

## FOR THE RECORD

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# Population Data of 15 STR in Chinese Han Population From North of Guangdong

**POPULATION:** Han population in north of Guangdong province of China ( $n = 102$ )

**KEYWORDS:** forensic science, DNA typing, short tandem repeat, population data, Chinese Han population, D3S1358, D8S1179, D21S11, D7S820, CSF1P0, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818, FGA, China

The samples were obtained from 102 unrelated, healthy individuals of Chinese Han population living in north of Guangdong province of China. Genomic DNA was extracted using the Chelex-100 protocol as described by Walsh et al. (1). Fifteen STR loci and Amelogenin locus were co-amplified by using the AmpFLSTR Identifiler kit following the amplification conditions recommended by the manufacturer. Detection and genotyping of all PCR products were accomplished using ABI3100 DNA Genetic Analyzer (Applied Biosystem). Allele designation was done using GeneScan 3.7 and Genotyper 3.7. Evaluation of Hardy–Weinberg equilibrium expectations was carried out using the exact test and further statistical parameters of forensic interest were determined by using Arlequin version 1.1 (2).

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

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### References

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. [\[PubMed\]](#)
2. Schneider S, Roessli SD, Excoffier L. A software for population genetics data analysis, Arlequin version 2.0. Geneva, Switzerland: Genetic and Biometry Laboratory, University of Geneva, 2000.

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TABLE 1—Allele frequencies and statistical parameters regarding the 15 STR loci of Chinese Han population ( $n = 102$ ).

Allele	D3S1358	D8S1179	D21S11	D7S820	CSF1P0	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA
6						0.098									
7					0.005	0.343								0.034	
8				0.1	0.005	0.044	0.294	0.005				0.603		0.010	
9				0.059	0.039	0.456	0.127	0.275				0.083		0.098	
9.3						0.020								0.201	
10		0.127		0.137	0.221	0.034	0.118	0.108				0.039		0.299	
11	0.005	0.142		0.402	0.245	0.005	0.240	0.265		0.005		0.255	0.005	0.230	
12		0.167		0.201	0.353		0.162	0.216		0.039		0.020	0.025	0.127	
12.2										0.044			0.005		
13		0.191		0.059	0.103		0.054	0.118		0.240			0.167		
13.2										0.088			0.025		
14	0.025	0.137			0.029		0.005	0.015		0.157	0.225		0.162		
14.2										0.083			0.015		
15	0.328	0.118							0.005	0.059	0.044		0.186		
15.2										0.206			0.010		
16	0.358	0.098							0.025	0.029	0.137		0.162		0.005
16.2										0.044			0.010		
17	0.240	0.015							0.108	0.005	0.279		0.074		
17.2										0.005			0.010		
18	0.039	0.005							0.083		0.221		0.069		0.010
18.2													0.010		
19	0.005								0.186		0.064		0.010		0.039
20									0.123		0.029		0.025		0.039
21									0.054				0.029		0.132
23									0.176				0.005		0.270
23.2															0.005
24									0.113						0.157
24.2															0.005
25									0.044						0.078
26									0.010						0.029
26.2															0.005
27			0.010												
28			0.039												
28.2			0.005												
29			0.230												
30			0.304												
30.2			0.020												
31			0.093												
31.2			0.064												
32			0.025												
32.2			0.162												
33			0.005												
33.2			0.034												
34.2			0.010												
H	0.704	0.857	0.812	0.752	0.754	0.661	0.797	0.782	0.877	0.852	0.797	0.563	0.872	0.790	0.824
PIC	0.661	0.851	0.802	0.732	0.730	0.658	0.789	0.771	0.874	0.849	0.786	0.557	0.871	0.771	0.815
PD	0.840	0.957	0.935	0.893	0.897	0.844	0.920	0.910	0.967	0.946	0.928	0.756	0.963	0.917	0.933
PPE	0.529	0.841	0.774	0.653	0.665	0.539	0.729	0.695	0.875	0.808	0.748	0.389	0.863	0.719	0.769
P	0.899	0.787	0.909	0.433	0.979	0.689	0.837	0.948	0.995	0.998	0.711	0.134	0.999	0.808	0.997

H: observed heterozygosity; PD: power of discrimination; PPE: probability of exclusion; PIC: polymorphism information content; P: probability values of exact tests for Hardy-Weinberg disequilibrium.