPOX were higher in comparison with F13B, LPL, F13A01 in Japanese. And in Chinese, those of VWA, CSF1PO, TH01 and TPOX were higher.

Table 1 Allele frequency distributions, χ^2-test for Hardy-Weinberg equilibrium and statistical parameters for the eight loci in the Japanese and Chinese populations

Allele	CSF1PO		F13AO1		F13B		FES/FPS	
	Japanse (n = 117)	Chinese (n = 91)	Japanese (n = 109)	Chinese (n = 86)	Japanese (n = 116)	Chinese (n = 98)	Japanese (n = 111)	Chinese (n = 91)
3.2			0.280	0.378				
4			0.092	0.122				
5			0.032	0.058				
6			0.596	0.436				
7	0.009			0.006		0.005		
8					0.078	0.082		
9	0.030	0.049			0.194	0.250	0.005	0.011
9.3								
10	0.252	0.275			0.728	0.663	0.086	0.038
11	0.209	0.165					0.342	0.500
12	0.410	0.418					0.360	0.225
13	0.056	0.077					0.194	0.220
14	0.034	0.016					0.014	0.005
15								
16								
17								
18								
19								
20								
χ^2	22.37	14.38	3.06	7.46	0.98	3.94	8.81	12.21
df	35	20	9	14	5	9	20	20
P	$0.950 < P < 0.975$	$0.750 < P < 0.900$	$0.950 < P < 0.975$	$0.900 < P < 0.950$	$0.950 < P < 0.975$	$0.900 < P < 0.950$	$0.975 < P < 0.990$	$0.900 < P < 0.950$
Ht.obs	0.709	0.736	0.550	0.721	0.448	0.460	0.757	0.560
Ht. exp	0.725 ± 0.0017	0.722 ± 0.0022	0.562 ± 0.0023	0.656 ± 0.0026	0.429 ± 0.0021	0.496 ± 0.0026	0.714 ± 0.0018	0.657 ± 0.0024
PD	0.876	0.874	0.740	0.81	0.623	0.679	0.861	0.821
PIC	0.697	0.692	0.525	0.615	0.551	0.460	0.681	0.621
MEC	0.484	0.479	0.301	0.380	0.215	0.249	0.454	0.392

Table 1 (continued)

Allele	LPL		THO1		TPOX		VWA	
	Japanese (n = 109)	Chinese (n = 84)	Japanese (n = 119)	Chinese (n = 94)	Japanese (n = 116)	Chinese (n = 93)	Japanese (n = 121)	Chinese (n = 91)
3.2								
4								
5								
6			0.256	0.176				
7	0.005		0.269	0.223				
8	0.005		0.071	0.037	0.466	0.500		
9	0.009	0.006	0.366	0.484	0.108	0.108		
9.3			0.025	0.053				
10	0.720	0.732	0.013	0.027	0.022	0.011		
11	0.101	0.089			0.366	0.344		
12	0.151	0.167			0.039	0.038		
13	0.009	0.006						
14							0.269	0.209
15							0.021	0.060
16							0.120	0.159
17							0.285	0.242
18							0.194	0.170
19							0.091	0.148
20							0.021	0.011
χ^2	25.89	2.74	22.49	29.91	14.03	19.34	15.71	23.71
df	27	14	20	20	14	14	27	27
P	$0.500 < P < 0.750$	$0.995 < P$	$0.250 < P < 0.500$	$0.050 < P < 0.100$	$0.250 < P < 0.500$	$0.100 < P < 0.250$	$0.950 < P < 0.975$	$0.500 < P < 0.750$
Ht.obs	0.440	0.476	0.723	0.638	0.716	0.613	0.752	0.813
Ht.exp	0.452 ± 0.0023	0.433 ± 0.0029	0.729 ± 0.0017	0.687 ± 0.0023	0.641 ± 0.0020	0.625 ± 0.0025	0.791 ± 0.0014	0.827 ± 0.0016
PD	0.660	0.634	0.873	0.854	0.799	0.786	0.921	0.941
PIC	0.431	0.409	0.698	0.658	0.602	0.584	0.770	0.804
MEC	0.249	0.227	0.475	0.445	0.367	0.349	0.581	0.634

