

FOR THE RECORD

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Allele Frequencies of Six STR Loci (D3S4536, D4S2633, D5S2500, D9S925, D9S1118 and D20S481) in Chinese Han Population

POPULATION: Over 265 unrelated individuals from Han population living in Wuhan, China

KEYWORDS: DNA typing, population genetics, D3S4536, D4S2633, D5S2500, D9S925, D9S1118, D20S481, Han population

Genomic DNA was obtained from peripheral blood extracted with Chelex-100 method (1). PCR was performed in a total reaction volume of 10 μ L containing 10 ng genomic DNA, 0.2 μ M each primer, 10 mM Tris-HCl buffer (pH 8.3), 50 mM KCl, 1.5 mM MgCl₂, 200 μ M each dNTP, and 0.5 U Taq DNA polymerase (BioStar, Canada). Primer sequences: D3S4536: 5'-ccc ctg caa aca aat ttt tt-3', 5'-gcg cta aag tta cta gtc ctg g-3'; D4S2633: 5'-aag gtt cca gga cac att ca-3', 5'-cct gga tct cca gct tac aa-3'; D5S2500: 5'-tta aag gag

tga tct ccc cc-3', 5'-gtt aca gta cct atg gtc atg cc-3'; D9S925: 5'-tgt gag cca agg cct tat ag-3', 5'-gtc tgg gtt ctc caa aga aa-3'; D9S1118: 5'-cag gat att atg tga tgg aat cc-3', 5'-ctg ctg act cca aaa ata tgc-3'; D20S481: 5'-tgg gtt atg agt gca cac ag-3', 5'-aac agc aaa aag aca cac agc-3'. PCR conditions: 95°C for 2 min soak, 30 cycles of 35 s at 94°C, 35 s at 61°C, 40 s at 72°C followed by a 5 min extension period at 72°C. The amplification products were separated in a vertical, native polyacrylamide gel (6% T; 5% C) and visualized by silver staining (2). Allele frequencies and other statistics parameters for forensic and paternity were determined for each locus by the PowerStats software packages (3). The Hardy-Weinberg

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TABLE 1—Allele frequencies of the STR loci D3S4536, D4S2633, D5S2500, D9S925, D9S1118, and D20S481 in the Chinese Han population.

Allele	D3S4536 (n = 288)	D4S2633 (n = 284)	D5S2500 (n = 284)	D9S925 (n = 266)	D9S1118 (n = 274)	D20S481 (n = 265)
7					0.2007	
8					0.0237	
9					0.0036	
10		0.0141	0.0141		0.0146	
11		0.2342	0.2764		0.0985	0.0170
12		0.0423	0.1708	0.0019	0.1752	0.0094
13		0.2905	0.0458	0.0113	0.0310	0.0774
14		0.2042	0.0863	0.1353	0.2500	0.1132
15	0.0104	0.1109	0.2940	0.2481	0.1807	0.4283
16	0.0174	0.0739	0.0986	0.2782	0.0201	0.2811
16.3				0.0038		
17	0.1545	0.0282	0.0141	0.2387	0.0018	0.0679
18	0.1667	0.0018		0.0752		0.0057
19	0.0694			0.0075		
20	0.1128					
21	0.1493					
22	0.1076					
23	0.0833					
24	0.0851					
25	0.0330					
26	0.0069					
27	0.0035					

n = number of unrelated individuals.

TABLE 2—Statistic parameters of the six loci analyzed in the Chinese Han population.

Locus	D3S4536	D4S2633	D5S2500	D9S925	D9S1118	D20S481
Forensic						
Matching probability	0.027	0.071	0.079	0.079	0.058	0.132
Express as 1 in . . .	37.4	14.2	12.6	12.7	17.4	7.6
Power of discrimination	0.973	0.929	0.921	0.921	0.942	0.868
PIC	0.87	0.77	0.76	0.74	0.80	0.67
Paternity						
Power of exclusion	0.696	0.598	0.604	0.433	0.660	0.492
Typical paternity index	3.35	2.49	2.54	1.68	2.98	1.92
Variability						
Heterozygosity observed	85.1%	79.9%	80.3%	70.3%	83.2%	74.0%
Heterozygosity expected	88.3%	80.0%	79.0%	78.2%	82.3%	71.6%
HWE-exact test	$P = 0.911$	$P = 0.465$	$P = 0.223$	$P = 0.446$	$P = 0.916$	$P = 0.490$

equilibrium test (HWE) was performed by an exact test (4). None of the analyzed loci showed deviations from HWE ($P > 0.05$) in the population studied. The complete data set is available to any interested researcher upon request to the authors.

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