

FOR THE RECORD

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Distribution of Nine STR Loci Alleles Frequencies in a Chinese Population

POPULATION: Chinese

KEYWORDS: forensic science, DNA typing, population genetic, short tandem repeats, polymerase chain reaction, Guilin, Guangxi, China

A total of 108 unrelated individuals were collected from Han ethnic group in Guilin City of China. DNA was extracted using Chelex method (1).

DNA samples were amplified by using reagents provided in CTT Multiplex, FFv Multiplex and SliverSTR™ III kit (Promega, Madison, WI) according to the technical manual, PCR amplifications were carried out in a GeneAmp PCR System 9600 (Perkin-Elmer, Norwalk, CT). The PCR products were separated in denaturing polyacrlamide gels according to the technical manual and visualized by sliver staining (2).

Data of population genetics and forensic science were analyzed using POWERSTATS program (3). The genotype distribution was analyzed for Hardy-Weinberg equilibrium according to Hou's

method (4), no deviation from Hardy-Weinberg equilibrium was observed.

The complete data can be accessed at <http://www.legalmed.org/dna/guilinstr.htm>.

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TABLE 1—*Allele frequencies of nine STR loci.*

Allele	VWA	D13S317	D7S820	CSF1PO	TH01	D16S539	TPOX	FESFPS	F13A01
3.2									0.162
4									0.296
5									0.079
6	0.009				0.0097				0.440
7		0.009	0.032	0.241		0.097			0.005
8	0.292	0.130	0.005	0.079	0.014	0.241			0.009
9	0.199	0.051	0.046	0.468	0.190	0.079	0.009		0.009
10	0.130	0.111	0.273	0.105	0.148	0.468	0.051		
11	0.153	0.417	0.259	0.005	0.273	0.106	0.347		
12	0.16	0.227	0.301	0.005	0.264	0.005	0.329		
13	0.037	0.046	0.069		0.083	0.005	0.231		
14	0.269	0.014	0.009	0.014		0.019		0.032	
15	0.019					0.009			
16	0.176								
17	0.269								
18	0.167								
19	0.088								
20	0.014								
*HWE	<i>p</i> > 0.05								

* Test for Hardy-Weinberg equilibrium.

TABLE 2—*Population genetics and forensic data of nine STR loci.*

Locus	PIC	DP	Pm	CE	H _o	H _e	SE
CSF1P0	0.72	0.903	0.097	0.494	0.741	0.763	0.0409
D13S317	0.806	0.926	0.074	0.609	0.806	0.809	0.0378
D16S539	0.76	0.914	0.086	0.575	0.787	0.794	0.0389
D7S820	0.71	0.880	0.120	0.609	0.806	0.744	0.0420
F13A01	0.63	0.835	0.165	0.420	0.694	0.689	0.0445
FESFPS	0.66	0.853	0.147	0.494	0.741	0.718	0.0433
TH01	0.66	0.864	0.136	0.406	0.685	0.699	0.0441
TPOX	0.56	0.794	0.206	0.271	0.583	0.626	0.0465
VWA	0.76	0.916	0.084	0.644	0.824	0.792	0.0391

* PIC (polymorphism information content), DP (power of discrimination), Pm (probability of match), H_o (observed heterozygosity), H_e (expected heterozygosity), SE (standard error).