## FOR THE RECORD

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## Allele Frequency of D8S1121 and D8S1130 in Two Populations

## POPULATIONS: Chinese Han and Thai

KEYWORDS: forensic science, short tandem repeat, D8S1121, D8S1130, Chinese Han, Thai, DNA typing, population genetics

Blood samples was collected from unrelated individuals of Chinese Han population living in Chengdu and a Thai population from Thailand. Genomic DNA were extracted using Chelex-100 (1). PCR was performed in a 20  $\mu$ L reaction mixture containing 20 ng, template DNA, 0.2  $\mu$ mol/L each primer, 200  $\mu$ mol/L dNTPs, 10 mmol/L Tris-HCl (pH 8.3), KCl 50  $\mu$ mol/L, 1.5 mmol/L MgCl<sub>2</sub> and 1.0 U Taq polymerase. Primer sequences are as follows:

D8S1121: 5'-tca ctc cat cag tgg gtc tt-3' 5'-ctt ttt tgc ttc agg aac ca-3'. D8S1122: 5'-gaa gat ttg gct ctg ttg ga-3' 5'-tgt ctt act gct ata gct ttc ata a-3'.

PCR conditions: start at 94°C for 3 min, followed by 32 cycles of 30 s at 94°C, 45 s at 60°C, 50 s at 72°C followed by a 10 min extention at 72°C. The amplified products were electrophoresed in 6% polyacrylamide followed by sliver staining (2). The amplified products were sequenced by ABI PRISM<sup>TM</sup> 377 Genetic Analyzer in order to make the right nomenclature. Data were analyzed by The Promega Software, POWERSTATS (3). No deviation from Hardy-Weinberg equilibrium was found in any population within the two loci. The complete dataset is available to any interested researcher by contacting kju@scu.edu.cn.

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TABLE 1—Allele frequencies for the loci D8S1121 and D8S1130 as well	Į				
as their forensic parameters in Chinese Han and Thai.					

Allele	D8S1121		D8S1130	
	Chinese $(n = 100)$	Thai $(n = 120)$	Chinese $(n = 103)$	Thai $(n = 120)$
12	0.035	0.013	0.097	0.038
13	0.040	0.029	0.223	0.188
14	0.180	0.154	0.180	0.233
15	0.400	0.425	0.160	0.179
16	0.205	0.225	0.228	0.229
17	0.135	0.108	0.087	0.113
18	0.005	0.046	0.024	0.021
HWE	p > 0.05	p > 0.05	p > 0.05	p > 0.05
Н	0.750	0.742	0.786	0.775
PM	0.118	0.121	0.068	0.067
PIC	0.71	0.69	0.80	0.78
DP	0.882	0.879	0.932	0.933
PE	0.510	0.496	0.574	0.553
PI	2.00	1.94	2.34	2.22

HWE: Hardy-Weinberg equilibrium test; H: Observed heterozygosity; heterozygosity; PM: Matching probability; PIC: Polymorphism information content; DP: Power of discrimination; PE: Power of exclusion; PI: Typical paternity index.

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