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Genetic polymorphisms of 22 autosomal STR loci in Chinese Han population

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ABSTRACT

Microreader™ 23sp ID system was a new STR multiplex system developed for forensic application, but there was a lack of population data in the Chinese Han population. This kit contained 21 non-CODIS STR loci (D6S477, D18S535, D19S253, D15S659, D11S2368, D20S470, D1S1656, D22-GATA198B05, D7S3048, D8S1132, D4S2366, D21S1270, D13S325, D9S925, D3S3045, D14S608, D10S1435, D12S391, D2S1338, D17S1290, D5S2500), one CODIS STR locus (D16S539) and the amelogenin locus. In this study, a population sample in Chengdu Han population was analyzed with the kit. Forensic genetic parameters and probability values of the Hardy–Weinberg equilibrium (HWE) were calculated with software PowerStats v1.2 and Arlequin v3.5. Allele frequencies of the 22 STR loci and further forensic genetic parameters were obtained. The results suggested that Microreader™ 23sp ID system can provide informative polymorphic data for identification and parentage testing in Chinese Han population.

1. Introduction

STRs was widely used in paternity test, individual identification and biological anthropology because they can be easily amplified by the polymerase chain reaction (PCR) [1], and its diversity and genetic differentiation of human populations. Nevertheless, there was an absence of genetic information for some countries or areas. In this study, 22 autosomal STR loci in the Chengdu Han population were investigated using the Microreader™ 23sp ID system, to obtain the data of population genetics and determine the genetic variability.

2. Materials and methods

Blood samples were collected from 152 unrelated individuals (109 males and 43 females) of the Han population living in Chengdu, northwest China after informed consent. Genomic DNA was isolated by the salting out extraction method and quantified by the NanoDrop1000 Spectrophotometer (Nano-Drop Technologies, Wilmington, DE, USA). The samples were amplified using the Microreader™ 23sp ID system (Suzhou Microread Genetics, Suzhou, Jiangsu, China), PCR amplification was carried out on a Mastercycler® pro (Eppendorf, Germany) following the manufacturer's instructions, and amplified products were separated by capillary electrophoresis on a 3130 DNA Genetic Analyzer (Applied Biosystems, USA). Electrophoresis results were analyzed using GeneMapper ID 3.2 software (Applied Biosystems). The experimental procedures were guided in keeping with laboratory internal control standards and kit controls. Forensic statistical parameters were calculated by PowerStats v1.2 software [2], observed heterozygosity, expected heterozygosity and the chi-square test of Hardy–Weinberg equilibrium (HWE) were analyzed with ARLEQUIN version 3.5 software [3].

3. Results and discussion

Allele frequencies and forensic parameters were listed in Table 1. The observed heterozygosity (Ho) ranged from 0.7171 (D10S1435) to 0.8684 (D2S1338) while the expected heterozygosity (He) ranged from 0.7294 (D10S1435) to 0.8733 (D7S3048). The power of discrimination (PD) ranged from 0.8831 (D10S1435) to 0.9627 (D11S2368) and the probability of excluding paternity (PE) ranged from 0.4552 (D10S1435) to 0.7315 (D2S1338). The combined power of discrimination (CPD) in the 22 STR loci was 0.99999999999999999999999996806 and combined probability of matching (CPE) was 3.1943×10^{-27}. The value of combined probability of exclusion was 0.99999999975. All of 22 STR loci showed no statistically significant deviation from Hardy–Weinberg equilibrium (HWE). Except D10S1435 (PIC = 0.6860) rest of the 21 STR loci presented high polymorphism (PIC > 0.7), and the most informative locus was D7S3048 (PIC = 0.8566).

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Table 1
Allele frequencies of the 22 autosomal STR loci and forensic parameters of Chengdu Han population in China ($N = 152$).

