ELSEVIER

Forensic Science International 129 (2002) 78–80

Forensic Science International

www.elsevier.com/locate/forsciint

Announcement of population data

Genetic profile of a multi-ethnic population from Guiné-Bissau (west African coast) using the new PowerPlex® 16 System kit

Rita Gonçalves, José Jesus, Ana Teresa Fernandes, António Brehm*

Human Genetics Laboratory, Center of Macaronesian Studies, University of Madeira, Penteada, 9000 Funchal, Portugal

Received 31 May 2002; accepted 3 June 2002

Abstract

Allele and haplotype frequencies of 15 chromosome STR loci included in the kit PowerPlex® 16 System from Promega, were determined in a sample of unrelated males from Guiné-Bissau, a country from the west African coast. All individuals were subjected to an interview in order to make sure that their ancestors belonged to the same ethnic group. This way we intended to look for possible inter-ethnic differences. PowerPlex 16 includes STRs not studied before in any multi-ethnic population. The kit includes two new allele markers (Penta D and Penta E), which are very useful either in forensics or population genetic studies. The Guinean population presents significant differences when compared with other African populations.

Keywords: STRs; Population data; Guiné-Bissau; Africa; Ethnic groups; PowerPlex® 16 System; Promega

Population: A sample of 100 healthy unrelated males from Guiné-Bissau was typed for 15 STRs. Males were subjected to an interview in order to ascertain about their ethnic origins and to give their informed consent. The individuals belong to the following ethnic groups and were coded as follows: Bijagós (from the Bijagós Archipelago), Balanta, Felupe (known as Diola or Djola), Mancanha, Manjaco, Papeis, Banhú, Beafadas, Nalú, Fula (also known as Peul or Fulbe), Mansonca, Susso and Mandinga (also known as Mandenka).

DNA extraction: Chelex method.

PCR and typing: PowerPlex® 16 System [1]. Although amelogenin is included in the Promega kit, we excluded it from the analysis. Typing was done using an ABI Prism 310 automatic sequencer.

Analyses of data: GENEPOP [2], haplotype and gene diversity according to Nei [3]. Population comparisons were done using Arlequin [4].

Results: Allele frequencies for 15 STR loci and parameters of genetic and forensic interest are presented in Table 1.

Access to the data: By request to lgh@uma.pt or directly on the laboratory's Web site http://www.uma.pt/ccbg/LGH/STRGuiné-Bissau.

Observations: There are no significant differences on allele frequencies between the different ethnic groups, something expected due to the small sample size for each group. Nevertheless, allele frequencies of the STRs studied separated by ethnic groups are available from the authors upon request. The Guinean population is in Hardy–Weinberg equilibrium for all loci. We have compared the allele frequencies of the Guinean population (taken as a whole) with other data using the available sets of loci. The Guinean population show significant differences when compared with Afro-Americans at loci D21S11, Penta E, CSF1PO, Penta D and TPO, [5,6] and in Moçambique [7] at loci D3S1358, D21S11, CSF1PO D8S1179, FGA, TH01 and TPO (in all cases, a *G*-test, using Fisher's method, $P < 0.01$). Nevertheless there are interesting features related to specific alleles that were not reported in a Moçambique survey [7] but appear in Caucasoid or north African populations. Such is the case of allele 13 of D3S1358 and allele 29.2 of D21S11 that have been reported with low frequency in Caucasoid individuals from the US [6] and Berbers [8] but not in Moçambique or the US Africans [6,7]. In Guiné-Bissau, the former allele was found exclusively in two ethnic groups, the Bijagós and Felupe and the

* Corresponding author. Tel.: +351-1291-705383; fax: +351-1291-705399.
E-mail address: brehm@uma.pt (A. Brehm).

0379-0738/02/$ – see front matter
PII: S0379-0738(02)00204-9

Table 1
Allele frequencies for 15 STR loci and parameters of genetic and forensic interest

