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FOR THE RECORD

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Allele Frequencies of D2S2960 and GATA149B10 in Two Populations

POPULATION: Chinese Han, Thai.

KEYWORDS: forensic science, Han in Sichuan, China, Thai, Thailand, DNA typing, short tandem repeats, polymerase chain reaction, population genetics, D2S2960, GATA149B10

Blood samples were collected from unrelated individuals of a Chinese Han population living in Chengdu and a Thai population from Thailand (Table 1). Genomic DNA was extracted using Chelex-100 (1). PCR was performed in a 20 μL reaction mixture containing 20 ng template DNA, 0.2 μmol/L each primer, 200 μmol/L dNTPs, 10 mmol/L Tris-HCl (pH 8.3), KCl 50 μmol/L, 1.5 mmol/L $MgCl_2$, and 1.0 U Taq polymerase. The primer sequences were as follows:

D2S2960: 5′-taagaagccgttcttggatg-3′
5′-tcaaattcaagttaacattcatca-3′.

GATA149B10: 5′-tattcagccttcagaatctgg-3′
5′-ctgtcatatcttcctatggttatca-3′.

The PCR conditions were as follows: start at 94°C for 5 min, followed by 30 cycles of 30 sec at 94°C, 45 sec at 60°C, and 55 sec at 72°C, followed by a 7-min extention at 72°C. The amplified products were electrophoresed in 6% polyacrylamide, followed by sliver staining (2). The amplified products were sequenced by an ABI PRISM™ 377 Genetic Analyzer (Applied Biosystems, Foster City, CA) in order to make the right nomenclature. Data were analyzed by the Promega Software, POWERSTATS http://www.promega.com/geneticidtools/powerstats. No deviation from Hardy–Weinberg equilibrium was found in any population within the two loci. The complete data can be accessed at http://www.fayi.cn/dna/d2s2960.htm or http://www.legalmed.org/dna/d2s2960.htm

TABLE 1—*Allele frequencies for the loci D2S2960 and GATA149B10 as well as their forensic parameters in Chinese Han and Thai.*

	D2S2960		GATA149B10	
Allele	Chinese ($n = 105$)	Thai ($n = 107$)	Chinese ($n = 121$)	Thai ($n = 98$)
9			0.008	0.031
10			0.165	0.107
11			0.545	0.638
12			0.198	0.184
13			0.083	0.041
14				
15				
16				
17	0.029	0.014		
18	0.229	0.196		
19	0.043	0.037		
20	0.062	0.047		
21	0.286	0.215		
22	0.290	0.308		
23	0.057	0.168		
24	0.005	0.014		
HWE	$p > 0.05$	$p > 0.05$	$p > 0.05$	$p > 0.05$
H	0.714	0.738	0.620	0.541
P_m	0.085	0.079	0.182	0.253
PIC	0.74	0.76	0.58	0.51
DP	0.915	0.921	0.818	0.747
P_e	0.451	0.490	0.315	0.226
P_i	1.75	1.91	1.32	1.09

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; P_i, typical paternity index.

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