Allele	D6S477	D18S535	D19S253	D15S659	D11S2368	D20S470	D1S1656	D22-GATA198B05	D16S539	D7S3048	D8S1132
6						0.0033					
7			0.1743								
8			0.0428	0.0033					0.0033		
9		0.1809				0.0066			0.2401		
10	0.0066	0.0559	0.0263	0.0099		0.1118			0.1513		
10.3				0.0033							
11	0.0066	0.0197	0.1349	0.1776		0.0329	0.0592		0.2401		
11.3				0.0033							
12	0.0493	0.0987	0.3454	0.2270		0.0559	0.0395		0.2566		
12.1											
12.3											
13	0.2138	0.2500	0.2072	0.1053		0.1283	0.0954		0.1020		
13.3											
14	0.2204	0.2895	0.0559	0.0329	0.0033	0.1382	0.1250	0.0033	0.0066		
15	0.2895	0.0954	0.0132	0.1250	0.0099	0.1941	0.3125	0.0099			0.0033
15.3											
16	0.1941	0.0099		0.1678	0.0461	0.1908	0.2007	0.0888			0.0164
16.2											
16.3							0.0033				
17	0.0197			0.1086	0.1645	0.0921	0.0658	0.1447		0.0033	0.1250
17.3							0.0658				
18				0.0329	0.1184	0.0428	0.0066	0.0592		0.0789	0.2303
18.3							0.0197				
19				0.0033	0.1414	0.0033	0.0033	0.0855		0.0987	0.1743
19.3							0.0033				
20					0.1447			0.1151		0.1776	0.1349
21					0.1908			0.2993		0.1151	0.1480
22					0.1184			0.1546		0.0789	0.0954
23					0.0493			0.0329		0.1875	0.0559
24					0.0099			0.0066		0.1118	0.0099
25										0.1184	0.0066
26					0.0033					0.0296	
27											
Ho	0.7632	0.8092	0.7895	0.8553	0.8618	0.8487	0.8487	0.8026	0.7763	0.8618	0.8158
He	0.7839	0.8012	0.7859	0.8508	0.8656	0.8661	0.8259	0.8351	0.7881	0.8733	0.8510
MP	0.0839	0.0771	0.0794	0.0490	0.0373	0.0389	0.0583	0.0519	0.0850	0.0387	0.0441
PD	0.9161	0.9229	0.9206	0.9510	0.9627	0.9611	0.9417	0.9481	0.9150	0.9613	0.9559
PIC	0.7464	0.7701	0.7538	0.8298	0.8472	0.8482	0.8034	0.8136	0.7511	0.8566	0.8301
PE	0.5325	0.6162	0.5797	0.7053	0.7183	0.6923	0.6923	0.6039	0.5558	0.7183	0.6287
TPI	2.1111	2.6207	2.3750	3.4545	3.6190	3.3043	3.3043	2.5333	2.2353	3.6190	2.7143
p	0.4313	0.3724	0.9053	0.2697	0.8935	0.3871	0.4230	0.3281	0.5685	0.1719	0.3943

Allele	D4S2366	D21S1270	D13S325	D9S925	D3S3045	D14S608	D10S1435	D12S391	D2S1338	D17S1290	D5S2500
6						0.0855					
7						0.2204					
8						0.0132	0.0164				
9	0.2928				0.3388	0.1118	0.0033				0.0066
10	0.0822	0.2862			0.0362	0.2467	0.0197			0.0428	0.0329
10.3											
11	0.3684	0.0625			0.0296	0.2138	0.1414			0.0559	0.3026
11.3											
12	0.1250	0.0493			0.1283	0.0855	0.4145			0.0132	0.1382
12.1		0.0033									
12.3		0.1020									
13	0.0625	0.1086		0.0099	0.2500	0.0164	0.2336			0.0132	0.0592
13.3		0.0329									
14	0.0658	0.2336		0.1217	0.1842	0.0066	0.1612			0.0329	0.0691
15	0.0033	0.0987		0.2237	0.0296		0.0066	0.0132		0.1974	0.2829
15.3		0.0099		0.0033							
16		0.0132		0.3289	0.0033		0.0033		0.0132	0.2533	0.0954
16.2										0.0033	
16.3				0.0263							
17			0.0066	0.2039				0.0658	0.0822	0.1776	0.0132
17.3				0.0066							
18			0.0428	0.0724				0.2336	0.1118	0.1151	
18.3											
19			0.2368	0.0033				0.2204	0.1711	0.0691	
19.3											
20			0.2763					0.1809	0.1020	0.0230	
21			0.2204					0.1184	0.0263	0.0033	
22			0.1546					0.0789	0.0395		
23			0.0428					0.0395	0.1908		
24			0.0164					0.0164	0.1908		
25			0.0033					0.0164	0.0625		

4. Conclusion

Our results showed that Microreader™ 23sp ID system could amplify 22 autosomal STR loci (contained 21 non-CODIS STR loci) and one sex-determining locus in a single reaction and it presented extremely high CPD and CPE value in the Chengdu Han population. Based on these we suggest that Microreader™ 23sp ID system could provide informative polymorphic data for identification and parentage testing in Chinese Han population, especially for deficiency cases of paternity test and the presence of STR mutation.

Conflict of interest

None.

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