Legal Medicine 15 (2013) 109–113

Contents lists available at SciVerse ScienceDirect

Legal Medicine

journal homepage: www.elsevier.com/locate/legalmed

Announcement of Population Data

Allelic polymorphic investigation of 21 autosomal short tandem repeat loci in a Chinese Bai ethnic group

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ARTICLE INFO

Article history:
Received 4 March 2012
Received in revised form 14 August 2012
Accepted 28 August 2012
Available online 5 October 2012

Keywords:
Short tandem repeat
Chinese Bai ethnic group
Allelic diversity

ABSTRACT

Population genetic data of 21 autosomal short tandem repeats (STRs) were obtained in a sample of 106 unrelated healthy individuals of Bai ethnic minority born in the Dali Bai Autonomous Prefecture in Yunnan Province. We observed 138 alleles with corresponding allelic frequencies ranging from 0.005 to 0.575. The genotypic frequency distributions at those STR loci were consistent with Hardy–Weinberg equilibrium (Bonferroni's correction was used for Hardy–Weinberg equilibrium tests). The combined probability of exclusion, power of discrimination, probability of matching value for all 21 STR loci were 0.9999975729, 0.999999999999999999872 and 1.28×10^{-19}, respectively. The population data in this study showed significant differences from the previously published population data of Tibetan and Salar groups in some loci.

Studied population: According to the 2000 census, the Bai ethnic group numbered 1,861,895 is the 15th largest of the 56 ethnic groups officially recognized by the People's Republic of China. And eighty percent of the Bais live in concentrated communities in the Dali Bai Autonomous Prefecture in Yunnan Province [1]. The Bais speak a language related to the Yi branch of the Tibetan–Myanmese group of the Chinese–Tibetan language family. The language contains a large number of Chinese words due to the Bais' long contact with the majority Chinese ethnic group–Han [2]. Although the Bai people believe in Buddhism, they also respectively worship their village god (Benzhu), Nature god, the Prince of the Nanzhao regime, or even a hero of folklore. There are different views about the Bai ethnic's origin in the academic. According to years of research and comprehensive analysis of all aspects of materials, Scholars tend to think that Bai is a national community of more than one source. The Bais merge in the Han, part of the Yi and the Achang because of the migration and wars of the Bai ancestors in the history [2]. The location of the Bai ethnic group (collected the samples) in China is showed in Supplementary Figure 1.

DNA extraction: After informed consent, bloodstained samples were obtained from 106 unrelated healthy individuals of the Bai population in the Dali Bai Autonomous Prefecture in Yunnan Province. The ancestors of all participants had to be born and live in the region for at least three generations and only individuals whose three generations must be Bais were selected. The genomic DNA was extracted by using the Chelex-100 protocol [3].

PCR: The extracted DNA was amplified using a commercially available AGCU 21+1 STR Fluorescence Assay Kit (AGCU ScienTech Incorporation, Wuxi, Jiangsu, China) in the GeneAmp 9700 PCR system (Applied Biosystems, Foster City, CA, USA) according to the manufacturer's recommendations. We identified twenty-one autosomal short tandem repeats including D6S474, D12ATA63, D22S1045, D10S1248, D1S1677, D11S4463, D1S1627, D3S4529, D2S441, D6S1017, D4S2408, D19S433, D17S1301, D1GATA113, D18S853, D20S482, D14S1434, D9S1122, D2S1776, D10S1435 and D5S2500 loci and the gender determination locus Amelogenin. PCR reactions were performed in 25 µl system containing 1–5 ng genomic DNA, 10 µl reaction mix, 5 µl 21+1 primers, 0.5 µl HS-TaqDNA polymerase and 9.5 µl ddH_2O.

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http://dx.doi.org/10.1016/j.legalmed.2012.08.012

Table 1
Allele frequencies and statistical parameters of 21 STR loci from Chinese Bai ethnic group ($n = 106$).

Allele	D6S474	D12ATA63	D22S1045	D10S1248	D1S1677	D11S4463	D1S1627	D3S4529	D2S441	D6S1017	D4S2408	D19S433	D17S1301	D1GATA113	D18S853	D20S482	D14S1434	D9S1122	D2S1776	D10S1435	D5S2500
7														0.505							
8										0.146	0.250									0.019	
9										0.009	0.354		0.019						0.127	0.005	
9.1									0.019												
10							0.066		0.212	0.434	0.278	0.005	0.028		0.009	0.038	0.127	0.052	0.042	0.024	
11			0.278	0.009	0.009				0.363	0.075	0.090		0.189	0.132	0.316	0.005	0.165	0.137	0.292	0.170	
11.3									0.085												
12		0.288		0.061	0.024	0.033	0.061		0.160	0.255	0.028	0.052	0.505	0.358	0.066	0.038	0.061	0.321	0.406	0.349	
12.2												0.005									
12.3									0.009										0.005		
13			0.014	0.354	0.123	0.222	0.575	0.245	0.009	0.080		0.288	0.241	0.005	0.222	0.217	0.250	0.420	0.094	0.274	
13.2												0.042									
14	0.382	0.038	0.042	0.231	0.396	0.330	0.292	0.189	0.123			0.236	0.019		0.297	0.434	0.377	0.061	0.028	0.151	0.396
14.2												0.113									
15	0.321	0.019	0.236	0.245	0.377	0.288	0.005	0.354	0.019			0.057			0.085	0.231	0.019	0.009	0.005	0.009	
15.2												0.151									
16	0.175	0.156	0.208	0.090	0.057	0.085		0.146				0.009			0.005	0.038					
16.2												0.042									
17	0.108	0.368	0.193	0.009	0.014	0.042		0.066													0.307
18	0.014	0.123	0.024																		0.184
19		0.009	0.005																		
20																					0.080
23																					0.033
MP	0.129	0.114	0.080	0.106	0.181	0.112	0.238	0.103	0.083	0.132	0.142	0.064	0.175	0.271	0.109	0.141	0.099	0.147	0.134	0.100	0.143
PD	0.871	0.886	0.920	0.894	0.819	0.888	0.762	0.897	0.917	0.868	0.858	0.936	0.825	0.729	0.891	0.859	0.901	0.853	0.866	0.900	0.857
PIC	0.657	0.699	0.750	0.709	0.625	0.707	0.512	0.714	0.744	0.671	0.677	0.793	0.597	0.520	0.709	0.662	0.709	0.645	0.680	0.710	0.657
PE	0.331	0.568	0.518	0.568	0.440	0.518	0.252	0.502	0.568	0.455	0.585	0.603	0.344	0.383	0.486	0.425	0.357	0.440	0.383	0.397	0.357
PI	1.359	2.304	2.038	2.304	1.710	2.038	1.152	1.963	2.304	1.767	2.409	2.524	1.395	1.514	1.893	1.656	1.432	1.710	1.514	1.559	1.432
HO	0.632	0.783	0.755	0.783	0.708	0.755	0.566	0.745	0.783	0.717	0.792	0.802	0.642	0.670	0.736	0.698	0.651	0.708	0.670	0.679	0.651
P	0.069	0.360	0.408	0.471	0.613	0.957	0.805	0.780	0.898	0.993	0.145	0.623	0.798	0.154	0.655	0.783	0.017	0.846	0.198	0.073	0.173

MP: matching probability; PD: power of discrimination; PIC: polymorphism information content; PE: probability of exclusion; HO: observed heterozygosity; *P*: probability values of exact tests for Hardy–Weinberg equilibrium.