

FOR THE RECORD

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Genetic Analysis of 15 STR Loci of Chinese Uigur Ethnic Population

POPULATION: Almost all the Uigurs are found in Xinjiang Uigur Autonomous Region that covers more than 1,709,400 square kilometers or approximately one sixth of China's total landmass, Uigers are mainly agricultural Turkic people, and they believe in Islam. Its national characters and languages belong to the Altai phylum and Turkic branch.

KEYWORDS: forensic science, short tandem repeats, population genetics, DNA typing, polymorphism chain reaction, Chinese Uigur ethnic group, China

The blood samples were obtained from 106 unrelated healthy individuals from Yili Uigur ethnic autonomous region, Xin Jiang Province of China. Genomic DNA was extracted using the Chelex-100 protocol as described by Walsh et al. (1). PCR for 15 STRs was performed in multiplex reaction using AmpFLSTR Identifiler kit; 0.9 μ L (2 ng/ μ L) genomic DNA samples were amplified in a total reaction volume of 10 μ L along with 2.9 μ L deionized water, 4 μ L dNTP, 0.2 μ L AmpliTaqGold DNA polymerase, and 2.0 μ L primer set. Thermal cycling was conducted with the below conditions: 95°C for 11 min; 28 cycles of 94°C for 60 sec, 59°C for 60 sec, 72°C for 60 sec; and a final extension of 60°C for 45min. Detection and genotyping of all PCR products were accomplished using ABI3100 DNA Genetic Analyzer (Applied Biosystem). Allele designation was done using GeneScan3.7 and Genotyper3.7.

Quality control was adhered to laboratory internal control standards and kit controls. Data analysis was carried out with SPSS11.0 version, genetic data analysis (GDA) (2) and GENEPOP (3) software packages. See Table 1 for results. As shown in Table 1, 129 alleles were observed, with the corresponding allele frequencies ranging from 0.0047 to 0.6038. The combined PM and PE value

for all 15 STR loci were 2.7269×10^{-17} and 0.999999997, respectively. Chi-square test showed that all STR loci followed the Hardy-Weinberg equilibrium ($p > 0.05$). These data were compared with the previously published population data of other ethnic groups or regions that were observed at the same 15 STR loci following the method of Bonferroni's correction (4). The comparison results between our studied population and population from Miao ethnic of China (5), Belgian (6) showed no significant difference at all 15 STR loci. We found that there were significant differences between studied population and population from Byelorussian minority living in Northeastern Poland (7) ($p = 0.015$) and Venezuela ethnic population (8) ($p = 0.044$) at D18S51 locus, but no significant difference at other loci. Results of present study are valuable for human identification and paternity tests in Chinese Uigur population.

The complete dataset is available upon request via e-mail from corresponding author: Liuyao2002cn@yahoo.com.cn or the first author zhubofeng7372@126.com.

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TABLE 1—Allele frequencies and statistical parameters regarding the 15 STR loci of Chinese Uigur ethnic group.

Allele	D3S1358	D21S11	vWA	D18S51	TPOX	FGA	D5S818	D8S1179	D7S820	CSFIPO	THO1	D13S317	D16S539	D2S1338	DS19S433
6											0.156				
7								0.014			0.250				
8					0.604		0.005	0.014	0.208		0.075	0.160	0.052		
9					0.052		0.052	0.005	0.071	0.014	0.288	0.113	0.193		
9.3											0.198				
10					0.028		0.113	0.123	0.226	0.259	0.033	0.123	0.080		
11				0.014	0.259		0.358	0.042	0.226	0.288		0.288	0.288		
12				0.080	0.057		0.321	0.080	0.231	0.321		0.222	0.250		0.042
13				0.137			0.142	0.297	0.024	0.094		0.075	0.123		0.255
13.2															0.042
14	0.052		0.127	0.241			0.005	0.226		0.014		0.019	0.014		0.245
14.2															0.080
15	0.382		0.066	0.169				0.146		0.009					0.160
15.2															0.104
16	0.278		0.198	0.127			0.005	0.042						0.005	0.033
16.2															0.024
17	0.198		0.325	0.071				0.024						0.099	0.009
17.2															0.005
18	0.085		0.208	0.047		0.024								0.175	
18.2						0.005									
19	0.005		0.066	0.052		0.019								0.165	
20			0.009	0.033		0.052								0.160	
20.2						0.005									
21				0.028		0.160								0.019	
21.2						0.005									
22						0.165								0.052	
22.2						0.005									
23						0.208								0.128	
23.2						0.009									
24						0.217								0.104	
25						0.085								0.075	
26						0.038								0.019	
27						0.005									
28		0.071													
28.2		0.005													
29		0.274													
29.2															
30		0.297													
30.2		0.028													
31		0.047													
31.2		0.085													
32		0.005													
32.2		0.146													
33.2		0.038													
34.2		0.005													
Ho	0.651	0.764	0.812	0.934	0.519	0.958	0.764	0.774	0.896	0.717	0.840	0.840	0.849	0.906	0.792
He	0.727	0.799	0.787	0.859	0.562	0.844	0.733	0.813	0.795	0.738	0.784	0.808	0.793	0.871	0.827
PIC	0.697	0.785	0.768	0.853	0.559	0.844	0.699	0.801	0.783	0.708	0.773	0.796	0.779	0.866	0.824
PD	0.885	0.931	0.922	0.956	0.725	0.952	0.880	0.945	0.918	0.889	0.903	0.928	0.917	0.961	0.937
PE	0.628	0.761	0.729	0.839	0.402	0.825	0.618	0.803	0.719	0.635	0.679	0.747	0.716	0.856	0.779
P	0.351	0.328	0.479	0.363	0.134	0.532	0.193	0.107	0.315	0.467	0.408	0.398	0.156	0.249	0.854

Ho: observed heterozygosity; He: expected heterozygosity; PD: power of discrimination; PE: probability of exclusion; PIC: polymorphism information content; P: probability values of exact tests for Hardy-Weinberg disequilibrium.

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