	D3S1358	D21S11	D18S51	Penta E	D5S818	D13S317	D7S820	D16S539	CSF1PO	Penta D	D8S1179	FGA	TH01	VWA	TPO
2.2										0.250					
3.2										0.010					
5				0.100						0.055			0.005		
6				0.005									0.085		0.100
7				0.045			0.005		0.110	0.045			0.350		0.035
8				0.180	0.085	0.015	0.235	0.025	0.095	0.100			0.255		0.215
9			0.005	0.080	0.035	0.005	0.120	0.180	0.050	0.060			0.200		0.220
9.3													0.105		
10			0.005	0.080	0.055	0.020	0.380	0.110	0.175	0.130	0.005				0.060
10.2			0.015												
11			0.010	0.085	0.170	0.285	0.165	0.320	0.170	0.130	0.025			0.010	0.325
12	0.005		0.075	0.085	0.405	0.480	0.085	0.220	0.345	0.095	0.100			0.010	0.045
13	0.020		0.065	0.095	0.230	0.145	0.010	0.130	0.055	0.100	0.205			0.025	
13.2			0.010												
14	0.070		0.025	0.045	0.015	0.050		0.015		0.010	0.335			0.080	
15	0.295		0.155	0.085	0.005					0.015	0.215			0.195	
16	0.310		0.150	0.070							0.115			0.260	
17	0.210		0.220	0.020										0.245	
18	0.085		0.145	0.010								0.005		0.095	
18.2												0.010			
19	0.005		0.055	0.015								0.035		0.050	
19.2												0.015			
20			0.025									0.020		0.020	
21			0.025									0.095		0.010	
21.2												0.005			
22			0.010									0.230			
22.2												0.010			
23			0.005									0.210			
24												0.110			
25												0.120.5			
26												0.060			
27			0.020									0.035			
28			0.190									0.025			
29			0.120									0.010			
29.2			0.010												
30			0.200												
30.2			0.015												
31			0.080												
31.2			0.055									0.005			
32			0.025												
32.2			0.135												
33			0.005												
33.2			0.045												
34			0.015												
34.2			0.015												
35			0.065												
36			0.005												
PD	0.904	0.972	0.969	0.983	0.898	0.835	0.901	0.924	0.932	0.969	0.916	0.966	0.900	0.943	0.922
CE	0.519	0.734	0.724	0.786	0.509	0.401	0.513	0.565	0.589	0.719	0.546	0.708	0.509	0.608	0.608
P	0.279	0.478	0.207	0.586	0.190	0.907	0.076	0.533	0.057	0.919	0.095	0.567	0.930	0.960	0.664
H_e	0.764	0.878	0.873	0.909	0.746	0.668	0.755	0.791	0.799	0.870	0.780	0.864	0.758	0.819	0.787
H_o	0.740	0.830	0.820	0.870	0.760	0.690	0.720	0.780	0.770	0.870	0.750	0.850	0.730	0.820	0.840

For all loci, the number of individuals studied was 100. H_o: observed heterozygosity; H_e: expected heterozygosity; PD: power of discrimination and exclusion; CE: a priori chance of exclusion; *P*: Hardy–Weinberg equilibrium, exact test based on more than 2000 shufflings, for S.E. < 0.01.

later in the Bijagós and Beafadas. Allele 7 of D7S820, which appeared in the Sussos of Guiné-Bissau, was not reported in Moçambique but in Caucasoids. Allele 12 of VWA appeared in the Mandinga and Fula, two ethnic groups known to be historically related to north Africans, are also absent from other Africans but do appear in Madeira and the Açores populations [9,10]. Finally, allele 21 of VWA was found in the Mandinga and Bijagós, absent in other African populations but appearing in Morocco, Açores and other Caucasoids. The new Penta E and Penta D systems included in the Promega kit revealed to be good markers for paternity testing (PD = 0.983 and 0.969, respectively).

Acknowledgements

This work was done under a research partnership with PROMEGA Corp. We acknowledge the collaboration of the Chairman of the Army Chiefs of Staff and the Ministry of Public Health of the Republic of Guiné-Bissau. ICCTI provided a travel grant to AB.

