

## FOR THE RECORD

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# Allele Frequency Distributions for 15 STR Loci in Chinese Chengdu Han Population

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**POPULATION:** Han population living in Chengdu China

**KEYWORDS:** forensic science, DNA typing, Han population, VWA, CFS1PO, D2S1338, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, D19S433, D21S11, FGA, TH01, TPOX

This study was to provide a 15 STRs database for a population sample of Chengdu, China for the use as a highly discriminatory system of genetic markers in forensic community. Whole blood specimens obtained by venipuncture was collected in EDTA vacutainer tubes from unrelated volunteer donors living in Chengdu, China. DNA was extracted using Chelex-100 and proteinase K (1). The multiplex amplified of all 15 STR loci was performed using commercially available multiplex kit AmpF $\ell$ STR<sup>®</sup> Identifier<sup>™</sup> (Applied Biosystems). Genotyping was performed using a 310 ABI Prism Genetic Analyzer. The forensic efficiency parameters were calculated by the Promega Software, POWERSTATS([www.promega.com/techserv/apps](http://www.promega.com/techserv/apps)).

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Hardy-Weinberg equilibrium test of all 15 loci were based on the Chi-square test. The combined values of the matching probability and the power of exclusion are  $3.52 \times 10^{-17}$  and 99.9999, respectively.

All data are available upon request at: [kjc@scu.edu.cn](mailto:kjc@scu.edu.cn)

## Reference

1. Wiegand P, Bajanowski T, Brinkmann B. PCR typing of debris from fingernails. *Int J Legal Med* 1993;106:81–4. [\[PubMed\]](#)

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TABLE 1—Allele frequencies in the Han population in Chengdu, China.

Allele	Frequency													FGA	TH01	TPOX
	VWA	CFS1PO	D2S1338	D3S1358	D5S818	D7S820	D8S1179	D13S317	D16S539	D18S51	D19S433	D21S11				
6	...	...	...	...	...	...	...	...	...	...	...	...	...	0.065	...	
7	...	...	...	...	0.032	0.005	0.002	0.002	...	...	...	...	...	0.304	...	
8	...	0.014	...	...	...	0.159	...	0.308	0.007	...	...	...	...	0.065	0.493	
9	...	0.113	...	...	0.054	0.068	0.002	0.137	0.282	0.006	...	...	...	0.493	0.155	
9.2	...	...	...	...	...	0.003	...	...	...	...	...	...	...	...	...	
9.3	...	...	...	...	...	...	...	...	...	...	...	...	...	0.036	...	
10	...	0.176	...	...	0.163	0.122	0.111	0.107	0.155	0.009	...	...	...	0.036	0.049	
11	0.007	0.204	...	...	0.320	0.383	0.101	0.269	0.275	0.003	...	...	...	...	0.289	
12	0.007	0.352	...	0.013	0.276	0.227	0.113	0.124	0.162	0.038	0.057	...	...	...	0.014	
13	0.002	0.120	...	0.018	0.153	0.021	0.187	0.040	0.106	0.175	0.409	...	...	...	...	
13.2	...	...	...	...	...	...	...	...	...	...	0.034	...	...	...	...	
14	0.292	0.021	...	0.033	...	0.013	0.207	0.012	0.014	0.160	0.170	...	...	...	...	
14.2	...	...	...	...	...	...	...	...	...	...	0.148	...	...	...	...	
15	0.040	...	...	0.321	0.002	...	0.200	...	...	0.148	0.080	...	...	...	...	
15.2	...	...	...	...	...	...	...	...	...	...	0.080	...	...	...	...	
16	0.191	...	0.024	0.354	...	...	0.059	...	...	0.154	...	...	...	...	...	
16.2	...	...	...	...	...	...	...	...	...	...	0.011	...	...	...	...	
17	0.188	...	0.083	0.195	...	...	0.012	...	...	0.071	0.011	...	0.003	...	...	
18	0.171	...	0.190	0.059	...	...	0.005	...	...	0.050	...	...	0.036	...	...	
19	0.092	...	0.119	0.008	...	...	...	...	...	0.080	...	...	0.044	...	...	
20	0.010	...	0.119	...	...	...	...	...	...	0.041	...	...	0.044	...	...	
21	...	...	0.024	...	...	...	...	...	...	0.033	...	0.003	0.103	...	...	
21.2	...	...	...	...	...	...	...	...	...	...	...	...	0.003	...	...	
22	...	...	0.071	...	...	...	...	...	...	0.015	...	...	0.205	...	...	
23	...	...	0.155	...	...	...	...	...	...	0.015	...	...	0.187	...	...	
23.2	...	...	...	...	...	...	...	...	...	...	...	...	0.010	...	...	
24	...	...	0.119	...	...	...	...	...	...	0.003	...	...	0.226	...	...	
24.2	...	...	...	...	...	...	...	...	...	...	...	...	0.010	...	...	
25	...	...	0.060	...	...	...	...	...	...	...	...	...	0.095	...	...	
25.2	...	...	...	...	...	...	...	...	...	...	...	...	0.003	...	...	
26	...	...	0.012	...	...	...	...	...	...	...	...	...	0.026	...	...	
27	...	...	0.024	...	...	...	...	...	...	...	...	...	0.008	...	...	
28	...	...	...	...	...	...	...	...	...	...	...	0.050	...	...	...	
29	...	...	...	...	...	...	...	...	...	...	...	0.243	...	...	...	
29.2	...	...	...	...	...	...	...	...	...	...	...	0.003	...	...	...	
30	...	...	...	...	...	...	...	...	...	...	...	0.290	...	...	...	
30.2	...	...	...	...	...	...	...	...	...	...	...	0.015	...	...	...	
31	...	...	...	...	...	...	...	...	...	...	...	0.078	...	...	...	
31.2	...	...	...	...	...	...	...	...	...	...	...	0.075	...	...	...	
32	...	...	...	...	...	...	...	...	...	...	...	0.038	...	...	...	
32.2	...	...	...	...	...	...	...	...	...	...	...	0.138	...	...	...	
33	...	...	...	...	...	...	...	...	...	...	...	0.008	...	...	...	
33.2	...	...	...	...	...	...	...	...	...	...	...	0.058	...	...	...	
34.2	...	...	...	...	...	...	...	...	...	...	...	0.005	...	...	...	
n	202	142	168	145	203	192	203	201	142	169	176	200	195	138	142	
H (%)	76.7	80.3	92.9	76.4	75.4	74.5	84.2	80.1	77.5	82.8	75.0	83.5	85.6	63.8	62.0	
MP	0.068	0.099	0.051	0.131	0.096	0.100	0.047	0.078	0.087	0.031	0.095	0.058	0.047	0.177	0.180	
PE	0.540	0.604	0.854	0.534	0.516	0.501	0.680	0.601	0.533	0.653	0.510	0.666	0.708	0.339	0.315	
PD	0.932	0.901	0.949	0.869	0.904	0.900	0.953	0.922	0.913	0.969	0.905	0.942	0.953	0.823	0.820	
P								>0.05								

H: heterozygosity; MP: matching probability; PE: power of exclusion; PD: power of discrimination.