

FOR THE RECORD

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Genetic Polymorphism for Two STR Loci D4S2639 and D4S1644 in a Chinese Population

POPULATION: Han in eastern China

KEYWORDS: forensic science, DNA typing, short tandem repeats, eastern Chinese population, population genetics, D4S2639, D4S1644

Blood samples or buccal swabs in this study were collected from unrelated donors residing in eastern China 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 final reaction volume is 37.5 μ 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 1—Allele frequencies of two STR loci in Chinese Han population.

Allele	D4S2639 (n = 105)	Allele	D4S1644 (n = 106)
10	0.014	11	0.080
11	0.200	12	0.524
12	0.081	13	0.283
13	0.243	14	0.094
14	0.181	15	0.019
15	0.148
16	0.076
17	0.048
18	0.001

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

Locus	PIC	DP	Pm	CE	H _o
D4S2639	0.810	0.942	0.058	0.714	0.848
D4S1644	0.570	0.798	0.202	0.316	0.575

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

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Additional information and reprint request:

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