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Announcement of population data

Genetic polymorphisms of 15 STR loci of Chinese Dongxiang and Salar ethnic minority living in Qinghai Province of China

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Abstract

Fifteen autosomal STRs loci were analyzed from two samples of 178 healthy unrelated autochthonous individuals of Chinese Dongxiang and Salar ethnic minority groups using a multiplex PCR system. Allele frequencies distribution and statistical parameters for all STR loci, D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818 and FGA, were determined by the AmpFISTR Identifiler Kit. The observed genotype frequencies and expected of genotype frequencies were evaluated by χ^2-test and the Fisher exact tests. χ^2-test showed that the agreement with Hardy–Weinberg equilibrium ($p > 0.05$) was for all studied STR loci of two populations. The data in the present study can be used greatly for routine forensic application in the region, and enrich Chinese ethnical genetic informational resources.

Keywords: Forensic science; Genetic polymorphisms; Short tandem repeats; Chinese Dongxiang ethnic group; Chinese Salar ethnic group; AmpFISTR Identifiler kit

General information on the studied population: Dongxiang ethnic minority: Dongxiang ethnic minority, with a population of 513,805 (According to the fifth population survey China in 2000) live in the part of the Linxia Hui Autonomous Prefecture situated south of the Yellow River and southwest of Lanzhou city, province of Gansu. Half of them dwell in the Dongxiang Autonomous County, and the rest are scattered in Hezheng and Linxia counties, the city of Lanzhou, the Xinjiang Uygur Autonomous Region, Qinghai Province of China, and some other places. The Dongxiangs are Moslems. According to legends and historical data, the Dongxiangs probably originated from the Mongolians. The Dongxiang language is basically similar to Mongolian, both belonging to the Mongolian branch of the Altaic language family. Chinese is accepted as their common written language.

Salar ethnic minority: According to the fifth population survey China in 2000, Salar population number is 104,503. Xunhua County, which the largest group of the Salars live, is a mountainous area situated along the banks of the Yellow River in southeastern Qinghai Province. There have been different theories put forward on the origin of the Salars. The prevalent view held at the moment is that the ancestors of the Salars came from the region of Samarkand in Central Asia during the Yuan Dynasty. The customs and habits as practiced among the Salars are deeply influenced by Islam. Language of the Salars belongs to the Tujue (Turkic) branch of the Altaic language family.

Population: The blood stained samples were obtained from 178 unrelated healthy individuals of Chinese Dongxiang

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Table 1
Allele frequencies and statistical parameters regarding the 15 STR loci of Chinese Dongxiang ethnic group ($n = 80$)

Allele	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	THO1	D13S317	D16S539	D2S1338	DS19S433	vWA	TPOX	D18S51	D5S818	FGA
6						0.0750									
7			0.0065	0.0127		0.3000								0.0125	
8			0.1558			0.0875	0.2875					0.4750			
9			0.0714	0.0506		0.4563	0.1188	0.2688				0.1625		0.0750	
9.3						0.0563									
10	0.0949		0.1753	0.2658		0.0188	0.1438	0.1250				0.0063		0.1938	
11	0.0443		0.3052	0.2532		0.0063	0.2438	0.3188				0.3250	0.0066	0.3313	
12	0.1013		0.2532	0.3291			0.1563	0.1938		0.0253		0.0250	0.0263	0.2500	
12.2										0.0127					
13	0.2468		0.0260	0.0823			0.0375	0.0813		0.3291	0.0063	0.0063	0.1842	0.1188	
13.2										0.0506					
14	0.2342		0.0065	0.0063	0.0443		0.0125	0.0125		0.2152	0.2000		0.2039	0.0063	
14.2										0.0886					
15	0.1266				0.3671					0.0506	0.0313		0.1447	0.0125	
15.2										0.1646					
16	0.1266				0.3038				0.0063	0.0253	0.1875		0.0987		
16.2										0.0253					
17	0.0253				0.1772				0.0443	0.0063	0.2750		0.0526		
17.2										0.0063					
18					0.1013				0.0886		0.1938		0.0592		0.0253
19					0.0063				0.1582		0.0938		0.1250		0.0380
20									0.1392		0.0125		0.0658		0.0506
21									0.0316				0.0197		0.1266
21.2															0.0063
22									0.0443						0.2025
22.2															0.0127
23									0.2152						0.1772
23.2															0.0253
24									0.1709				0.0066		0.1962
25									0.0949				0.0066		0.0759
26									0.0063						0.0570
27															0.0063
28		0.0500													
28.2		0.0188													
29		0.2563													
30		0.2125													
30.2		0.0125													
31		0.1500													
31.2		0.1438													
32		0.0313													
32.2		0.0813													
33.2		0.0438													
Ho	0.7848	0.8750	0.7403	0.7215	0.7089	0.6500	0.8000	0.7375	0.8481	0.7595	0.8750	0.6500	0.9474	0.7875	0.8481
He	0.8303	0.8335	0.7818	0.7474	0.7293	0.6850	0.7972	0.7662	0.8582	0.8032	0.8017	0.6416	0.8663	0.7702	0.8585
PIC	0.8200	0.8265	0.7638	0.7230	0.6974	0.6781	0.7894	0.7549	0.8533	0.8014	0.7899	0.6296	0.8610	0.7464	0.8578
PD	0.9425	0.9353	0.9172	0.8819	0.8799	0.8406	0.9144	0.9087	0.9547	0.9303	0.9153	0.7856	0.9539	0.9016	0.9556
PPE	0.7923	0.7772	0.7162	0.6255	0.6185	0.5455	0.7172	0.6904	0.8347	0.7623	0.7116	0.4380	0.8318	0.6790	0.8366
P	0.5213	0.4528	0.5862	0.4349	0.6745	0.1194	0.5395	0.4983	0.6832	0.4592	0.4893	0.5497	0.6717	0.8945	
ET	0.3286	0.4573	0.7238	0.3479	0.5396	0.3187	0.6127	0.5219	0.7028	0.4167	0.5473	0.6472	0.5376	0.7648	

Ho, observed heterozygosity; He, expected heterozygosity; PD, power of discrimination; PPE, probability of exclusion; PIC, polymorphism information content; *p*, probability values of exact tests for Hardy–Weinberg disequilibrium; ET, exact test.

($n = 80$) and Salar ($n = 98$) ethnic group living in Qinghai province of China after informed consent was acquired. Their ancestors had lived in the region at least the three generations. The aim of study is to found forensic DNA database in the region.

DNA extraction: Genomic DNA was extracted using the Chelex-100 protocol as described by Walsh et al. [1].

PCR: PCR for 15 euchromosome STRs was performed in multiplex reaction using AmpFISTR Identifiler kit (Applied Biosystems, Foster City, CA, USA). The amplification reactions 10 μl in total contained 0.9 μl (2 ng/μl) genomic DNA samples. Thermal cycling conditions were conducted according to the manufacturer's protocols of the kit using GeneAmp PCR system 9700 (PE Applied Biosystems, Foster City, CA, USA).

Typing: Detection and genotyping of all PCR products were accomplished using ABI3130 DNA Genetic Analyzer (Applied Biosystem). Allele designations were determined