

FOR THE RECORD

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Genetic Polymorphism for Two New STR Loci D9S925, D2S1772 in a Chinese Population

POPULATION: Chinese Han

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The sample population contained unrelated Han individuals living in Jiangsu, Zhejiang, Anhui province and Shanghai city were collected after obtaining their informed consent. Ethnic origin was determined by appearance and self-declaration. Genomic DNA was extracted from EDTA anticoagulated peripheral blood or buccal swabs using a Chelex method (1). PCR was performed using 2–4 ng of genomic DNA in a 37.5 μ L final reaction volume that contained 2–4 ng human genome DNA, 6 μ L dNTP (1 mmol/mL), 1.5 μ Taq polymerase, 3.75 μ L 10 \times buffer (Mg²⁺ 1.5 mmol/l), 0.3 μ L primers (50 nmol/mL). 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.

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

Allele	D9S925 (n = 102)	Allele	D2S1772 (n = 100)
12	0.005	12	0.035
15	0.142	13	0.025
16	0.196	14	0.025
17	0.343	15	0.085
18	0.221	16	0.145
19	0.078	17	0.080
20	0.015	18	0.025
		19	0.260
		20	0.075
		21	0.035
		22	0.080
		23	0.095
		24	0.035

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

Locus	PIC	DP	Pm	CE	H _o
D9S925	0.730	0.902	0.098	0.553	0.775
D2S1772	0.860	0.960	0.040	0.795	0.900

* PIC: polymorphism information content, DP: power of discrimination, Pm: probability of match, H_o: observed heterozygosity.

Tables 1 and 2 contain the summary of allele frequencies and forensic values for the two STR loci, respectively. The complete data can be obtained from the authors on request to: yuzhengao@suda.edu.cn.

References

- Walsh BS, Petzger DA, Higuchi R. Chelex-100 as medium for simple extraction of DNA for PCR-based typing from forensic material. *Biotechniques* 1991;10:506–10. [PubMed]
- Allen CR, Graves G, Budowle B. Polymerase chain reaction amplification products separated on rehydratable polyacrylamide gels and stained with silver. *Biotechniques* 1990;7:736–44.
- DNA recommendations. Report concerning further recommendations of the DNA commission fo the ISFH regarding PCR-based polymorphisms in STR (short tandem repeat) systems. *Int J Legal Med* 1994;107:159–60.
- http://www.premega.com
- Hou Y, Zhang J, Li Y, Wu J, Zhang S, Prize M. Allele sequence of six new Y STR loci and haplotype in the Chinese Han population. *Forensic Sci Int* 2001;118:147–52. [PubMed]

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