Legal Medicine 26 (2017) 41–44

Contents lists available at ScienceDirect

Legal Medicine

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

Announcement of Population Data

Population genetic analysis of Xiamen Han population on 21 short tandem repeat loci

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ARTICLE INFO

Article history:
Received 26 September 2016
Received in revised form 19 January 2017
Accepted 1 March 2017
Available online 7 March 2017

Keywords:
Forensic science
Short tandem repeat
GlobalFiler™ Express
Xiamen
Han

ABSTRACT

GlobalFiler™ Express amplification kit incorporates 21 commonly used autosomal short tandem repeat (STR) loci and three gender determination loci. In this study, we analyzed GlobalFiler STR loci on 1006 unrelated individuals sampled of the Han population from Xiamen city, Fujian province, China. No deviations from Hardy–Weinberg equilibrium were observed. The combined probability of exclusion (CPE) for all 21 STR loci were >0.99999999771. A comparison of the allele frequencies in the population under study has been performed with other published from East Asian population for the same loci. Multiple STR loci showed significant differences between Han population from Xiamen and Korea, as well as Japan.

1. Introduction

A set of highly polymorphic short tandem repeat (STR) loci for human individual identification (HID) has proven to be successful in forensic investigations [1] . A total of 24 autosomal STR loci were commonly used in forensics [2], which were embedded in several multiplex amplification kits. Recently, the six-dye GlobalFiler™ Express Amplification kit were developed by Thermo Fisher Scientific company [3], which includes 21 autosomal STRs of above 24 markers and three gender determination loci (Amelogenin, Yindel, and DYS391). The autosomal STR loci in GlobalFiler kit are D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, VWA, TPOX, D18S51, D5S818, FGA, D12S391, D1S1656, D2S441, D10S1248, D22S1045, and SE33.

Xiamen city, In China's southeast coast, south of Fujian province, among the new commercial Human Identification (HID) kits, population studies based on the GlobalFiler kit (Thermo Scientific) have not been reported. In this study, to estimate the allele frequencies and forensic statistical parameters of 21 GlobalFiler STR loci on Han population from Xiamen, we typed a total of 1006 samples.

2. Materials and methods

2.1. Samples and experiments

A total of 1006 unrelated Han blood donors were sampled from Xiamen after acquiring their informed consent. All DNA samples were amplified using GlobalFiler™ STR kit (Thermo Fisher Scientific Company, Carlsbad, USA) in the GeneAmp PCR System 9700 (Thermo Fisher Scientific Company) according to manufacturer's recommendation. A total of 24 loci were amplified, including 21 autosomal STR loci and three gender determination loci. The PCR products were separated by capillary electrophoresis in an ABI PRISM 3730xL Genetic Analyzer (Thermo Fisher Scientific Company), and the GeneMapper® ID-X Software v1.4 (Thermo Fisher Scientific Company) was used for genotype assignment. DNA typing and assignment of nomenclature were based on the ISFG recommendations [4,5].

2.2. Statistical analyses

The allele frequencies were estimated from corresponding genotype counts. The exact tests of Hardy-Weinberg equilibrium (HWE) and linkage disequilibrium (LD) were performed using Arlequin v3.5 [6], and the observed heterozygosity (Ho) were also estimated. Match probability (MP), power of discrimination (PD), and power of exclusion (PE) were estimated using Modified-Powerstates [7]. The exact test of population differentiation was

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http://dx.doi.org/10.1016/j.legalmed.2017.03.002
1344-6223/

Table 1
Allele frequencies of 21 autosomal STR obtained for a population of 1006 Han individuals from Xiamen, China.

