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FOR THE RECORD

Yanyun Wang,[1] M.D.; Zhuo Wang,[1] M.D.; Bin Zhou,[1] Ph.D.; Bin Du,[1] Ph.D.; Beilei Zhang,[1] M.D.; Gengqian Zhang,[1] Ph.D.; Yi Jia,[1] Ph.D.; Yesheng Wei,[1] Ph.D.; and Lin Zhang,[1,2] Ph.D.

Allele Frequencies for Two Short Tandem Repeat Loci in the Chinese Han Population from Chengdu, China, and a Thai Population from Thailand

POPULATION: Chinese Han and Thai.

KEYWORDS: forensic science, DNA typing, short tandem repeat, polymerase chain reaction, population genetics, Chinese Han, Thai, D4S1645, D7S3062

Blood samples were collected from unrelated individuals of the Chinese Han population living in Chengdu and a Thai population from Thailand. Genomic DNA was extracted using Chelex-100 (1). PCR products were electrophoresed in 6% polyacrylamide, followed by sliver staining (2). The amplicons 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 (3). No deviation from Hardy–Weinberg equilibrium was found in any population within the two loci.

The complete data set is available to any interested researcher by contacting wyanyun@gmail.com (Table 1).

TABLE 1—*Allele frequencies for the loci D4S1645and D7S3062 as well as their forensic parameters in Chinese Han and Thai.*

	D4S1645			D7S3062	
Allele	Chinese ($n = 100$)	Thai ($n = 97$)	Allele	Chinese ($n = 100$)	Thai ($n = 100$)
5			20	0.010	0.010
6	0.100	0.155	21	0.030	0.010
7	0.045	0.021	22	0.085	0.055
8	0.050	0.021	23	0.220	0.215
9	0.275	0.196	24	0.190	0.175
10	0.240	0.289	25	0.210	0.265
11	0.210	0.196	26	0.160	0.165
12	0.060	0.119	27	0.075	0.065
13	0.020	0.005	28	0.015	0.025
14			29	0.005	0.015
HWE	p>0.05	p>0.05	HWE	p>0.05	p>0.05
H_o	0.740	0.804	H_o	0.820	0.790
P_m	0.073	0.079	P_m	0.053	0.058
PIC	0.78	0.77	PIC	0.81	0.79
DP	0.927	0.921	DP	0.947	0.942
P_e	0.493	0.607	P_e	0.637	0.581
PI	1.92	2.55	PI	2.78	2.38

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

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Additional information and reprint requests:
Lin Zhang, Ph.D.
Institute of Forensic Biology
Sichuan University
Chengdu, 610041 Sichuan
China
E-mail: zhanglin@scu.edu.cn

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[1] College of Forensic Medicine, Sichuan University, Chengdu, 610041 Sichuan, China.

[2] State Key Laboratory of Biotherapy, Sichuan University, Chengdu, 610041 Sichuan, China.