

## FOR THE RECORD

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# Han Chinese Population Data for Ten STR Loci in Changsha, China

**POPULATIONS:** Han Chinese in Changsha,  $N = 108$

**KEYWORDS:** forensic science, DNA typing, population genetics, polymerase chain reaction, short tandem repeat, Chinese, D3S1358, D2S1338, D16S539, D18S51, D19S433, D21S11, vWA, D8S1179, TH01, FGA

Whole blood obtained by venipuncture was collected in EDTA vacutainer tubes from unrelated individuals residing in Changsha, China. The DNA was extracted by phenol chloroform method (1). PCR amplification was performed using the AmpF $\ell$ STR Profiler Plus<sup>TM</sup> PCR amplification kit (PE-Biosystems, Foster City, CA) following the manufacturer's protocol (2). The amplified products

were separated and detected using the ABI Prism<sup>TM</sup> 377 DNA sequencer (PE-Biosystems, Foster City, CA). The data were analyzed using The Promega Software, POWERSTATS.

Summary data for the ten loci are shown in Table 1. The complete data are available to any interested researcher upon request by contacting Kun Xia via e-mail: nlmglcy@public.cs.hn.cn. All loci, except TH01, meet Hardy-Weinberg expectations.

## References

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TABLE 1—STR allele frequencies data for Han Chinese in Changsha (N = 108).

Allele	D3S1358	D2S1338	D16S539	D18S51	D19S433	D21S11	vWA	D8S1179	TH01	FGA
6	—	—	—	—	—	—	—	—	0.121	—
7	—	—	—	—	—	—	—	—	0.266	—
8	—	—	0.014	—	—	—	—	0.005	0.037	—
9	—	—	0.273	—	—	—	0.005	—	0.514	—
9.3	—	—	—	—	—	—	—	—	0.023	—
10	—	—	0.12	—	—	—	—	0.097	0.033	—
11	—	—	0.25	—	—	—	0.005	0.097	0.005	—
12	—	—	0.241	0.032	0.028	—	0.005	0.125	—	—
12.2	—	—	—	—	0.005	—	—	—	—	—
13	—	—	0.079	0.144	0.301	—	—	0.181	—	—
13.2	—	—	—	—	0.051	—	—	—	—	—
14	0.014	—	0.019	0.181	0.213	—	0.264	0.218	—	—
14.2	—	—	—	—	0.093	—	—	—	—	—
15	0.324	—	0.005	0.19	0.088	—	0.042	0.171	—	—
15.2	—	—	—	—	0.171	—	—	—	—	—
16	0.431	0.028	—	0.185	0.009	—	0.162	0.097	—	—
16.2	—	—	—	—	0.037	—	—	—	—	—
17	0.167	0.056	—	0.079	—	—	0.278	0.009	—	—
18	0.056	0.125	—	0.037	—	—	0.176	—	—	0.014
18.2	—	—	—	—	0.005	—	—	—	—	—
19	0.009	0.176	—	0.06	—	—	0.056	—	—	0.074
20	—	0.144	—	0.037	—	—	0.009	—	—	0.042
21	—	0.019	—	0.037	—	—	—	—	—	0.134
22	—	0.046	—	0.005	—	—	—	—	—	0.162
22.2	—	—	—	—	—	—	—	—	—	0.005
23	—	0.204	—	—	—	—	—	—	—	0.255
23.2	—	—	—	—	—	—	—	—	—	0.009
24	—	0.13	—	0.014	—	—	—	—	—	0.19
24.2	—	—	—	—	—	—	—	—	—	0.005
25	—	0.046	—	—	—	—	—	—	—	0.056
25.2	—	—	—	—	—	—	—	—	—	0.009
26	—	0.019	—	—	—	—	—	—	—	0.037
27	—	0.009	—	—	—	—	—	—	—	0.005
28	—	—	—	—	—	0.051	—	—	—	0.005
28.2	—	—	—	—	—	0.005	—	—	—	—
29	—	—	—	—	—	0.278	—	—	—	—
30	—	—	—	—	—	0.25	—	—	—	—
30.2	—	—	—	—	—	0.014	—	—	—	—
31	—	—	—	—	—	0.046	—	—	—	—
31.1	—	—	—	—	—	0.005	—	—	—	—
31.2	—	—	—	—	—	0.102	—	—	—	—
32	—	—	—	—	—	0.032	—	—	—	—
32.2	—	—	—	—	—	0.176	—	—	—	—
33.2	—	—	—	—	—	0.042	—	—	—	—
Hets	0.63	0.843	0.806	0.88	0.759	0.833	0.722	0.88	0.648	0.898
DP	0.834	0.963	0.916	0.963	0.94	0.937	0.927	0.951	0.819	0.95
PIC	0.62	0.85	0.75	0.85	0.79	0.79	0.76	0.83	0.6	0.82
PEP	0.328	0.68	0.609	0.754	0.526	0.662	0.463	0.754	0.352	0.792
HWE test*	$P > 0.05$	$P > 0.05$	$P > 0.05$	$P > 0.05$	$P > 0.05$	$P > 0.05$	$P > 0.05$	$P > 0.05$	$0.05 > P > 0.01$	$P > 0.05$

\*: *P*-value  
 Hets: heterozogosity  
 DP: discriminating power  
 PIC: polymorphism  
 PEP: excluding probability of paternity