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Frequency data for 15 STR loci and forensic use in a Beijing-Han population

Yacheng Liu^{*}, Zhen Yi Huo, Hui Tang, Jing Wang, Zhangping Jiao, Wanshan Ma, Jiangwei Yan, Jian Yang, Shuqin Jia, Xiaojun Zhu

Forensic Medical Examination and Identification Centre of Beijing Public Security Bureau, Beijing, China

Abstract

Short tandem repeats (STR) are useful to forensic science and are characterized by their small range of alleles, their high sensitivity and their suitability if the DNA is degraded. In our research, allele frequencies of 15 STR loci (CSF1PO, TPOX, TH01, D5S818, D7S820, D13S317, D16S539, D21S11, D18S51, FGA, vWA, D8S1179, D3S1358, PentaE, PentaD), together with the Amelogenin locus, were obtained in a sample of over 200 people from the Beijing-Han population, China. The results suggest that the 15 loci are excellent markers for identity and paternity testing. This is the first report on statistical data of all the 15 loci in the Beijing-Han population. © 2003 Elsevier Science B.V. All rights reserved.

Keywords: STR; Marker; DNA typing

1. Introduction

The purpose of our study was to investigate the distribution of 15 STR loci (CSF1PO, TPOX, TH01, D5S818, D7S820, D13S317, D16S539, D21S11, D18S51, FGA, vWA, D8S1179, D3S1358, PentaE, PentaD) in the Beijing-Han population and evaluate these markers in identity and paternity testing in forensic science.

^{*} Corresponding author. 1 Longgang Road, Qinghe District, Beijing 100085, China. Tel.: +86-106-290-9016; fax: +86-106-290-2582.

E-mail address: www.fmeicbjpsb.sohu.com (Y. Liu).

 Table 1

 Allele frequencies and statistical parameters of 15 STR loci in Beijing-Han population

	D3S1358	VWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	TH01	TPOX	CSF1PO	D16S539	PentaE	PentaD
														0.0657	
i										0.0805					0.0060
							0.0268	0.0058		0.2860					
								0.2543	0.1412	0.0508	0.5368	0.0092		0.0057	0.0542
				0.0056			0.0685	0.1445	0.0765	0.4894	0.1165	0.0583	0.2874	0.0029	0.3102
.3										0.0339					
0				0.1045			0.2083	0.1590	0.1618	0.0593	0.0142	0.3098	0.1782	0.0400	0.0813
0.2															
1				0.0791		0.0162	0.3512	0.2514	0.4059		0.3040	0.2055	0.2126	0.1371	0.2078
2				0.1328		0.0357	0.2045	0.1532	0.1912		0.0256	0.3344	0.1925	0.1200	0.1777
3		0.0028		0.2034		0.1916	0.1250	0.0202	0.0206		0.0028	0.0767	0.1121	0.0571	0.1205
4	0.0351	0.2955		0.1554		0.2370	0.0149	0.0116	0.0029			0.0061	0.0172	0.0971	0.0392
5	0.4211	0.0369		0.2486		0.1299								0.0971	0.0030
6	0.3070	0.1506		0.0593		0.1136								0.0886	
7	0.1871	0.2557		0.0113		0.1006								0.0686	
8	0.0409	0.1477	0.0145			0.0552								0.0771	
9	0.0088	0.0966	0.0494			0.0649								0.0371	
)		0.0142	0.0378			0.0260								0.0200	
1			0.1105			0.0065								0.0429	
1.2			0.0029												
2			0.1831			0.0065								0.0200	
2.2			0.0087												

23			0.2122			0.0130								0.0171	
23.2			0.0203												
24			0.2267			0.0032								0.0057	
25			0.0872												
26			0.0320												
27			0.0058												
28					0.0298										
28.2					0.0089										
29					0.3006										
29.2															
30					0.3423										
30.2					0.0060										
31					0.0923										
31.2					0.0565										
32					0.0149										
32.2					0.1190										
33					0.0030										
33.2					0.0268										
34.2															
$H_{\rm obs}$	0.7018	0.8125	0.8131	0.8356	0.7773	0.8261	0.7857	0.7803	0.7412	0.6664	0.8023	0.7117	0.7874	0.8571	0.8373
PD	0.8329	0.9150	0.9680	0.9670	0.9339	0.9733	0.9076	0.9286	0.8938	0.8319	0.9506	0.8843	0.9216	0.9831	0.9274
PE	0.4346	0.5941	0.7886	0.7399	0.6599	0.8004	0.5607	0.6065	0.5321	0.4273	0.6698	0.5074	0.5850	0.8294	0.6183
PIC	0.6362	0.7616	0.8868	0.8565	0.8032	0.8932	0.7360	0.7725	0.7116	0.6168	0.8133	0.6968	0.7581	0.9097	0.7770

2. Materials and methods

2.1. Sample collection

A total of 201 blood samples were obtained from unrelated Beijing-Han volunteer donors. DNA was extracted either with 5% chelex-100 or organic reagents.

2.2. DNA typing

Target DNA (about 2 ng) was amplified using the PowerplexTM 16 System kit (Promega) following the PCR protocol described in the Technical Manual [1]. The amplified fragments were separated and detected using the PE-310 Genetic Analyzer with reference to allelic ladders. The genotype results of the 15 loci were obtained through the Genotyper software applied by Promega [1]. Preliminary data has been used to generate the population statistics displayed in Table 1.

3. Results and discussions

The genotype frequencies of the 15 STR loci showed no deviations from HWE expectations based on the χ^2 test. The study of the genetic mode of two generations from 100 families demonstrated that all these loci conform to Mendelian laws of inheritance.

Through our genetic research on PentaE and PentaD in the Beijing-Han population, the 5-bp core repeat systems were found to cause none or minimal "stutter" [4].

The results suggest that all these 15 loci are excellent markers in forensic science. Multiplex PCR of all these 15 loci could help us in identity and paternity testing especially when dealing with degraded or trace evidence samples where no signals were obtained for the larger fragment loci but good results were obtained for many smaller fragment size loci.

References

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