

FOR THE RECORD

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Distribution of D6S2418, D2S1327 and GATA156D11 Alleles in Chinese Population Sample

POPULATION: Chinese.

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A total 100 EDTA-blood samples were obtained from unrelated individuals of Chinese Han ethnic group in Chengdu of China. DNA was extracted by utilizing the Chelex-100 method as described by Walsh et al. (1). The allelic variation at three STR loci named as D6S2418, D2S1327 and GATA156D11 were analyzed by PCR amplification whose respective conditions can be accessed at Nucleotide Database updated by NCBI (<http://www.ncbi.nlm.nih.gov>); however, their annealing temperatures do not totally amount to those recommended by Database. The details of PCR conditions are described in Table 1. The volume of PCR reaction for each locus was 20 μ L containing 2–10 ng DNA, 1 \times Taq buffer, 1.5 mM MgCl₂, 200 μ M each dNTP (Pharmacia Biotech, Sweden), 2.0 U Taq polymerase and 0.3 μ M each primer. PCR amplifications were carried out in a GeneAmp PCR System 9600 (Perkin-Elmer).

The PCR products were analyzed by vertical non-denaturing polyacrylamide gel electrophoresis with 1 \times TBE continuous buffer system and visualized by silver staining (2). Data of population genetics and forensic science were analyzed by using

TABLE 1—Details of PCR conditions.

Locus	Pre-denaturing	Denaturing	Annealing	Extension
D6S2418	94°C 3 min	94°C 35 sec	57°C 35 sec	72°C 55 sec
D2S1327	94°C 3 min	94°C 35 sec	56°C 35 sec	72°C 55 sec
GATA156D11	94°C 3 min	94°C 35 sec	60°C 35 sec	72°C 55 sec

Total of 32 cycles finally are followed by 6 min extension at 72°C.

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TABLE 2—Allele frequencies of three STR loci in Chinese population.

Allele	Frequency		
	D6S2418 (N = 100)	D2S1327 (N = 100)	GATA156D11 (N = 100)
8	0.015	0.02	0.005
9	0.01	0.1	0.055
10	0.455	0.015	0.23
11	0.265	0.065	0.525
12	0.125	0.35	0.15
13	0.065	0.325	0.035
14	0.05	0.075	...
15	...	0.035	...
16	0.015	0.015	...
17
18
Total	1.000	1.000	1.000
HWE*	P > 0.05	P > 0.05	P > 0.05

Test for Hardy-Weinberg equilibrium.

TABLE 3—Population genetics and forensic data of three STR loci.

Locus	PIC	DP	Pm	EP	H _o	H _e
D6S2418	0.66	0.859	0.141	0.398	0.68	0.70
D2S1327	0.71	0.878	0.122	0.637	0.82	0.75
GATA156D11	0.60	0.82	0.18	0.246	0.56	0.65

PIC: polymorphism information content; DP: power of discrimination; Pm: probability of match; EP: power of Exclusion; H_o: observed heterozygosity; H_e: expected heterozygosity.

POWERSTATS program (3). The details of distribution data are described in Tables 2 and 3. The genotype distribution was analyzed for Hardy-Weinberg equilibrium according to Hou's method (4). No deviation from Hardy-Weinberg equilibrium was observed.

All of the above data can be accessed by any interest party at <http://www.smth.edu.cn/pc/index.php?id=wne> or <http://wcumswne.chiname.cn/51143.asp>

References

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