

FOR THE RECORD

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Genetic Analysis of Six STR Polymorphisms in a Southern Chinese Population

POPULATION: A total of 105 unrelated and healthy individuals from the Han ethnic group of Nanning city in south China.

KEYWORDS: forensic sciences, DNA typing, population genetics, polymerase chain reaction, short tandem repeat, Nanning city, southern Chinese population, Han ethnic group, CSF1PO, TH01, D16S539, D2S1338, D19S433, TPOX

DNA extraction: Genomic DNA was extracted from whole blood using the Chelex method (1).

Amplification and genotyping: Multiplex amplification of six STR was according to the manufacturer's protocol with modification (Applied Biosystems, Foster, CA); the volume of reaction was 10 μ L, which contained approximately 0.5 ng genomic DNA, 2.2 μ L reaction mix, 2.2 μ L prime set, and 1 U AmpliTaq Gold DNA polymerase. The amplified products were genotyped using an ABI Prism 3100 genetic analyzer (Applied Biosystems).

Genetic analysis: Allele frequencies, observed heterozygosity, expected heterozygosity, power of discrimination, probability of exclusion, and polymorphic information content were calculated utilizing Powerstats software (2). The genetic data are listed in Table 1. Hardy-Weinberg equilibrium for genotype distribution was analyzed according to Hou's method (3), and no departure from Hardy-Weinberg equilibrium was observed.

The complete dataset is available via e-mail from the corresponding author at lovekoushui@sina.com

References

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TABLE 1—Allelic frequencies of six STR in a southern Chinese population.

Allele	CSF1PO	TH01	D16S539	D2S1338	D19S433	TPOX
6		0.095				
7		0.319				
8	0.005	0.071	0.005			0.576
9	0.019	0.414	0.286			0.095
9.3		0.024				
10	0.233	0.067	0.100			0.048
11	0.286	0.005	0.229		0.019	0.271
12	0.400	0.005	0.295		0.057	0.010
12.2					0.010	
13	0.048		0.076		27.6%	
13.2					0.043	
14	0.010		0.010		0.190	
14.2					0.105	
15					0.086	
15.2					0.157	
16				0.014	0.014	
16.2					0.033	
17				0.095		
17.2					0.010	
18				0.052		
19				0.224		
20				0.105		
21				0.048		
22				0.081		
23				0.190		
24				0.148		
25				0.033		
26				0.005		
27				0.005		
PD	0.832	0.873	0.901	0.956	0.950	0.764
PIC	0.65	0.66	0.72	0.84	0.82	0.520
PE	0.530	0.392	0.530	0.766	0.581	0.218
H_e	0.701	0.708	0.763	0.859	0.838	0.583
H_o	0.762	0.676	0.762	0.886	0.790	0.533

PD, power of discrimination; PIC, polymorphic information content; PE, power of exclusion; H_e , expected heterozygosity; H_o , observed heterozygosity.

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