Population genetic data for the STR loci using the AmpFlSTR® Identifiler™ Kit in Bahia, Brazil

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Abstract. The AmpFlSTR® Identifiler™ is a multiplex kit which coamplifies 16 STR loci, including the segment of the X–Y homologus gene Amelogenin. The study of these STR loci is important for the formation of local human identification databases in order to statistically evaluate the evidence. This report presents allele frequency data for 15 STR loci in 150 unrelated individuals from Bahia, Brazil. The genotype frequencies of the 15 STR loci showed no deviations from HWE expectations. The combined power of exclusion is estimated as 99.99996% and the combined power of discrimination is 99.9999999999999999%. © 2003 Elsevier B.V. All rights reserved.

Keywords: Bahia, Brazil population; STR loci; Population genetic data

1. Introduction

The Brazilian culture and origin has been diversified with the arrival of immigrants, namely the European (mainly the Portuguese) and African groups.

The purpose of this study was to determine the distribution of 15 loci: D19S433, D3S1358, D5S8118, D8S1179, vWA, TH01, D13S317, D21S11, TPOX, FGA, D7S820, D16S539, D18S51, CSF1PO and D2S1338, in the Bahian population.

2. Materials and methods

The bloodstains of 150 unrelated (in three generations) voluntary healthy donors from Bahia, Brazil were collected and extracted using Chelex procedures [1] and, if necessary, purified by the modified salt-chloroform method.

Amplification was done according to the AmpFlSTR® Identifiler™ kit [2] protocol using a 9600 thermal cycler. Amplified products were analysed by capillary electropho-

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Table 1
Allele frequencies and statistical analysis in the Bahian population ($n = 150$)

Allele	D3S1358	VWA	FGA	TH01	TPOX	CSF1PO	D5S818	D13S317	D7S820	D8S1179	D21S11	D18S51	D16S539	D2S1338	D19S433
6				0.220	0.023										
7				0.283	0.013	0.013	0.017		0.007						
8				0.150	0.460	0.020	0.023	0.057	0.136	0.007			0.033		
9				0.127	0.147	0.020	0.010	0.087	0.117	0.010			0.140		0.003
9.3				0.207											
10				0.013	0.077	0.313	0.063	0.047	0.320	0.060		0.013	0.100		
11		0.010			0.250	0.284	0.347	0.336	0.260	0.057		0.017	0.287		0.017
12					0.030	0.277	0.360	0.296	0.120	0.107		0.137	0.277		0.090
12.2															0.013
13	0.007	0.010				0.063	0.160	0.127	0.040	0.286		0.114	0.150		0.304
13.2															0.037
14	0.103	0.066				0.010	0.017	0.040		0.257		0.120	0.010	0.003	0.240
14.2								0.003							0.033
15	0.330	0.147					0.003			0.173		0.170	0.003		0.130
15.2												0.003			0.07
16	0.270	0.240								0.033		0.150		0.040	0.047
16.2															0.013
17	0.197	0.270							0.007	0.010		0.103		0.200	
17.2															0.003
18	0.090	0.133	0.017									0.057		0.053	
18.2															
19	0.003	0.100	0.087									0.047		0.107	
20		0.017	0.090									0.053		0.123	
20.2															
21		0.007	0.177									0.013		0.063	
21.2															

22			0.177									0.003		0.087	
22.2			0.003											0.087	
23			0.123											0.113	
23.2			0.003												
24			0.157											0.093	
25			0.090											0.027	
26			0.033											0.003	
27			0.033								0.037				
28			0.007								0.140				
29											0.250				
30											0.207				
30.2											0.033				
31											0.060				
31.2											0.107				
32											0.013				
32.2											0.087				
33.2											0.047				
34											0.003				
34.2											0.003				
35											0.010				
36											0.003				
42.2			0.003												
Minimum frequency	0.003	0.007	0.003	0.013	0.013	0.010	0.003	0.003	0.007	0.007	0.003	0.003	0.003	0.003	0.003
X^2 test	0.207	0.738	0.706	0.450	0.253	0.114	0.319	1.850	0.165	0.300	0.775	0.734	0.186	0.919	0.703
Exp. H	0.763	0.818	0.874	0.792	0.699	0.742	0.722	0.771	0.784	0.805	0.851	0.886	0.791	0.891	0.818
Obs. H	0.833	0.740	0.880	0.793	0.687	0.773	0.720	0.747	0.760	0.787	0.847	0.887	0.787	0.860	0.773
PE	0.539	0.637	0.741	0.583	0.466	0.502	0.482	0.564	0.579	0.617	0.700	0.763	0.587	0.774	0.646
PD	0.904	0.941	0.970	0.923	0.865	0.887	0.874	0.913	0.920	0.934	0.960	0.975	0.924	0.977	0.944

Exp. H, expected heterozygosity; Obs. H, observed heterozygosity; PE, power of exclusion and PD, power of discrimination.

resis on the ABI PRISM® 310 Genetic Analyzer using Liz 500 as Internal Lane DNA Standard and employing ABI software [3].

Statistical analysis was done using Genepop version 3.1a software package [4] and Microsoft Excel, respectively, in accordance with Refs. [5 and 6].

3. Results and discussion

The observed allele frequencies and results of the statistical tests are shown in Table 1. The genotype frequencies of the 15 STR loci showed no deviations from HWE expectations. The combined power of exclusion is estimated as 99.99996% and the combined power of discrimination is 99.9999999999999999%.

The allele frequencies did not show significant differences in comparison with the other Brazilian populations [7–13].

In conclusion, these systems have been shown to be a useful tool for personal identification, justifying their use for the Bahian population.

Acknowledgements

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