Table 2 Comparison of allele frequency distributions between the Japanese and Chinese populations by the χ^2-test of 2 × C contingency test

Locus	χ^2	df	P
CSF1PO	4.999	6	$0.500 < P < 0.750$
F13AO1	11.167	4	$0.025 < P < 0.050$
F13B	3.371	3	$0.100 < P < 0.250$
FES/FPS	17.105	5	$0.002 < P < 0.005$
LPL	2.088	6	$0.900 < P < 0.950$
THO1	12.973	5	$0.010 < P < 0.025$
TPOX	1.122	4	$0.750 < P < 0.900$
vWA	11.68	6	$0.050 < P < 0.100$

References

1. Hammond HA, Jin L, Zhong Y, Caskey CT, Chakraborty R (1994) Evaluation of 13 short tandem repeat loci for use in personal identification applications. Am J Hum Genet 55:175–189
2. Alford RL, Hammond HA, Coto I, Caskey CT (1994) Rapid and efficient resolution of parentage by amplification of short tandem repeat. Am J Hum Genet 55:190–195
3. Polymeropoulos MH, Rath DS, Xiao H, Merril CR (1991) Tetranucleotide repeat polymorphism at the human coagulation factor XIII A subunit gene (F13A1). Nucleic Acids Res 19:4306
4. Nishimura DY, Murray JC (1992) A tetranucleotide repeat for the F13B locus. Nucleic Acids Res 20:1167
5. Polymeropulos MH, Rath DS, Xiao H, Merril CR (1991) Tetranucleotide repeat polymorphism at the human c-fes/fps proto-oncogene (FES). Nucleic Acid Res 19:4018
6. Zuliani G, Hobbs HH (1990) Tetranucleotide repeat polymorphism in the LPL gene. Nucleic Acid Res 18:4958
7. Edwards A, Civitello A, Hammond HA, Caskey CT (1991) DNA typing and genetic mapping with trimeric and tetrameric tandem repeats. Am J Hum Genet 49:746–756
8. Edwards A, Hammond HA, Jin L, Caskey CT, Chakraborty R (1992) Genetic variation at five trimeric and tetrameric repeat loci in four human population groups. Genomics 12:241–253
9. Puers C, Hammond HA, Jin L, Caskey CT, Schumm JW (1993) Identification of repeat sequence heterogeneity at the polymorphic short tandem repeat locus HUMTH01 [AATG]n and reassignment of alleles in population analysis by using a locus-specific allelic ladder. Am J Hum Genet 53:953–958
10. Anker R, Steinbrueck T, Donnis-Keller H (1992) Tetranucleotide repeat polymorphism at a human thyroid peroxidase (hTPO) locus. Hum Mol Genet 1:137
11. Kimpton CP, Walton A, Gill P (1992) A further tetranucleotide repeat polymorphism in the vWF gene. Hum Mol Genet 1:287
12. Fisher RA (1951) Standard calculations for evaluating a blood group system. Heredity 5:95–102
13. Grunbaum BW, Selvin S, Pace N, Black DM (1978) Frequency distribution and discrimination probability of twelve protein genetic variants in human blood as functions of race, sex, and age. J Forensic Sci 23:577–587
14. Bostein 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
15. 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
16. Nagai A, Yamada S, Watanabe Y, Bunai Y, Ohya I (1996) Analysis of the STR loci HUMF13A01, HUMFXIIIB, HUMLIPOL, HUMTH01, HUMTPOX and HUMAWFA31 in a Japanese population. Int J Legal Med 109:34–36
17. Kozma Z, Nishimura A, Ushiyama I, Setalo J, Bajnoczky I, Nishi K (1997) HUMTH01, HUMTPOX and HUMCSF1PO STR loci: allele frequency distributions in a Hungarian and Japanese population groups. Acta Crim Japon 63:105–111
18. Lee JCI, Chen CH, Tsai LC, Linacre A, Chang JG (1997) The screening of 13 short tandem repeat loci in the Chinese population. Forensic Sci Int 87:137–144