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Announcement of Population Data

Genetic polymorphisms of 15 STR loci in two Tibetan populations from Tibet Changdu and Naqu, China

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Abstract

The allelic distribution of 15 short tandem repeat (STR) loci included in the AmpFl STR® Identifiler™ kit was examined in 100 Changdu Tibetan and 118 Naqu Tibetan unrelated individuals living in the Tibet Province, PR China. The distribution of these observed genotypes was not significantly different from the expected distribution according to Hardy–Weinberg equilibrium.

Keywords: Forensic science; Short tandem repeats (STR); Genetic polymorphism; Population data; Tibetan; Chinese

General information on the studied population: Changdu area and Naqu area are Tibetan inhabitancy under the jurisdiction of Tibet, abutting on Sichuan Province and Qinghai Province of China, respectively. People residing in these areas speak in unique dialect and have distinct lifestyle. The geographical distribution of Tibetan in Tibet Province is shown in Fig. 1 [1]. We detected 15 highly polymorphic short tandem repeats (STR) of the two populations and compared the difference between them and other populations living in China.

Population: Blood samples were collected from randomly selected individuals in the regions.

DNA extraction: Genomic DNA was extracted using the Chelex-100 protocol as described by Walsh et al. [2] and quantified spectrophotometrically.

PCR: Target DNA was amplified following the manufacturer's instruction (AmpFl STR® Identifier™ PCR Amplification, Applied Biosystems) with some modifications: total reaction volume was reduced from 25 μl recommended to 8 μl, in which was included 0.5–1.0 ng DNA, 3 μl reaction mix, 1.8 μl prime set and 0.25 μl AmpliTaq Gold DNA polymerase (5 U/μl).

Typing: ABI Prism® 3100 Genetic Analyzer using the recommended protocol (AmpFl STR® Identifier™ PCR Amplification, Applied Biosystems) electrophoresis results were analyzed by data collection software (Version1.1), Genescan analysis (Version 3.7) and Genotyper (Version 3.6) software (Applied Biosystems).

Results: See Tables 1 and 2.

Quality control: Laboratory internal control standards and kit controls.

Data analysis: Allele frequencies (since autosomal co-dominant) were computed using the gene counting method. The potential usefulness of the studied markers for forensic studies in the Changdu Tibetan and Naqu Tibetan was assessed by calculating discrimination power (DP) [3], probability of paternity exclusion (PE) [4] and the heterozygosity value (*H*) [5]. The STR DP, PE and *H* were calculated with the allelic frequency as shown in Tables 1 and 2. R × C contingency test was employed for pairwise interpopulation comparisons [6,7]. Excel program and SPSS 11.5 for windows software were used for analysis of data.

Access to the data: The complete data are available to any interested researchers via mail from author (klongli@yahoo.com).

Other remarks: The population samples were highly polymorphic. There was less genetic diversity among Changdu Tibetan and Naqu Tibetan populations than in the Chinese Han

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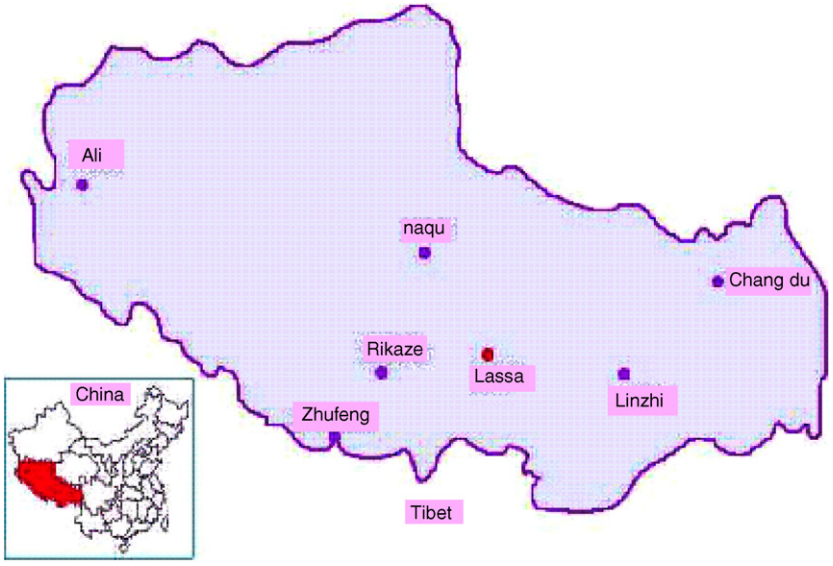

Fig. 1. Distribution of Tibetan living in Tibet, China.

Table 1
Allele frequencies for 15 STR loci of Changdu Tibetan in China ($n = 100$)

Allele	D19S433	VWA	D18S51	D8S1179	D21S11	D13S317	D16S539	D2S1338	D5S818	D7S820	CSF1PO	D3S1358	TH01	FGA	TPOX
6							0.0064						0.0577		
7									0.0130		0.0128		0.2885		0.0130
8						**0.2244**	0.0321			0.1218	0.0064		0.0513		**0.5455**
9				0.0064		0.1154	0.1795		0.0714	0.0833	0.0577		**0.5449**		0.1299
9.3													0.0513		
10				0.1090		0.0962	0.1859		0.2078	0.1154	0.2949		0.0064		0.0065
11				0.0385		0.2179	**0.3269**		**0.3766**	**0.3269**	0.2179				0.2662
12	0.0390			0.1538		0.1923	0.1731		0.1948	0.2949	**0.3590**				0.0390
12.2	0.0065														
13	**0.2727**		**0.3297**	0.2051		0.1282	0.0705		0.1234	0.0577	0.0385				
13.2	0.0390														
14	0.1883	0.1382	0.0867	**0.2115**		0.0192	0.0256		0.0065		0.0128				
14.2	0.1429														
15	0.1169	0.0395	0.1467	0.1795		0.0064			0.0065			0.3846			
15.2	0.1299	0.0066													
16		**0.2697**	0.1667	0.0833								**0.3974**		0.0132	
16.2	0.0325														
17	0.0263	0.2500	0.0933					0.0658				0.1731			
18	0.0065	0.1447	0.0467	0.0128				0.0329				0.0449		0.0263	
19		0.1382	0.0600					0.2368						0.0263	
20		0.0132	0.0267					0.1579						0.0263	
21			0.0067					0.0395						0.0461	
21.2														0.0066	
22			0.0067					0.0395						0.1776	
22.2														0.0132	
23			0.0200					**0.2961**						**0.2303**	
23.2														0.0263	
24			0.0133					0.1118						0.1711	
24.2														0.0197	
25								0.0197						0.1184	
25.2														0.0066	
26					0.0064									0.0592	
26.2					0.0064										
27					0.0064									0.0132	
28					0.0064									0.0197	
28.2					0.0449										
29					**0.3077**										
30					0.2372										
30.2					0.0192										