

FOR THE RECORD

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Distribution of D2S2958, D2S1769, and D18S872 Alleles in a Chinese Population Sample

POPULATION: Chinese.

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More than 100 EDTA-blood samples were collected from unrelated healthy individuals of Chinese Han ethnic group in Chengdu City of Sichuan Province. Genomic DNA samples were extracted using the Chelex-100 method (1). The allelic variation at three STR loci named as D2S2958, D2S1769, and D18S872 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 the Database. The details of the PCR conditions are given in Table 1. The volume of PCR reaction for each locus is 25 μ L. Primer sequences are available on CHLC (<http://gai.nci.nih.gov/html-chlc/ChlcMarkers.html>).

PCR amplifications were carried out in a GeneAmp PCR System 9600 (Perkin Elmer, Norwalk, CA). The PCR products were separated by vertical non denaturing polyacrylamide gel electrophoresis with 1 $\times$ TBE continuous buffer system and visualized by silver staining (2). The amplified products were sequenced using ABI PRISMTM 377 Genetic Analyzer (Applied Biosystems, Foster City, CA) in order to make the right nomenclature. Data of population genetics and forensic science were analyzed by using Modified-powerstate program (3). The details of the distribution data are illustrated in Table 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 within the three loci. The complete dataset is available to any interested researcher by contacting rechtsme@wcums.edu.cn or visiting <http://www.legalmed.org/dna/d2s2958.htm>, <http://www.fayi.cn/dna/d2s2958.htm> or <http://w1.88ko.net/vip/jiangshi/lhb.xls>

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

Allele	Frequency		
	D2S2958 (N = 106)	D2S1769 (N = 101) (%)	D18S872 (N = 100) (%)
9		0.5%	1.0%
10		1.5%	41.5%
11		30.7%	39.0%
12		40.1%	16.5%
13		24.3%	2.0%
14		3.0%	
19	3.3%		
21	17.0%		
22	17.0%		
23	18.9%		
24	17.0%		
25	12.7%		
26	11.3%		
28	2.8%		
Total	1.000	1.000	1.000
HWE*	0.05 > p	0.05 > p	0.05 > p

*Test for Hardy–Weinberg equilibrium.

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

Locus	PIC	DP	PM	EP	PI	H
D2S2958	0.83	0.956	0.044	0.603	2.52	0.802
D2S1769	0.62	0.826	0.174	0.514	2.02	0.752
D18S872	0.58	0.816	0.184	0.291	1.25	0.600

PIC, polymorphism information content; DP, power of discrimination; PM, matching probability; EP, power of exclusion; PI, typical of paternity index; H, observed heterozygosity.

TABLE 1—Details of PCR conditions.

Locus	Pre-Denaturing	Denaturing	Annealing Extension
D2S2958	94°C 3 min	94°C 30 sec	58°C 45 sec 72°C 45 sec
D2S1769	94°C 3 min	94°C 30 sec	57°C 45 sec 72°C 45 sec
D18S872	94°C 3 min	94°C 30 sec	56°C 45 sec 72°C 45 sec

A total of 32 cycles finally are followed by a 6-min extension at 72°C.

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