

FOR THE RECORD

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Population Genetics for Six STR Loci in the Population from Southern China

POPULATION: A total of 157 unrelated individuals from the Han ethnic group of Southern China (Nanning City, Guangxi, China)

KEYWORDS: forensic science, vWA, FGA, D21S11, D18S51, D13S317, D7S820, short tandem repeats, Chinese population, population genetics, DNA typing

The loci studied were named as vWA, FGA, D21S11, D18S51, D13S317 and D7S820. Samples were collected from unrelated adults after informed consent. Genomic DNA was isolated utilizing Chelex method (1). Locus-specific primers of these STR were labeled with fluorescent dye. The volume of PCR reaction was 25 μ L, and the amplified condition were accordant with the protocol of manufacture. Amplification were carried out with a GeneAmp PCR system 9700 thermocycler (Applied Biosystem, Foster city, CA). The amplicons were analyzed on ABI PRISM 3100 Genetic Analyzer (Applied Biosystems, Foster city, CA).

Allelic frequencies, data of population genetics and values of forensic science were calculated using software POWERSTATS (2). Allelic frequencies of these loci were list in the Table 1, and data of population genetics and forensic science were presented in the

Table 2. A total of 9, 14, 13, 15, 7 and 8 alleles was observed at VWA, FGA, D21S11, D18S51, D13S317 and D7S820, respectively, in the population studied. The conventional Chi-square analysis was used to detect significant departures from Hardy-Weinberg equilibrium expectations.

The complete dataset can be accessed via e-mail at lovekoushui@sina.com.

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. [\[PubMed\]](#)
2. <http://www.promega.com>

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TABLE 1—Distribution of allelic frequencies at six loci in the population studied.

Allele	VWA (N = 314)	FGA (N = 314)	D21S11 (N = 314)	D18S51 (N = 314)	D13S317 (N = 314)	D7S820 (N = 314)
7						0.6%
8					29.3%	15.3%
9					15.9%	8.6%
10					14.6%	14.6%
11				0.3%	25.2%	36.3%
12				4.8%	13.1%	21.7%
13	0.3%			15.9%	1.6%	2.5%
14	29.9%			18.8%	0.3%	0.3%
15	2.2%			22.3%		
16	14.0%			13.4%		
17	23.6%			6.4%		
18	18.5%	1.9%		6.7%		
19	8.9%	6.4%		4.1%		
19.2				0.3%		
20	1.9%	5.1%		2.5%		
21	0.6%	17.2%		1.6%		
22		20.4%		1.0%		
23		20.7%		1.3%		
23.2		0.6%				
24		14.6%		0.6%		
24.2		0.3%	0.3%			
25		6.1%				
25.2		1.0%				
26		4.1%				
27		1.3%				
28		0.3%	5.4%			
29			28.0%			
30			22.0%			
30.2			1.0%			
31			9.6%			
31.2			10.2%			
32			2.2%			
32.2			15.3%			
33			0.6%			
33.2			4.8%			
34			0.3%			

N: the number of chromosomes.

TABLE 2—Population genetics and forensic data of six loci in the population studied.

Locus	VWA	FGA	D21S11	D18S51	D13S317	D7S820
Power of Discrimination	0.918	0.958	0.943	0.952	0.913	0.906
PIC	0.76	0.83	0.80	0.84	0.75	0.74
Power of Exclusion	0.664	0.702	0.740	0.702	0.580	0.535
He	0.792	0.852	0.824	0.858	0.787	0.768
Ho	0.834	0.854	0.873	0.854	0.790	0.764
H-WE	$P > 0.05$	$P > 0.05$	$P > 0.05$	$P > 0.05$	$P > 0.05$	$P > 0.05$

PIC: polymorphic information content, He: expected heterozygosity, Ho: observed heterozygosity, H-WE: test for Hardy-Weinberg equilibrium.