

FOR THE RECORD

Yonggang Wei,¹ M.D.; Tingting Liu,² Ph.D.; Jingdong Li,³ M.D.; Lin Zhang,⁴ Ph.D.; Binwu Ying,⁵ Ph.D.; and Bo Li,¹ M.D.

Genetic Diversity of Five STR Loci in Southeastern China

POPULATION: Chinese

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Blood samples were collected from 150 unrelated people of Han ethnic group in Fuzhou of China. The DNA was extracted from whole blood using the Chelex-100 extraction method (1), and the DNA concentration was determined by the ethidium bromide dot quantization method (2). Target DNA ranging from 0.5 to 1.25 ng was amplified in 8 μ L of total reaction volume containing 3 μ L Reaction Mix, 1.8 μ L Primer Set, and 0.25 μ L AmpliTaq Gold DNA polymerase (5 U/ μ L) using the AmpFLSTR[®] Identifiler[™] PCR Amplification Kit (Applied Biosystems, Foster City, CA). The cycling conditions provided with the kit were exactly followed. The PCR product of 1 μ L was mixed with 0.3 μ L internal LIZ size standard (GS-500 LIZ, Applied Biosystems) and 8.7 μ L Hi-Di formamide (Applied Biosystems), and electrophoresed in ABI Prism[®] 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). Data of population genetics and forensic science were analyzed using powerstats program (Promega Corporation, Madison, WI) (3).

The complete data (also including some statistical parameters) are available to any interested researcher upon request to corresponding author at: doclijd@gmail.com.

¹Department of General Surgery, West China Hospital, Sichuan University (West China University of Medical Sciences), Chengdu 610041, Sichuan, China.

²Department of Orthodontics, West China College of Stomatology, Sichuan University (West China University of Medical Sciences), Chengdu 610041, Sichuan, China.

³Department of General Surgery, Affiliated Hospital of North Sichuan Medical College, Nanchong, Sichuan 637000, China.

⁴College of Preclinical Medicine and Forensic Science, Sichuan University (West China University of Medical Sciences), Chengdu 610041, Sichuan, China.

⁵Department of Laboratory Medicine, West China Hospital, Sichuan University (West China University of Medical Sciences), Chengdu 610041, Sichuan, China.

TABLE 1—Allele frequencies and forensic efficiency data of five STR loci in Han ethnic group of Chinese population.

Allele	Frequency				
	D3S1358	TH01	D21S11	D18S51	D5S818
6		8.7%			
7		6			2.0%
8		9.0%			
9		49.7%			9.7%
9.3		2.7%			
10		5.0%		0.7%	16.7%
11		0.3%		1.0%	29.3%
12		0.3%		2.3%	28.7%
13	0.3%			19.3%	11.3%
14	6.7%			19.7%	1.3%
15	30.7%			14.0%	1.0%
16	35.3%			17.0%	
17	20%			9.7%	
18	5.7%			2.3%	
19	1.3%			5.3%	
20				2.3%	
21				2.0%	
22				4.0%	
23				0.3%	
27.2			0.3%		
28			3.0%		
28.2			1.0%		
29			25.3%		
30			31.3%		
30.2			0.7%		
31			11.3%		
31.2			3.3%		
32			3.3%		
32.2			15.0%		
33			1.0%		
33.2			4.0%		
34.2			0.3%		
Pm	0.123	0.152	0.090	0.041	0.080
PD	0.877	0.848	0.910	0.959	0.920
PIC	0.69	0.63	0.77	0.84	0.75
PE	0.504	0.379	0.662	0.637	0.460
X ²	0.0925	0.0809	1.0430	2.2653	3.5963
P	0.7611	0.7760	0.3071	0.1323	0.0579

PD, power of discrimination; PE, power of exclusion; Pm, probability of match; d.f. = 1.

References

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3. Available at: <http://www.promega.com>.

Additional information and reprint requests:

Li Bo, M.D.

Department of General Surgery

West China Hospital

Sichuan University (West China University of Medical Sciences)

Chengdu 610041, Sichuan

China

E-mail: doclijd@gmail.com