

## FOR THE RECORD

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# Polymorphism Study on Nine STRs Loci of Han Ethnic Group in Hanzhong Region (West of China)

**POPULATION:** Chinese Han ethnic group ( $n = 165$ )

**KEYWORDS:** forensic science, DNA typing, short tandem repeat, population genetics, Hanzhong, China, D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820

Blood samples were obtained from 165 unrelated healthy volunteer donors born in Hanzhong region, a relative isolated mountainous area in the west of China. Genomic DNA was extracted using the Chelex-100 protocol as described by Walsh et al. (1). A 1.0 ng template were amplified using AmpFISTR Profiler Plus™ PCR amplification kit (ABI Applied Biosystems) following the manufacturer's instructions. ABI PRISM 3100 Avant Genetic Analyzer and reference sequenced ladders (Applied Biosystems Divi-

sion, Foster City, CA). Data were analyzed using Excel Program designed by authors and SPSS 10.0 for Windows (SPSS Inc.).

The complete data are available to any interested researcher upon request.

## Reference

1. Walsh PS, Metzger DA, Higuchi R. Chelex 100 as a medium for simple extraction of DNA for PCR-based from forensic material. *Biotechniques* 1991;10:506-13. [\[PubMed\]](#)

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TABLE 1—Allele frequencies of 9 STR loci of Han ethnic group in Hanzhong region, West of China (n = 165).

Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820
7	...	...	...	...	...	...	0.0030	...	...
8	...	...	...	0.0212	...	...	0.0061	0.2636	0.1212
9	...	...	...	0.0121	...	0.0030	0.0545	0.1333	0.0818
10	...	...	...	0.0939	0.0121	0.0061	0.1667	0.1788	0.1727
11	...	...	0.0030	0.0909	0.0242	...	0.3758	0.2182	0.3182
12	0.0030	0.0091	0.0152	0.1333	0.0182	0.0455	0.1939	0.1545	0.2061
13	0.0030	0.0121	0.0303	0.2545	0.0091	0.1848	0.1273	0.0455	0.0152
14	0.0485	0.2879	0.0061	0.1788	0.0030	0.2061	0.0030	0.0030	0.0152
15	0.3697	0.0333	0.0091	0.1515	...	0.1788	...	...	0.0212
16	0.2697	0.1818	0.0061	0.0485	...	0.1273	...	...	0.0364
17	0.2242	0.1667	0.0030	0.0152	...	0.0273	...	0.0030	0.0091
18	0.0667	0.1818	0.0152	...	...	0.0424	...	...	0.0030
19	0.0061	0.1061	0.0545	...	...	0.0515	...	...	...
20	0.0091	0.0152	0.0333	...	...	0.0182	...	...	...
21	...	0.0061	0.1030	...	...	0.0273	...	...	...
21.2	...	...	0.0030	...	...	...	...	...	...
22	...	...	0.1667	...	...	0.0182	...	...	...
22.2	...	...	0.0091	...	...	...	...	...	...
23	...	...	0.2091	...	...	0.0242	...	...	...
23.2	...	...	0.0152	...	...	...	...	...	...
24	...	...	0.1818	...	...	0.0091	...	...	...
24.2	...	...	0.0061	...	...	...	...	...	...
25	...	...	0.0515	...	...	0.0091	...	...	...
25.2	...	...	0.0061	...	...	...	...	...	...
26	...	...	0.0424	...	0.0030	0.0121	...	...	...
26.2	...	...	...	...	...	0.0061	...	...	...
27	...	...	0.0242	...	...	0.0030	...	...	...
28	...	...	0.0061	...	0.0424	...	...	...	...
28.2	...	...	...	...	0.0030	...	...	...	...
29	...	...	...	...	0.2394	...	0.0212	...	...
30	...	...	...	...	0.2667	...	0.0212	...	...
30.2	...	...	...	...	0.0333	...	0.0030	...	...
31	...	...	...	...	0.0788	...	0.0091	...	...
31.2	...	...	...	...	0.0606	...	0.0061	...	...
32	...	...	...	...	0.0212	...	...	...	...
32.2	...	...	...	...	0.1273	...	0.0091	...	...
32.3	...	...	...	...	0.0030	...	...	...	...
33	...	...	...	...	0.0030	...	...	...	...
33.2	...	...	...	...	0.0515	...	...	...	...
H	0.7356	0.8128	0.8764	0.8448	0.8408	0.8682	0.7754	0.8096	0.8052
DP	0.8831	0.9333	0.9646	0.9455	0.9462	0.9551	0.8948	0.9322	0.9119
PIC	0.5995	0.7897	0.8729	0.8067	0.7632	0.7679	0.5875	0.7585	0.6886
CE	0.4009	0.6320	0.7670	0.6640	0.6180	0.6100	0.3930	0.5851	0.5106

H: observed heterozygosity; PD: power of discrimination; PIC: polymorphism information content; CE: chance of exclusion.