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Evaluation of Genetic Parameters of 22 STR loci in two Minorities Population from Yunnan Province of China

Research Article

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Abstract

A total of 22 Short Tandem Repeat (STR) loci (include 3 Expanded U.S. Core Loci D2S441, D22S1045, D10S1248 and 19 non-CODIS STR D1S1627, D3S4529, D17S974, D6S1017, D4S2408, D9S2157, D6S474, D1GATA113, D18S853, D20S482, D14S1434, D20S1082, D17S1301, D12ATA63, D1S1677, D11S4463, D9S1122, D2S1776, D5S2500) were analyzed in two minorities population from Yunnan Province of China with 298 (Wa200, Bai98) unrelated individuals. The allele frequency distribution and forensic parameters of the two populations were reported in this paper. The results show these 22 STR loci have high or medium power of discrimination and probabilities of exclusion. The Hardy–Weinberg Equilibrium of each locus were tested. The genetic distances (i.e., Fst) among the two population and other Chinese populations were estimated. The results showed that these loci are available in forensic genetics and may prove useful in both human identification and kinship analysis.

Keywords: Allele Frequencies; Chinese Minorities Population; Non-CODIS loci Paternity Testing STR.

Introduction

Short tandem repeats (STR) are one of highly polymorphism genetic markers in the human genome [1]. The Identifiler™ [2], Promega Fusion System [3] and DNA Typer 15plus™ [4] PCR amplification kits have high Discrimination Power and Probability of Paternity Exclusion. In most cases, using these kits would be sufficient for human individual identification and standard trio paternity testing. However, in some complex relationships cases, such as single parent/child paternity analysis, uncle–nephew, grandparents–grandchildren, more STR loci are required to determine more precisely the relationships [5-9]. In this study, 22 STR from a polymorphism systems constructed by our own laboratory were tested to evaluate their performance in both single source comparison and kinship analysis for the two minorities from Yunnan Province, China. The distributions of allelic frequencies and forensic statistical parameters of these 22 STRs loci in the two population were generated. Hardy-Weinberg Equilibrium of each locus tested. The genetic distances (i.e., Fst) among the two population and other Chinese populations were estimated.

Materials and Methods

Population samples

A total of 200 samples from healthy unrelated Wa volunteers and 98 samples from Bai volunteers were collected, with informed consent, from Yunnan province of China.

PCR amplification and electrophoresis

PCR reactions were performed in a total volume of 10μl containing one 1.0mm blood card, 2×buffer mix, 2×primer mix (Institute of Forensic Science of China). Amplification was carried out by GeneAmp 9700 (Applied Biosystems, USA) with some modification of PCR condition. Pre-PCR denaturation was performed at 95°C for 11 min, followed by 28 cycles of denaturing

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at 94°C for 45s, annealing at 59°C for 2min, extension at 72°C for 1min, and a final extension at 60°C for 30 min. PCR products were analyzed by an ABI 3730xl Genetic Analyzer (Applied Biosystems, USA). Data were analyzed using Genemapper ID 3.2 software (Applied Biosystems, USA) and the alleles were determined by comparing with the allelic ladders.

Statistical analysis

We calculated the allele frequency at each locus from the numbers of alleles in the population samples. Forensic statistical parameters were calculated with the software PowerStatsV1.2 (Promega, USA) [10]. Hardy–Weinberg Equilibrium (HWE) expected Heterozygosity (He) of each locus and the genetic distance (Fst) between the two population and other Chinese populations were tested by using the Genepop Version 4.2 software package (http://genepop.curtin.edu.au).

Results and Discussion

The observed allele frequencies and forensic statistical parameters of the loci in the two population are shown in Table 1-4. The genotype frequency distributions in the 22 STR loci showed no deviations from the Hardy–Weinberg equilibrium by an exact test. Deviations from HWE were detected at D3S4529 (p-value = 0.0031) in Wa population and (p-value = 0.0316) in Bai population. After Bonferroni correction (i.e., p-value = 0.05/22 = 0.00227), no locus was significant.