References

[1] PowerPlex® 16 System kit, Promega Corporation, Technical Manual.
[2] M. Raymond, F. Rousset, GENEPOP (Version 1.2): population genetic software for exact tests and ecumenicism, J. Hered. 86 (1995) 248–249.
[3] M. Nei, Molecular Evolutionary Genetics, Columbia University Press, New York, 1987.
[4] S. Schneider, J.-M. Kueffer, D. Roessli, L. Excoffier, Arlequin (Version 1.1): A Software for Population Genetic Data Analysis, Genetics and Biometry Laboratory, University of Geneva, Switzerland, 1997.
[5] B. Budowle, A. Masibay, S. Anderson, C. Barna, L. Biega, S. Brenneke, B. Brown, J. Cramer, G. DeGroot, D. Douglas, B. Duceman, A. Eastman, R. Giles, J. Hamill, D. Haase, D. Janssen, T. Kupferschmid, T. Lawton, C. Lemire, B. Llewellyn, T. Moretti, J. Neves, C. Palaski, S. Schueler, J. Sgueglia, C. Sprecher, C. Tomsey, Yet STR primer concordance study, Forensic Sci. Int. 124 (2001) 47–54.
[6] C. Holt, C. Stauffer, J. Wallin, K. Lazaruk, T. Nguyen, B. Budowle, P. Walsh, Practical applications of genotypic surveys for forensic STR testing, Forensic Sci. Int. 112 (2000) 91–109.
[7] C. Alves, L. Gusmão, A. Amorim, STR data (AmpFlSTR Profiler Plus and GenePrint CTTv) from Mozambique, Forensic Sci. Int. 119 (2001) 131–133.
[8] A. Pérez-Lezaun, F. Calafell, J. Clarimón, E. Bosch, E. Mateu, L. Gusmão, A. Amorim, N. Benchemsi, J. Bertranpetit, Allele frequencies of 13 short tandem repeats in population samples from the Iberian Peninsula and northern Africa, Int. J. Legal Med. 113 (2000) 208–214.
[9] A. Fernandes, A. Brehm, C. Alves, L. Gusmão, A. Amorim, Genetic profile of the Madeira Archipelago population using the new PowerPlex® 16 System kit, Forensic Sci. Int. 125 (2002) 281–283.
[10] R. Velosa, A. Fernandes, A. Brehm, Genetic profile of the Açores Archipelago population using the new PowerPlex® 16 System kit, Forensic Sci. Int., in press.

	D3S1358	D21S11	D18S51	PE	D5S818	D13S317	D7S820	D16S539	CSF1PO	PD	D8S1179	FGA	TH01	VWA	TPO
2,2										0,250					
3,2										0,010					
5				0,100						0,055			0,005		
6				0,005									0,085		0,100
7				0,045			0,005		0,110	0,045			0,350		0,035
8				0,180	0,085	0,015	0,235	0,025	0,095	0,100			0,255		0,215
9			0,005	0,080	0,035	0,005	0,120	0,180	0,050	0,060			0,200		0,220
9,3													0,105		
10			0,005	0,080	0,055	0,020	0,380	0,110	0,175	0,130	0,005				0,060
10,2			0,015												
11			0,010	0,085	0,170	0,285	0,165	0,320	0,170	0,130	0,025			0,010	0,325
12	0,005		0,075	0,085	0,405	0,480	0,085	0,220	0,345	0,095	0,100			0,010	0,045
13	0,020		0,065	0,095	0,230	0,145	0,010	0,130	0,055	0,100	0,205			0,025	
13,2			0,010												
14	0,070		0,025	0,045	0,015	0,050		0,015		0,010	0,335			0,080	
15	0,295		0,155	0,085	0,005					0,015	0,215			0,195	
16	0,310		0,150	0,070							0,115			0,260	
17	0,210		0,220	0,020										0,245	
18	0,085		0,145	0,010								0,005		0,095	
18,2												0,010			
19	0,005		0,055	0,015								0,035		0,050	
19,2												0,015			
20			0,025									0,020		0,020	
21			0,025									0,095		0,010	
21,2												0,005			
22			0,010									0,230			
22,2												0,010			
23			0,005									0,210			
24												0,110			
25												0,120			
26												0,060			
27		0,020										0,035			

28		0,190										0,025			
29		0,120										0,010			
29,2		0,010													
30		0,200													
30,2		0,015													
31		0,080													
31,2		0,055										0,005			
32		0,025													
32,2		0,135													
33		0,005													
33,2		0,045													
34		0,015													
34,2		0,015													
35		0,065													
36		0,005													
PD	0,904	0,972	0,969	0,983	0,898	0,835	0,901	0,924	0,932		0,916	0,966	0,900		0,922
CE	0,519	0,734	0,724	0,786	0,509	0,401	0,513	0,565	0,589		0,546	0,708	0,509		0,608
P	0,279	0,478	0,207	0,586	0,190	0,907	0,076	0,533	0,057	0,919	0,095	0,567	0,930	0,960	0,664
He	0,764	0,878	0,873	0,909	0,746	0,668	0,755	0,791	0,799	0,870	0,780	0,864	0,758	0,819	0,787
Ho	0,740	0,830	0,820	0,870	0,760	0,690	0,720	0,780	0,770	0,870	0,750	0,850	0,730	0,820	0,840