

FOR THE RECORD

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Allele Frequency Distributions for 9 STR Loci of Tibetan Population in Chinese Tibet*

POPULATION: Tibetan population living in Changdu, China

KEYWORDS: forensic science, DNA typing, Tibetan population, vWA, D3S1358, D5S818, D7S820, D8S1179, D13S317, D18S51, D21S11, FGA, population genetics

The aim of this study was to provide a 9 STRs database for a population sample of Changdu China for the use as a highly discriminatory system of genetic markers in forensic community. Whole blood specimens obtained by venipuncture was collected in EDTA vacutainer tubes from unrelated volunteer donors living in Changdu, Tibet, China. DNA was extracted using Chelex-100 and proteinase K(1). The multiplex amplified of all 9 STR loci was performed using commercially available multiplex kit Profile PlusTM. Genotyping was performed using a 310 ABI Prism Genetic Analyzer.

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The forensic efficiency parameters were calculated by the Promega Software, POWERSTATS (www.promega.com/techserv/apps).

Hardy-Weinberg equilibrium test of all 9 loci were based on the Chi-square test. The combined values of the power of exclusion are 99.99986, respectively.

All data are available upon request at: kjc@scu.edu.cn

Reference

1. Wiegand P, Bajanowski T, Brinkmann B. [PCR typing of debris from fingernails](#). *Int J Legal Med* 1993;106:81-4. [[PubMed](#)]

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TABLE 1—Allele frequencies in the Tibetan population in Changdu, China.

Alleles	D3S1358	VWA	FGA	D8S1179	D21S11	D18S51	D5S818	D7S820	D13S317
7	0.010	0.010	0.010
8	0.015	0.195	0.200
9	0.005	0.060	0.055	0.120
10	0.165	...	0.010	0.145	0.120	0.145
11	0.100	...	0.005	0.365	0.315	0.260
12	0.155	...	0.045	0.270	0.250	0.205
13	0.005	0.185	...	0.135	0.130	0.040	0.005
13.2	0.070
14	0.020	0.255	...	0.140	...	0.130	0.005	0.005	0.010
14.2	0.060
15	0.305	0.005	...	0.210	...	0.170	...	0.010	...
16	0.325	0.170	...	0.035	...	0.160
17	0.270	0.250	...	0.010	...	0.045
18	0.075	0.185	0.020	0.075
18.2	0.005
19	...	0.120	0.050	0.020
20	...	0.010	0.025	0.025
21	...	0.005	0.110	0.005
22	0.160	0.025
23	0.215	0.005
23.2	0.010
24	0.205	0.010
25	0.130
26	0.035
27
28	0.005	...	0.030
29	0.010	...	0.010
29.2	0.280
30	0.210
30.2	0.035
31	0.090
31.2	0.075
32	0.050
32.2	0.160
33	0.005
33.2	0.050
34.2	0.005
H*	0.8	0.74	0.87	0.87	0.81	0.75	0.74	0.82	0.86
DP	0.846	0.924	0.952	0.945	0.934	0.971	0.902	0.91	0.928
PE	0.599	0.493	0.735	0.735	0.618	0.51	0.493	0.637	0.715
PIC	0.67	0.76	0.83	0.82	0.81	0.88	0.71	0.75	0.79
PM	0.154	0.076	0.048	0.055	0.066	0.029	0.098	0.09	0.072

* H: heterozygosity; MP: matching probability; PE: power of exclusion; PD: power of discrimination.