

## FOR THE RECORD

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# Genetic Polymorphism of Two STR Loci D1S1609 and D18S976 in a Chinese Population

**POPULATION:** Han in eastern China

**KEYWORDS:** forensic science, DNA typing, short tandem repeats, eastern Chinese population, population genetics, D1S1609, D18S976

TABLE 1—Allele frequencies of two STR loci in Chinese Han population.

Allele	D1S1609 (n = 105)	Allele	D18S976 (n = 115)
15	0.029	11	0.004
16	0.267	12	0.109
17	0.214	13	0.278
18	0.148	14	0.313
19	0.100	15	0.213
20	0.057	16	0.052
21	0.110	17	0.026
22	0.062	19	0.004
23	0.014	...	...

Either blood samples or buccal swabs were taken from healthy unrelated Han individuals living in Jiangsu, Zhejiang, Anhui province and Shanghai city after obtaining their informed consent. A Chelex method was used for extracting genomic DNA (1). PCR was performed in an Eppendorf Mastercycler gradient system and the total volume is 37.5  $\mu$ L. The PCR products were analyzed by non-denaturing polyacrylamide gel electrophoresis and visualized by silver staining (2). Allele designation was established following the recommendations of the DNA commission of the ISFH (3). Genetic data were analyzed using Powerstats program (4). The genotype distribution was analyzed for Hardy-Weinberg equilibrium according to Hou's method (5) and no deviation from Hardy-Weinberg equilibrium was observed.

Table 1 contains the summary of allele frequencies and forensic values for the two STR loci. The complete dataset is available upon request at email: yuzhengao@suda.edu.cn

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TABLE 2—Forensic statistics of two STR loci in Chinese Han population.

Locus	PIC	DP	Pm	CE	H <sub>o</sub>
D1S1609	0.810	0.938	0.062	0.682	0.829
D18S976	0.730	0.909	0.091	0.515	0.722

\* PIC: polymorphism information content; DP: power of discrimination; Pm: probability of match; CE: power of exclusion; H<sub>o</sub>: observed heterozygosity.

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