Among the 22 STR loci in Wa population, 14 loci had He greater than 0.7, and 5 loci had DP greater than 0.9. The power of discrimination ranged from 0.7649 (D1GATA113) to 0.9287 (D9S2157), whereas the power of exclusion ranged from 0.2849 (D1S1677) to 0.6753 (D3S4529). The expected heterozygosity, power of discrimination and polymorphism information content of D9S2157 was the highest among the loci. The others had medium probability of exclusion and discrimination power. The cumulative discrimination power across these 22 loci in Wa population was >0.9 999 999 999 99. The combined probability of exclusion trios is 0.9999990508.

Among the 22 STR loci in Bai population, 13 loci had He greater than 0.7, and 5 loci had DP greater than 0.9. The power of discrimination ranged from 0.7722 (D1S1627) to 0.9248 (D2S441), whereas the power of exclusion ranged from 0.3455 (D1S1627) to 0.6105 (D2S441). The expected heterozygosity, power of discrimination and polymorphism information content of D2S441 was the highest among the loci. The others had medium probability of exclusion and discrimination power. The cumulative discrimination power across these 22 loci in Bai

Table 1. Allele frequencies of 22 STR in Wa population (n =200).

Allele	D1S1627	D3S4529	D2S441	D17S974	D6S1017	D4S2408	D9S2157	D6S474	D1GATA113	D18S853	D20S482
7				0.0025			0.0375		0.3975		
8				0.1200	0.2075	0.1950			0.0125		
9				0.2275		0.3250					
9.1			0.0025								
10	0.0775		0.2650	0.3250	0.3675	0.3375					0.0700
10.3			0.0025								
11	0.0050		0.2825	0.2525	0.0825	0.1250	0.0150		0.1050	0.4250	0.0025
11.3			0.1950								
12	0.1100		0.1200	0.0725	0.2425	0.0175	0.1050		0.4600	0.1450	0.0600
13	0.4775	0.2975	0.0075		0.1000		0.1800		0.0250	0.1200	0.2475
14	0.3150	0.1750	0.1250				0.1500	0.3425		0.1400	0.3350
15	0.0150	0.3050					0.3200	0.3075		0.1650	0.2125
16		0.2000					0.1725	0.1550		0.0050	0.0725
17		0.0225					0.0200	0.1525			
18								0.0425			
Allele	**D14S1434**	**D20S1082**	**D17S1301**	**D12ATA63**	**D22S1045**	**D10S1248**	**D1S1677**	**D11S4463**	**D9S1122**	**D2S1776**	**D5S2500**
7			0.0025								
8					0.2425						
9		0.0050	0.0575							0.0950	
10	0.1125		0.0125		0.0050			0.0375	0.0350	0.0225	
11	0.1325	0.4975	0.1150		0.0125	0.0125	0.0025	0.2700	0.1425	0.2525	
12	0.0025	0.0350	0.4825	0.2600	0.4425	0.0600	0.0075	0.2950	0.3100	0.5200	
13	0.3350	0.0025	0.3025	0.0225	0.1300	0.2900	0.0825	0.2675	0.4175	0.0925	
14	0.3875	0.0175	0.0275	0.0425	0.1525	0.2150	0.4825	0.1000	0.0575	0.0150	0.3700
15	0.0275	0.2650		0.0200	0.0150	0.3125	0.3500	0.0275	0.0350	0.0025	
16	0.0025	0.1575		0.3350		0.0850	0.0575	0.0025	0.0025		0.0100
17		0.0200		0.1675		0.0250	0.0175				0.3375
18				0.1425							0.2000
19				0.0100							0.0025
20											0.0675
21											0.0025
23											0.0100

Table 2. Allele frequencies of 22 STR in Bai population (n =98).

