

FOR THE RECORD

Shi Jiang,¹ M.D.; Wei Wu,¹ M.D.; Libin Yun,¹ M.D.; Peng Bai,¹ M.D.; Jinliang Hu,² M.D.; Li Liu,¹ M.D.; Haibo Luo,¹ M.D.; Jin Wu,¹ M.D.; Yingbi Li,¹ M.D.; and Yiping Hou,¹ M.D.

Distribution of D9S2150, GATA164F07, and D10S2469 Alleles in a Chinese Population Sample

POPULATION: Chinese ($n = 100$).

KEYWORDS: forensic science, Han in Sichuan, China, short tandem repeats, DNA typing, polymerase chain reaction, population genetics, D9S2150, GATA164F07, D10S2469

One hundred EDTA-blood samples were collected from unrelated healthy individuals of Chinese Han ethnic group in Chengdu of Sichuan. Genomic DNA samples were extracted using Chelex-100 method (1). The allelic variation at three short tandem repeat loci named as D9S2150, GATA164F07, and D10S2469 were analyzed by PCR amplification whose respective conditions can be accessed at Nucleotide Database updated by NCBI (<http://www.ncbi.nlm.nih.gov>), however, their annealing temperatures do not totally amount to those recommended by database.

The details of PCR conditions are available to any interested researcher by contacting rechtsme@wcums.edu.cn or visiting our Web site (<http://w1.88ko.net/vip/jiangshi/>).

TABLE 1—Allele frequencies of three STR loci in Chinese population.

Allele	Frequency		
	D9S2150 ($n = 100$)	GATA164F07 ($n = 100$)	D10S2469 ($n = 100$)
7		0.380	
8		0.070	
9	0.005	0.285	
10	0.045	0.195	
11	0.220	0.070	0.170
12	0.275		0.280
13	0.320		0.430
14	0.13		0.120
15	0.005		
Total	1.000	1.000	1.000
HWE*	$p > 0.05$	$p > 0.05$	$p > 0.05$

*Test for Hardy–Weinberg equilibrium (HWE).
STR, short tandem repeats.

TABLE 2—Population genetics and forensic data of three STR loci.

Locus	PIC	DP	P_m	EP	H_o	H_e
D9S2150	0.71	0.890	0.110	0.562	0.78	0.758
GATA164F07	0.68	0.882	0.118	0.444	0.71	0.730
D10S2469	0.64	0.840	0.160	0.413	0.69	0.697

PIC, polymorphism information content; DP, power of discrimination; P_m , probability of match; EP, power of exclusion; H_o , observed heterozygosity; H_e , expected heterozygosity; STR, short tandem repeats.

PCR amplifications were carried out in a GeneAmp PCR System 9600 (Applied Biosystems, Foster City, CA). The PCR products were separated by vertical nondenaturing polyacrylamide gel electrophoresis with $1 \times$ TBE continuous buffer system and visualized by silver staining (2). The amplified products were sequenced by ABI PRISMTM 377 Genetic Analyzer (Applied Biosystems) in order to make the right nomenclature. Data of population genetics and forensic science were analyzed by using POWERSTATS program (3). The details of distribution data are described in Tables 1 and 2. The genotype distribution was analyzed for Hardy–Weinberg equilibrium according to Hou's method (4). No deviation from Hardy–Weinberg equilibrium was observed within the three loci.

The complete data set is available to any interested researcher by contacting rechtsme@wcums.edu.cn or visiting our Web sites (<http://w1.88ko.net/vip/jiangshi/> or <http://legalmed.org/dna/d9s2150>).

References

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¹ Institute of Forensic Medicine, West China Medical Center, Sichuan University, Chengdu 610041, Sichuan, China.

² Department of Public Health, West China Medical Center, Sichuan University, Chengdu 610041, Sichuan, China.

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Additional information and reprint requests:

Shi Jiang, M.D.

Institute of Forensic Medicine

Sichuan University (West China University of Medical Sciences)

Chengdu 610041, Sichuan

China

E-mail: shijiang2008@sina.com