

FOR THE RECORD

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Genetic Profiles of Five STR loci in Eastern Chinese Population

POPULATION: Han in eastern China.

KEYWORDS: forensic science, DNA typing, short tandem repeats, eastern Chinese Han population, population genetics, D8S1179, D7S820, D16S539, D3S1358, D13S317

TABLE 1—Allele frequencies and forensic statistics for five STR loci in eastern Chinese population.

Allele	D8S1179 (n = 109)	D7S820 (n = 102)	D16S539 (n = 114)	D3S1358 (n = 103)	D13S317 (n = 108)
7	0.009
8	...	0.152	0.218
9	...	0.069	0.281	...	0.144
10	0.087	0.176	0.096	...	0.125
11	0.064	0.382	0.25	...	0.287
12	0.106	0.206	0.219	...	0.153
13	0.275	0.010	0.145	...	0.060
14	0.216	...	0.009	0.063	0.005
15	0.174	0.005	...	0.359	...
16	0.069	0.286	...
17	0.009	0.223	...
18	0.068	...

Population samples were collected from unrelated Han individuals living in Jiangsu, Zhejiang province and Shanghai City after obtaining their informed consent. Genomic DNA was extracted from EDTA anticoagulated peripheral blood or buccal swabs using a Chelex method (1). PCR was performed using 1–30 ng of genomic DNA in a 37.5 μ L final reaction volume. An Eppendorf Mastercycler gradient system was used for amplification. 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.

Tables 1 and 2 contain the summary of allele frequencies and forensic values for the five STR loci, respectively.

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TABLE 2—Forensic statistics of five STR loci in eastern Chinese population.

Locus	PIC	DP	Pm	CE	H ₀
D8S1179	0.800	0.934	0.066	0.770	0.881
D7S820	0.720	0.884	0.116	0.530	0.735
D16S539	0.740	0.908	0.092	0.629	0.798
D3S1358	0.680	0.832	0.168	0.695	0.854
D13S317	0.780	0.924	0.076	0.688	0.833

PIC: polymorphism information content; DP: power of discrimination; CE: power of exclusion; and H₀: observed heterozygosity.

The complete dataset can be obtained from the authors on request to: yuzhengao@suda.edu.cn

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