Allele	D1S1627	D3S4529	D2S441	D17S974	D6S1017	D4S2408	D9S2157	D6S474	D1GATA113	D18S853	D20S482
7				0.046			0.036		0.434		
8				0.153	0.194	0.245			0.005		
9				0.240		0.311	0.005				
9.1			0.026								
10	0.066		0.255	0.296	0.434	0.286					0.020
11	0.005		0.306	0.189	0.046	0.128	0.015		0.184	0.418	
11.3			0.082								
12	0.077		0.128	0.066	0.260	0.031	0.077		0.342	0.061	0.082
12.3			0.015								
13	0.587	0.235	0.020	0.010	0.061		0.327	0.015	0.036	0.214	0.189
14	0.25	0.286	0.143				0.179	0.332		0.25	0.444
15	0.015	0.265	0.026		0.005		0.296	0.393		0.056	0.189
16		0.148					0.046	0.158			0.077
17		0.066					0.020	0.082			
18								0.020			
Allele	**D14S1434**	**D20S1082**	**D17S1301**	**D12ATA63**	**D22S1045**	**D10S1248**	**D1S1677**	**D11S4463**	**D9S1122**	**D2S1776**	**D5S2500**
7								0.005			
8			0.005		0.255					0.005	
9			0.041					0.005		0.112	
10	0.082		0.031		0.005	0.005	0.020	0.097	0.071	0.046	
11	0.148	0.383	0.214		0.036	0.005	0.005	0.184	0.184	0.311	
12	0.015	0.020	0.439	0.301	0.25	0.041	0.026	0.311	0.281	0.367	
13	0.240	0.041	0.184		0.296	0.337	0.071	0.260	0.418	0.128	
14	0.505	0.046	0.077	0.026	0.143	0.245	0.424	0.097	0.031	0.026	0.413
15	0.010	0.362	0.010	0.061	0.015	0.230	0.367	0.031	0.010	0.005	
16		0.148		0.209		0.128	0.087	0.010	0.005		0.005
17				0.327		0.010					0.301
18				0.061							0.209
19				0.005							
20				0.010							0.071

Table 3. Forensic statistical parameters of 22 STR in Wa population.

Allele	D1S1627	D3S4529	D2S441	D17S974	D6S1017	D4S2408	D9S2157	D6S474	D1GATA113	D18S853	D20S482
He	0.6600	0.8400	0.7950	0.7050	0.7450	0.7550	0.7950	0.7400	0.6350	0.7150	0.8000
PIC	0.5970	0.7025	0.7475	0.7194	0.7056	0.6775	0.7729	0.6948	0.5430	0.7024	0.7320
DP	0.8250	0.8723	0.9105	0.9071	0.8912	0.8720	0.9287	0.8841	0.7649	0.8939	0.9005
PE	0.3691	0.6753	0.5898	0.4360	0.5013	0.5184	0.5898	0.4928	0.3350	0.4518	0.5990
Pm	0.1750	0.1278	0.0896	0.0929	0.1088	0.1280	0.0714	0.1159	0.2352	0.1062	0.0995
P	0.9064	0.0031	0.7006	0.0628	0.9184	0.3965	0.8068	0.9768	0.6650	0.4407	0.3061
Allele	**D14S1434**	**D20S1082**	**D17S1301**	**D12ATA63**	**D22S1045**	**D10S1248**	**D1S1677**	**D11S4463**	**D9S1122**	**D2S1776**	**D5S2500**
He	0.7350	0.6300	0.6500	0.7700	0.6450	0.7700	0.5950	0.7150	0.6650	0.6250	0.7150
PIC	0.6562	0.6036	0.6042	0.7340	0.6603	0.7218	0.5697	0.7151	0.6557	0.6006	0.6504
DP	0.8551	0.8362	0.8306	0.9035	0.8664	0.8966	0.8085	0.8968	0.8635	0.8272	0.8559
PE	0.4845	0.3284	0.3552	0.5446	0.3484	0.5446	0.2849	0.4518	0.3762	0.3220	0.4518
Pm	0.1449	0.1639	0.1694	0.0966	0.1336	0.1035	0.1916	0.1033	0.1366	0.1728	0.1442
P	0.4080	0.4187	0.7679	0.9751	0.0557	0.7986	0.2305	0.1532	0.2114	0.4742	0.7845

