J Forensic Sci, January 2008, Vol. 53, No. 1
doi: 10.1111/j.1556-4029.2007.00632.x
Available online at: www.blackwell-synergy.com

FOR THE RECORD

Ga Liao,[1] Ph.D.; Tingting Liu,[2] Ph.D.; Binwu Ying,[3,4] Ph.D.; Lei Sun,[5] M.D.; Yi Zou,[1] Ph.D.; Zhengrong Wang,[1] Ph.D.; Hong Fan,[3,4] Ph.D.; and Fuqiang Wen,[3] M.D.

Population Genetic Study of 15 STR Loci in a Chinese Population

POPULATION: Chinese (n = 501).

KEYWORDS: forensic science, Han ethnic group, Guangzhou City, Guangdong Province, China, DNA typing, short tandem repeats, polymerase chain reaction, population genetics, D3S1358, THO1, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penta D, VWA, D8S1179, TPOX, FGA

Blood samples were collected from 501 unrelated people of the Han ethnic group in Guangzhou, China. DNA was extracted using Chelex method (1). Individual DNA samples were amplified for 16 STR loci (including Amelogenin) by PCR using Powerplex 16™ kit (Promega Corporation, Madison, WI) under the conditions recommended by the manufacturer in a reaction volume of 12.5 μL in PE 9600 thermal cycler (Perkin-Elmer, Foster City, CA) (2,3). The PCR product of 1 μL was mixed with 0.3 μL internal LIZ size standard (GS-500 LIZ; Applied Biosystems, Foster City, CA) and 8.7 μL Hi-Di formamide (Applied Biosystems), and electrophoresed in ABI 3100 Genetic Analyzer (Applied Biosystems) using the recommended protocol from the kit. The results were analyzed by Data Collection (Version 1.1), GeneScan (Version 3.7), and Genotyper (Version 3.6) softwares (Applied Biosystems) (Tables 1 and 2).

Evaluation of Hardy–Weinberg expectations was carried out using the chi-squared test; the power of discrimination (PD), the probability of paternity exclusion (PE), the polymorphic information content (PIC), and the observed heterozygosity (Ho) were calculated using Powerstate of the Version 1.2 package (4,5).

The complete data (also including some statistical parameters) are available to any interested researcher upon request.

References

1. Walsh BS, Petzger DA, Higuchi R. Chelex-100 as medium for simple extraction of DNA for PCR-based typing from forensic material. Biotechniques 1991;10:506–10.
2. Promega Corporation. PowerPlexR 16 system kit, technical manual, http://www.promega.com. Accessed March 2006.
3. Krenke BE, Tereba A, Anderson SJ, Buell E, Culhan S, Finis CJ, et al. Validation of a 16-locus fluorescent multiplex system. J Forensic Sci 2002;47:773–85.
4. Tereba A. Tools for analysis of population statistics: profiles in DNA, Vol. 2, 1999; 203. Available at http://www.promega.com/geneticidentity/. Accessed March 2006.
5. Ying BW, Wei YG, Sun XM, Liu TT, Hou YP. STR data for the AmpFlSTR profiler plus from western China. J Forensic Sci 2005; 50(3):716–7.

Additional information and reprint requests:
Fuqiang Wen, M.D.
Department of Respiratory Medicine
Sichuan University (West China University of Medical Sciences)
Chengdu 610041, Sichuan
China
E-mail: fwen78@yahoo.com/bioion@gmail.com

[1]Biomedical Engineering Department, West China School of Preclinical and Forensic Medicine, Sichuan University, Chengdu 610041, China.
[2]Department of Orthodontics, West China College of Stomatology, Sichuan University, Chengdu 610041, Sichuan, China.
[3]Department of Respiratory Medicine, West China Hospital, Sichuan University, Chengdu 610041, Sichuan, China.
[4]Department of Laboratory Medicine, West China Hospital, Sichuan University, Chengdu 610041, Sichuan, China.
[5]Department of Paediatrics, The 2nd West China Hospital, Sichuan University, Chengdu 610041, Sichuan, China.

