J Forensic Sci, July 2006, Vol. 51, No. 4
doi:10.1111/j.1556-4029.2006.00193.x
Available online at: www.blackwell-synergy.com

FOR THE RECORD

Zhiyong Liu,[1] M.D.; Baohua Zhang,[2] B.S.; Guodi Chen,[1] M.D.; Lin Yu,[1] M.D.; Miao Liao,[1] B.S.; Jing Wang,[1] M.D.; Bing Long,[1] M.D.; and Lin Zhang,[1] Ph.D.

Allele Frequencies for Three STR Loci in Chinese Han Populations

POPULATION: Chinese.

KEYWORDS: forensic science, Han in Sichuan, China, DNA typing, short tandem repeats, polymerase chain reaction, population genetics, D18S536, GATA140E03, D12S1064

A total 100 EDTA blood samples were obtained from unrelated individuals of Chinese Han ethnic group in Chengdu of China. DNA was extracted by utilizing the Chelex-100 method as described by Walsh et al. (1). The allelic variation at three STR loci named as D18S536, GATA140E03, and D12S1064 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 described as followed: predenaturing condition of three loci is 94°C 3 min, denaturing is 94°C 35 sec, and extension is 72°C 55 sec. The annealing is 57°C for D18S536, 56°C for GATA140E03, 55°C for D12S1064, though all the lasting time for them is 35 sec. The volume of PCR reaction for each locus was 20 μL containing 2–10 ng DNA, 1 × Taq buffer, 1.5 mM $MgCl_2$, 200 μM each dNTP (Pharmacia Biotech, Uppsala, Sweden), 2.0 U Taq polymerase, and 0.3 μM each primer. PCR amplifications were carried out in a GeneAmp PCR System 9600 (Perkin-Elmer, Wellesley, MA).

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

	Frequency		
Allele	D18S536 ($N = 100$)	GATA140E03 ($N = 100$)	D12S1064 ($N = 100$)
8	0.02	—	—
9	0.01	—	—
10	0.205	—	0.035
11	0.28	0.075	0.045
12	0.41	0.15	0.045
13	0.07	0.42	0.14
14	0.005	0.265	0.22
15		0.08	0.335
16		0.005	0.14
17		0.005	0.035
18		—	0.005
Total	1.000	1.000	1.000
HWE*	$p > 0.05$	$p > 0.05$	$p > 0.05$

*Test for Hardy–Weinberg equilibrium.

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

Locus	PIC	DP	P_m	EP	H_o	H_e
D18S536	0.66	0.866	0.134	0.428	0.70	0.71
GATA140E03	0.68	0.874	0.126	0.476	0.73	0.72
D12S1064	0.77	0.924	0.076	0.618	0.81	0.80

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.

The PCR products were analyzed by vertical nondenaturing polyacrylamide gel electrophoresis with 1 × TBE continuous buffer system and visualized by silver staining (2). 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.

All the data can be read on the URL: http://spaces.msn.com/members/liuzhiyong35

[1]Institute of Forensic Medicine, West China Medical Center, Sichuan University, Chengdu, 610041, Sichuan, China.
[2]Center of Forensic Sciences, Public Security Bureau of Yantian District, Shenzhen 518082, Guangdong, China.

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Additional information and reprint requests:
Associate Prof. Guodi Chen, M.D.
Institute of Forensic Medicine
West China Medical Center
Sichuan University
17#, Section 3
Renmin Nan Road
Chengdu 610041, Sichuan
China
E-mail: scupress@yahoo.com.cn