He: expected heterozygosity, PIC: polymorphism information content,
DP: discrimination power, PE: probability of paternity exclusion Pm: Matching probability
P: probability values of exact tests for Hardy–Weinberg disequilibrium.

population was >0.9 999 999 999 99. The combined probability of exclusion trios is 0.9999980034.

The population data of this study were compared with previously published data from other Chinese populations [11] using the Genepop Version 4.2 software package. Table 5 shows the genetic distance (Fst) between the Wa population, Bai population and Chinese Han population. Apparently, Wa population is distant from Bai population, and both the two populations are distant from Chinese Han population, the Fst values are all more than 0.01 with the 22 loci. This observation further confirms that the Wa and Bai population are relatively isolated from the other

Table 4. Forensic statistical parameters of 22 STR in Bai population.

Allele	D1S1627	D3S4529	D2S441	D17S974	D6S1017	D4S2408	D9S2157	D6S474	D1GATA113	D18S853	D20S482
He	0.6429	0.6633	0.8061	0.7551	0.6429	0.7857	0.7755	0.6735	0.6429	0.6837	0.7041
PIC	0.5311	0.7273	0.7680	0.7577	0.6526	0.6989	0.7284	0.6519	0.5946	0.6620	0.6811
DP	0.7722	0.9069	0.9248	0.9130	0.8676	0.8805	0.9040	0.8576	0.8230	0.8746	0.8846
PE	0.3455	0.3737	0.6105	0.5185	0.3455	0.5728	0.5544	0.3884	0.3455	0.4035	0.4346
Pm	0.2278	0.0931	0.0752	0.0870	0.1324	0.1195	0.0960	0.1424	0.1770	0.1254	0.1154
P	0.2508	0.0316	0.8796	0.3504	0.1823	0.3915	0.8588	0.4664	0.6666	0.5168	0.6847
Allele	**D14S1434**	**D20S1082**	**D17S1301**	**D12ATA63**	**D22S1045**	**D10S1248**	**D1S1677**	**D11S4463**	**D9S1122**	**D2S1776**	**D5S2500**
He	0.6735	0.6633	0.7041	0.7041	0.7347	0.7143	0.6735	0.7245	0.7347	0.7551	0.7143
PIC	0.6108	0.6432	0.6808	0.7101	0.7229	0.7157	0.6149	0.7495	0.6581	0.6951	0.6328
DP	0.8263	0.8478	0.8836	0.8975	0.9077	0.8963	0.8288	0.9188	0.8536	0.8886	0.8274
PE	0.3884	0.3737	0.4346	0.4346	0.4839	0.4507	0.3884	0.4672	0.4839	0.5185	0.4507
Pm	0.1737	0.1522	0.1164	0.1025	0.0923	0.1037	0.1712	0.0812	0.1464	0.1114	0.1726
P	0.8079	0.4295	0.6769	0.2454	0.4519	0.2926	0.9665	0.1389	0.5892	0.7381	0.6516

He: expected heterozygosity, PIC: polymorphism information content,
DP: discrimination power, PE: probability of paternity exclusion Pm: Matching probability
P: probability values of exact tests for Hardy–Weinberg disequilibrium.

Table 5. Population pair wise Fst among three populations.

population	Wa	Bai	Han in China
Wa	-	-	-
Bai	0.039	-	-
Han in China	0.044	0.024	-

populations in China. Generally, these statistical analysis results of this study suggest that these 22 loci had high or medium polymorphism and can be used as genetic markers in human identity testing in the Wa and Bai populations from Yunnan province, China.

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