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FOR THE RECORD

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Analysis of Short Tandem Repeat Polymorphisms in the Southwest Chinese Population

POPULATION: The southwest Chinese ($n = 103$).

KEYWORDS: forensic science, DNA typing, short tandem repeats, polymerase chain reaction, population genetics, polymorphism, Han in Chengdu, China, D19S719, D19S431

Blood samples were collected from unrelated individuals of the Chinese Han ethnic group in Chengdu of China. DNA was extracted using the Chelex method (1). The volume of polymerase chain reaction (PCR) for each locus was 20 mL. The PCR products were analyzed by horizontal nondenaturing polyacrylamide gel electrophoresis with a discontinuous buffer system and visualized by silver staining (2,3). Data were analyzed using POWERSTATS program (4). The genotype distribution was analyzed for Hardy–Weinberg equilibrium according to the Hou's method (5) and no deviation from Hardy–Weinberg equilibrium was observed (Tables 1 and 2).

The complete data can be obtained from the authors on request to: jacky800817@sohu.com.

TABLE 1—*Two STR Allele frequency data for the southwest Chinese population.*

D19S719 ($N = 100$)		D19S431 ($N = 103$)	
Allele	Frequency	Allele	Frequency
10	0.590	27	0.015
11	0.055	28	0.107
12	0.155	29	0.024
13	0.150	30	0.102
14	0.035	31	0.442
15	0.015	32	0.189
		33	0.121
Total	1.000	Total	1.000
HWE*	$p > 0.05$	HWE*	$p > 0.05$

*Test for Hardy–Weinberg equilibrium.
STR, short tandem repeat.

TABLE 2—*Population genetics and forensic data of two STR loci.*

Locus	PIC	DP	Pm	EP	Ho	He
D19S719	0.56	0.802	0.198	0.225	0.540	0.601
D19S431	0.70	0.857	0.143	0.369	0.660	0.732

STR, short tandem repeat; PIC, polymorphism information content; DP, power of discrimination; Pm, probability of match; EP, power of exclusion; Ho, observed heterozygosity; He, expected heterozygosity.

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