Allele	D13S179	D16S539	D5S818	TH01	D8S1179	CSF1PO	D10S1248	TPOX	D2S441	D7S820	D19S441
3			0.0005								
5	0.0005			0.0005							
6				0.0970							
6.3				0.0005							
7	0.0020	0.0005	0.0309	0.2450		0.0020		0.0005	0.0005	0.0010	
7.3				0.0005							
8	0.2750	0.0080	0.0030	0.0523		0.0005	0.0005	0.5290	0.0010	0.1320	
8.1									0.0005	0.0010	
8.3				0.0060							
9	0.1405	0.2910	0.0749	0.5053	0.0005	0.0480		0.1150		0.0665	0.0005
9.1									0.0330	0.0040	
9.2										0.0010	
10	0.1510	0.1200	0.1900	0.0547	0.1240	0.2580		0.0335	0.2130	0.1640	0.0070
10.1									0.0025	0.0020	
10.3										0.0010	
11	0.2340	0.2610	0.3248	0.0020	0.1280	0.2400	0.0010	0.2930	0.3235	0.3490	0.0126
11.3									0.0730	0.0005	0.0019
12	0.1600	0.2100	0.2329		0.1303	0.3635	0.0730	0.0270	0.2070	0.2460	0.0440
12.1		0.0010				0.0010					
12.2											0.0050
12.3										0.0005	
13	0.0330	0.0910	0.1320		0.1942	0.0730	0.3680	0.0015	0.0160	0.0300	0.2810
13.2											0.0380
13.3		0.0005									
14	0.0040	0.0160	0.0100		0.1880	0.0110	0.2380		0.1190	0.0010	0.2470
14.2											0.1180
15		0.0010	0.0010		0.1550	0.0030	0.2003	0.0005	0.0110	0.0005	0.0690
15.2											0.1340
16					0.0630		0.1002				0.0080
16.2											0.0300
17					0.0140		0.0180				0.0010
17.2											0.0030
18					0.0030		0.0010				
Ob.H	0.8140	0.7620	0.7660	0.6840	0.8340	0.7400	0.7510	0.5980	0.7830	0.7470	0.8000
PD	0.9290	0.9170	0.9190	0.8440	0.9590	0.8820	0.9000	0.7930	0.9230	0.9120	0.9430
PE	0.6250	0.5300	0.5380	0.4040	0.6640	0.4920	0.5120	0.2890	0.5680	0.5040	0.5990
MP	0.0710	0.0830	0.0810	0.1560	0.0410	0.1180	0.1000	0.2070	0.0770	0.0880	0.0570
PIC	0.7700	0.7500	0.7500	0.6300	0.8300	0.6900	0.7100	0.5600	0.7600	0.7300	0.8000
P	0.2976	0.1572	0.2797	0.2969	0.1451	0.8593	0.9289	0.1723	0.7806	0.1002	0.1192

Allele	D22S1045	D3S1358	vWA	D1S1656	D2S1338	SE33	D18S51	D21S11	D12S391	FGA
9			0.0005							
10	0.0005			0.0010			0.0010			
11	0.2080			0.0570			0.0050			
12	0.0005	0.0010		0.0580			0.0410			
13	0.0040	0.0020	0.0030	0.1150		0.0005	0.1713			
14	0.0240	0.0490	0.2550	0.0670		0.0030	0.2044			
14.2						0.0010				
15	0.2740	0.3280	0.0337	0.2850		0.0088	0.1890		0.0120	
15.3				0.0010						
16	0.2640	0.2980	0.1560	0.2150	0.0190	0.0160	0.1263		0.0080	
16.1						0.0010				
16.3				0.0080						
17	0.1970	0.2370	0.2593	0.0826	0.0680	0.0470	0.0900		0.0800	0.0005
17.3				0.0730						
18	0.0230	0.0750	0.1953	0.0153	0.1080	0.0730	0.0560		0.2330	0.0220
18.1									0.0010	
18.3				0.0201						
19	0.0010	0.0090	0.0837	0.0010	0.1980	0.0740	0.0370		0.2015	0.0540
19.1									0.0010	
19.2						0.0018				
19.3				0.0010						0.0005
20	0.0010	0.0010	0.0130		0.1260	0.0650	0.0250		0.1740	0.0540
20.1										0.0005
20.2						0.0020				
20.3									0.0005	
21	0.0015		0.0005		0.0340	0.0320	0.0213		0.1160	0.1060
21.2						0.0200				0.0050
22					0.0370	0.0110	0.0230		0.0870	0.1680
22.2						0.0440				0.0070
23	0.0015				0.1860	0.0030	0.0045		0.0534	0.2110
23.2						0.0370		0.0010		0.0070
24					0.1390	0.0005	0.0022		0.0176	0.1870
24.1										0.0005