TABLE 1—*Allele frequencies of 15 STR loci in a Chinese population.*

	Frequency (%), n = 501														
Allele	D3S1358	THO1	D21S11	D18S51	Penta E	D5S818	D13S317	D7S820	D16S539	CSF1PO	Penta D	VWA	D8S1179	TPOX	FGA
5					5.9										
6		10.5							0.2						
7		26.6			0.2	2.2		0.2		0.2	0.5				
8		5.0			1.0	0.3	30.7	12.4	1.0	0.3	5.9			53.6	
9		48.6			1.7	8.2	16.1	8.1	27.0	4.0	34.6			10.6	
9.3		4.5													
10		4.8		0.1	4.8	19.2	13.0	17.2	11.7	25.6	12.9		11.9	1.5	
11				0.6	15.2	28.7	23.5	37.0	26.2	26.4	12.3		10.2	30.9	
12	0.4			3.0	12.5	27.0	12.3	22.8	21.6	35.0	17.9		13.2	3.2	
13				18.6	4.5	13.4	3.9	2.1	11.3	6.9	10.4		21.2	0.2	0.2%
14	3.7			19.6	7.7	0.8	0.6	0.3	1.0	1.5	3.9	26.5	17.1		
15	37.0			19.4	9.0	0.2					1.2	3.2	16.7		
16	30.0			14.1	6.0						0.5	17.4	8.7		0.1
17	21.0			7.5	8.9							25.5	1.0		0.2
18	7.1			4.9	7.1							15.7	0.2		2.8
19	0.5			5.0	6.5							10.3			2.9
20	0.3			2.1	3.8							1.3			5.2
21				2.9	2.6							0.1			11.6
21.2															0.3
22				1.0	1.1										17.9
22.2															2.3
23				0.8	0.6										18.6
23.2															0.8
24					0.8										19.1
24.2															1.4
25				0.4	0.3										10.1
25.2															0.5
26				0.2											5.0
27			0.2												1.0
28			5.3												0.1
28.2			0.6												
29			26.6												0.1
29.2			0.4												
30			25.5												
30.2			1.2												
31			10.8												
31.2			7.5												
32			3.8												
32.2			13.1												
33			0.2												
33.2			4.1												
34.2			0.6												
35.2			0.1												

TABLE 2—*Forensic data, paternity data, and HWE data of 15 loci in a Chinese population.*

	D3S1358	THO1	D21S11	D18S51	Penta E	D5S818	D13S317	D7S820	D16S539	CSF1PO	Penta D	VWA	D8S1179	TPOX	FGA
Forensic															
MP	0.125	0.149	0.053	0.041	0.017	0.084	0.078	0.095	0.083	0.119	0.064	0.070	0.044	0.222	0.033
PD	0.875	0.851	0.947	0.959	0.983	0.916	0.922	0.905	0.917	0.881	0.936	0.930	0.956	0.778	0.967
PIC	0.67	0.63	0.80	0.84	0.91	0.75	0.76	0.72	0.75	0.69	0.78	0.77	0.83	0.54	0.85
Paternity															
PE	0.442	0.336	0.699	0.699	0.841	0.611	0.596	0.560	0.563	0.497	0.596	0.600	0.715	0.324	0.664
TPI	1.72	1.37	3.39	3.39	6.42	2.58	2.48	2.26	2.28	1.94	2.48	2.51	3.58	1.34	3.02
Ho	70.9%	63.6%	85.2%	85.2%	92.2%	80.6%	79.8%	77.8%	78.0%	74.3%	79.8%	80.0%	86.0%	62.7%	83.4%
HWE															
df = 1 χ^2	0.5222	3.6280	2.7512	0.1324	0.1650	1.5912	0.1235	0.9223	0.0829	0.1189	0.0276	0.0102	0.4377	0.9708	4.5943
P	0.4698	0.0568	0.0971	0.7159	0.6845	0.2071	0.7252	0.3368	0.7734	0.7302	0.8679	0.9194	0.5082	0.3244	0.0320

MP, matching probability; PD, power of discrimination; PE, power of exclusion; TPI, typical paternity index; Ho, heterozygotes; HWE, Hardy–Weinberg expectations; PIC, polymorphic information content.