

FOR THE RECORD

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Genetic Analysis of 15 STR Loci of Chinese Ewenki Ethnic Population

POPULATION: Almost all the Ewenki are found in HulunBuir Ewenki Autonomous Banner, Inner Mongolia province of China. Some Ewenki are nomads; others are farmers or farmer-hunters. A small number of them are hunters. Its national characters and languages belong to the Altai phylum.

KEYWORDS: forensic science, short tandem repeats, population genetics, DNA typing, polymorphism chain reaction, Chinese Ewenki ethnic group, China, loci: D3S1358, D21S11, vWA, D18S51, TPOX, FGA, D5S818, D8S1179, D7S820, CSF1PO, TH01, D13S317, D16S539, D2S1338, D19S433

The blood samples were obtained from 103 unrelated healthy individuals from HulunBuir Ewenki ethnic autonomous banner, Inner Mongolia Province of China. Genomic DNA was extracted using the Chelex-100 protocol as described by Walsh et al. (1). Polymerase chain reaction (PCR) for 15 short tandem repeats (STRs) was performed in multiplex reaction using AmpFLSTR Identifier kit (Applied Biosystems, Foster City, CA); 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, 0.2 μ L dNTP, 0.2 μ L Amp-liTaqGold 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 ex-

tension of 60°C for 45 min. Detection and genotyping of all PCR products were accomplished using ABI3100 DNA Genetic Analyzer (Applied Biosystems). Allele designation was carried out using GeneScan3.7 and Genotyper3.7 (Applied Biosystems). Quality control was adhered to laboratory internal control standards and kit controls. Data analysis was carried with SPSS11.0 version, genetic data analysis (2) and GENEPOP (3) software packages. See Table 1 for results. As shown in Table 1, 143 alleles were observed, with the corresponding allele frequencies ranging from 0.0047 to 0.5097. χ^2 test showed that all STR loci followed the Hardy—Weinberg equilibrium ($p > 0.05$). Results of present study are valuable for human identification and paternity tests in Chinese Ewenki population.

TABLE 1—Allele frequencies and statistical parameters regarding the 15 (short tandem repeat) STR loci of Chinese Ewenki ethnic group.

Allele	D3S1358	D21S11	vWA	D18S51	TPOX	FGA	D5S818	D8S1179	D7S820	CSF1PO	TH01	D13S317	D16S539	D2S1338	D19S433
6									0.005		0.073				
7							0.024		0.005	0.010	0.311				
8					0.510			0.005	0.180	0.010	0.053	0.238	0.010		
8.2									0.005						
9					0.092		0.073		0.039	0.029	0.5	0.136	0.320		
9.2				0.010					0.005						
9.3											0.053				
10					0.024		0.209	0.102	0.175	0.201	0.010	0.107	0.126		
10.2										0.005					
11				0.005	0.345		0.325	0.083	0.286	0.255		0.272	0.277		0.010
12				0.015	0.029		0.252	0.102	0.262	0.436		0.194	0.180		0.019
12.2															0.005
13				0.162			0.102	0.194	0.034	0.039		0.044	0.083		0.330
13.2				0.005											0.034
14	0.049		0.248	0.293			0.015	0.248	0.005	0.015		0.010	0.005		0.189
14.2				0.025											0.121
15	0.311		0.010	0.136				0.165							0.102
15.2	0.010		0.015												0.155

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TABLE 1—Continued.

Allele	D3S1358	D21S11	vWA	D18S51	TPOX	FGA	D5S818	D8S1179	D7S820	CSF1PO	TH01	D13S317	D16S539	D2S1338	D19S433
16	0.330		0.136	0.096				0.092						0.010	0.005
16.2															0.024
17	0.209		0.262	0.101				0.005						0.049	
17.2															0.005
18	0.087		0.214	0.020		0.020		0.005						0.117	
18.2			0.005												
19	0.005		0.068	0.051		0.049								0.180	
19.2			0.005	0.005											
20			0.039	0.025		0.059								0.083	
21				0.025		0.098								0.029	
22				0.010		0.167								0.024	
23				0.015		0.25								0.252	
24						0.176								0.150	
24.2						0.010									
25						0.132								0.083	
22						0.034								0.024	
27		0.005				0.005									
28		0.024													
28.2		0.015													
29		0.243													
29.2		0.005													
30		0.282													
30.2		0.024													
31		0.117													
31.2		0.102													
32		0.024													
32.2		0.087													
33.2		0.063													
34.2		0.010													
H_e	0.741	0.824	0.799	0.844	0.611	0.844	0.770	0.838	0.784	0.701	0.642	0.800	0.766	0.850	0.804
H_o	0.709	0.874	0.854	0.808	0.612	0.804	0.777	0.825	0.699	0.804	0.689	0.845	0.748	0.816	0.913
PD	0.883	0.941	0.906	0.9999	0.769	0.949	0.900	0.950	0.918	0.863	0.810	0.925	0.911	0.953	0.923
PE	0.626	0.791	0.689	0.853	0.410	0.816	0.676	0.817	0.710	0.582	0.487	0.738	0.693	0.830	0.740
p	0.301	0.196	0.171	0.432	0.143	0.451	0.567	0.794	0.098	0.441	0.410	0.649	0.453	0.503	0.268

H_o , observed heterozygosity; H_e , expected heterozygosity; PD, power of discrimination; PE, probability of exclusion; p , probability values of exact tests for Hardy–Weinberg disequilibrium.

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