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FOR THE RECORD

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Population Genetics for Five STR Loci in Tibetan Group of Chinese Population

POPULATION: Chinese ($n = 131$).

KEYWORDS: forensic science, Tibetan ethnic group, China, DNA typing, short tandem repeats, polymerase chain reaction, population genetics, D3S1358, THØ1, D21S11, D18S51, D5S818

Blood samples were collected from 131 unrelated people of Tibetan ethnic group in Lasa of China. DNA was extracted using the Chelex method (1). PCR amplification was carried out on a thermal cycler using, as primers, the same sequences contained in the "PowerPlex 16 System" kit (2). Each PCR reaction was performed with 2.5 µL extract (5–250 ng DNA), 0.5 µM of each primer, 2.5 µL Taq buffer (10 × PCR Buffer II, Applied Biosystems, Foster City, CA), 2 µL $MgCl_2$ 25 µM (Applied Biosystems), 0.5 µL dNTPs mix (10 µM PCR nucleotide mix, Promega), 1 U Taq polymerase (DyNAzyme II DNA Polymerase, Finnzymes) in a total volume of 25 µL. A total of 30 cycles were carried out with an initial incubation (preliminary denaturation) step at 96°C for 2 min and then, for the first 10 cycles, as follows: at 94°C for 1 min (denaturation), at 60°C for 1 min (annealing) and at 70°C for 1.5 min (extension) and, for the last 20 cycles, as follows: at 90°C for 1 min (denaturation), at 60°C for 1 min (annealing) and at 70°C for 1.5 min (extension). A final extension step at 60°C for 30 min was also performed. The amplification products were vertically electorphoresed on ultrathin (0.2–0.4 mm) layer polyacrylamide denaturing gels (6% urea, 7 M) in TBE buffer 1 × and then revealed by silver staining (3). Data of female population genetics and forensic science were analyzed using the POWERSTATS program (4) (Table 1).

The complete data (also including some statistical parameters) are available to any interested researcher upon request to Dr. Bin Wu Ying at yingbw@hotmail.com

TABLE 1—*Allele frequencies and forensic efficiency data of five STR loci in Tibetan ethnic group of Chinese population.*

Allele			Frequency		
	D3S1358	THØ1	D21S11	D18S51	D5S818
6		9.5%			
7		27.5%			1.5%
8		6.9%			0.4%
9		48.5%			6.9%
9.3		1.9%			
10		5.7%			15.3%
11				0.8%	21.8%
12				3.8%	22.9%
13				18.3%	19.8%
14	5.3%			18.7%	8.8%
15	35.9%			18.3%	2.3%
16	28.2%			13.7%	0.4%
17	22.1%			8.4%	
18	8.0%			6.5%	
19				3.8%	
20	0.4%			3.4%	
21				3.1%	
22				1.1%	
23			0.4%		
28			5.7%		
29			28.2%		
30			24.0%		
30.2			0.4%		
31			10.3%		
31.2			5.7%		
32			2.3%		
32.2			16.4%		
33			0.4%		
33.2			5.7%		
34.2			0.4%		
P_m	0.112	0.149	0.062	0.042	0.066
PD	0.888	0.851	0.938	0.958	0.934
PIC	0.69	0.63	0.79	0.85	0.80
PE	0.456	0.323	0.546	0.797	0.645
X^2	0.2296348	1.413532	1.9040731	1.375311	0.0084898
P	0.6317947	0.2344711	0.1676232	0.240902	0.9265868

PIC, polymorphism information content; PD, power of discrimination; PE, power of exclusion; P_m, probability of match; df = 1.

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