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FOR THE RECORD

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Allele Frequencies of D16S764 and D10S2470 in Two Populations

POPULATION: Chinese Han ($n = 103$) and Thai ($n = 110$).

KEYWORDS: forensic science, Han in Sichuan, China, Thai, Thailand, DNA typing, short tandem repeats, polymerase chain reaction, population genetics, D16S764, D10S2470

Blood samples were collected from unrelated individuals of Chinese Han population living in Chengdu and a Thai population from Thailand. Genomic DNA were extracted using Chelex-100 (Bio-Rad, Shanghai, China) (1). PCR was performed in a 20 μL reaction mixture containing 20 ng template DNA, 0.4 μmol/L each primer, 200 μmol/L dNTPs, 10 mmol/L Tris-HCl (pH 8.3), 1.5 mmol/L $MgCl_2$, and 1.0 U Taq polymerase. Primer sequences are as follows:

TABLE 1—*Allele frequencies for the loci D16S764 and D10S2470 as well as their forensic parameters in Chinese Han and Thai.*

	D16S764		D10S2470	
Allele	Chinese ($n = 103$)	Thai ($n = 110$)	Chinese ($n = 103$)	Thai ($n = 110$)
7				0.005
8	0.010			
9	0.206	0.212		0.005
10	0.557	0.414		
11	0.196	0.283		
12	0.031	0.091	0.160	0.125
13			0.280	0.275
14			0.240	0.285
15			0.180	0.185
16			0.100	0.090
17			0.040	0.030
HWE	$p > 0.05$	$p > 0.05$	$p > 0.05$	$p > 0.05$
H	0.526	0.687	0.770	0.840
P_m	0.205	0.158	0.088	0.090
PIC	0.55	0.64	0.76	0.75
DP	0.795	0.842	0.912	0.910
P_e	0.211	0.408	0.545	0.675
PI	1.05	1.60	2.17	3.13

HWE, Hardy–Weinberg equilibrium test; H, observed heterozygosity; P_m, matching probability; PIC, polymorphism information content; DP, power of discrimination; P_e, power of exclusion; PI, typical paternity index.

D16S764: 5′-ttg tta agt gag gca tga tg-3′
5′-ctg tgc ttg gac ctg aag at-3′.
D10S2470: 5′-cag tga cag ttt aat ggc atg ctg-3′
5′-gcc tat ttt ggg acc cca tg-3′.

PCR conditions: start at 94°C for 2 min, followed by 30 cycles for D16S764 and 28 cycles for D10S2470 of 30 sec at 94°C, 45 sec at 63°C, 55 sec at 72°C, finally extend at 72°C for 7 min. The products were detected by nondenaturing polyacrylamide gel electrophoresis followed by silver staining (2). Data were analyzed by The Promega Software, POWERSTATS (3). No deviation from Hardy–Weinberg equilibrium was found in any population within the two loci (Table 1). The complete dataset is available to any interested researcher by contacting yzhih73@126.com

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