

FOR THE RECORD

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Allele Frequency Distribution of STR Loci D5S1486 in Three Populations*

POPULATIONS: 100 unrelated Chinese volunteer donors, 100 unrelated Thai volunteer donors, 100 unrelated Germany volunteer donors.

KEYWORDS: forensic science, D5S1486, short tandem repeat, Chinese, Thai, Germany

TABLE 1—Allele frequency distributions of D5S1486 in three populations.

Allele	Populations		
	Chinese (n = 100)	Thai (n = 100)	Germany (n = 100)
11	0.010	0.015	0.020
12	0.070	0.125	0.095
13	0.245	0.335	0.230
14	0.325	0.355	0.520
15	0.295	0.160	0.115
16	0.055	0.010	0.020
DP	0.876	0.874	0.828
Het	0.670	0.640	0.680
PE	0.383	0.342	0.398
PIC	0.690	0.670	0.610
HWE test*		P > 0.05	

* Probability values.

DP: power of discrimination.

Het: heterozygosity.

PE: power of exclusion.

PIC: polymorphism information content.

Blood Specimens were obtained from 100 unrelated Chinese volunteer donors, 100 unrelated Thai volunteer donors, 100 unrelated Germany volunteer donors respectively. DNAs were extracted from blood specimens using Chelex-100 (1). Genotyping were carried out by PCR in a PE9600 cyclor. The components of a 20 µL reaction mixture were as follows: template DNA 20 ng, primer 0.2 µmol/L each, dNTPs 200 µmol/L each, KCl 50 µmol/L, Tris-HCl (pH 8.3)

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TABLE 2—Genotype distributions of D5S1486 in three populations.

Genotypes	Populations		
	Chinese (n = 100)	Menggu (n = 100)	Germany (n = 100)
10–10	0	0	0
10–11	1	2	0
11–11	4	2	1
10–12	1	0	1
11–12	1	10	2
12–12	8	14	5
10–13	0	1	3
11–13	2	3	13
12–13	20	19	29
13–13	11	18	23
10–14	0	0	0
11–14	2	6	2
12–14	10	10	4
13–14	19	11	10
14–14	10	2	3
10–15	0	0	0
11–15	0	0	0
12–15	1	0	0
13–15	2	1	3
14–15	8	1	1
15–15	0	0	0
Total	100	100	100

10 mmol/L, MgCl₂ 1.5 mmol/L, Taq polymerase 1 U. Primer sequences: D5S1486: 5'-agctaaacaaggctagactgtatc-3', 5'-tcagctgtcctaaaagccag-3'. PCR conditions: start at 94°C for 4 min, followed by 36 cycles consist of 35 s at 94°C, 40 s at 57°C, 50 s at 72°C followed by a 10 min extention at 72°C. The amplified products were electrophoresed in 6% polyacrylamide gel by using 100 bp ladder and allelic markers as size markers, followed by silver staining. The amplified products were examined by an ABI PRISM™ 310 Genetic Analyzer. Data were analyzed by The Promega

Software, POWERSTATS. The complete dataset is available to any interested researcher by contacting kju@scu.edu.cn.

Reference

1. Singer-Sam J, Tanguary RL, Riggs AD. Use of Chelex to improve the PCR signal from a small number of cells. *Amplification* 1989;3:11.

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