Int J Legal Med (2005) 119: 107–110
DOI 10.1007/s00414-004-0505-9

SHORT COMMUNICATION

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The Fang population of Equatorial Guinea characterised by 15 STR-PCR polymorphisms

Received: 23 June 2004 / Accepted: 14 October 2004 / Published online: 24 November 2004

Abstract Allele frequencies for 15 STR loci (D8S1179, D21S11, D7S820, CSF1PO, D19S433, HUMVWA31A, HUMTPOX, D18S51, D3S1358, HUMTHO1, D13S317, D16S539, D2S1338, D5S818 and HUMFGA) were analysed in the Fang population of Bioko Island, Equatorial Guinea. No deviation from Hardy-Weinberg equilibrium was found for all loci. Statistical parameters demonstrated the forensic utility of the analysed systems.

Keywords STR polymorphisms · Forensic genetics · Populations genetics · Fang · Equatorial Guinea

Introduction

Bioko is a volcanic island in the Bight of Biafra (Gulf of Guinea, South Atlantic Ocean), 160 km north-west of mainland Equatorial Guinea with about 62,000 inhabitants. The indigenous ethnic group is the Bubi, but for the last 30 years it has been increasingly inhabited by the Fang (an ethnic group of Bantu origin) originally from the mainland, who maintain tribal village and family links with the mainland and frequently travel there [1]. Today they constitute 80% of the population of Equatorial Guinea (http://www.nationmaster.com/encyclopedia/Demographics-of-Equatorial-Guinea).

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Because they are the largest ethnic group of this country, it is interesting to obtain accurate allele frequency data and other genetic parameters of forensic interest in order make comparisons with other ethnic groups of Bantu origin. For this purpose 15 short tandem repeat loci (STRs) [2, 3] included in the Identifiler kit (Applied Biosystem, Foster City, CA) were studied. Data obtained can be used to provide estimates of the frequency of the DNA profile in human identity testing.

Material and methods

DNA was extracted by Chelex method [4] from blood samples taken from healthy unrelated Fang individuals (n=129) from Bioko Island. PCR amplification was performed following the recommendations of the Identifiler kit (Applied Biosystem, Foster City, CA). Amplified products were analysed using an ABI Prism 310 Genetic Analyzer automated laser sequencer [5]. Deviations from Hardy-Weinberg equilibrium [6] were calculated with the Popgen program. All forensic parameters were calculated with Powerstat (Promega, Madison, WI).

Results and discussion

The allele frequencies and the Hardy-Weinberg equilibrium probabilities (p) for the Fang population observed in each locus are shown in Table 1. The forensic parameters (h, heterozygosity index, CE, chance of exclusion and PD, power of discrimination) are summarised in Table 2. No significant deviations from Hardy-Weinberg expectations were found. The combined power of discrimination (PD) and the combined chance of exclusion (CE) for the 15 studied loci were >0.9999999 and 0.99999724, respectively. The expected heterozygosity and the power of discrimination calculated from the gene frequencies obtained for the Fang population revealed that in combination, the 15 systems have a high forensic efficiency.

Table 1 Allele frequency distributions for D5S818, D13S317, D7S820, D16S539, HUMTH01, HUMVWA, D8S1179, HUMTPOX, HUMFGA, HUMCSF1PO, D21S11, D18S51, D2S1338, D19S433 and D3S1358 in the Fang population

Allele	D5S818	D13S317	D7S820	D16S539	HumTH01	HumVWA	D8S1179	HumTPOX	HumFGA	HumCSF1PO	D21S11	D18S51	D2S1338	D19S433	D3S1358
4					0.0040										
5				0.0082											
6					0.1120			0.0470							
7			0.0127		0.3800			0.0470		0.0637					
8	0.0714	0.0080	0.2585	0.0287	0.2680			0.3120		0.0588					
9	0.0159	0.0040	0.1059	0.2295	0.1680			0.2308		0.0343				0.0240	
9.3					0.0400										
10	0.0397	0.0040	0.3602	0.1352	0.0280			0.0641		0.2598					
11	0.1944	0.2760	0.1864	0.3033		0.0127	0.0543	0.2821		0.2010				0.0840	
11.2														0.0040	
12	0.3968	0.4400	0.0551	0.1926			0.1357	0.0171		0.3137		0.0196	0.0042	0.0880	
12.2														0.0440	
13	0.2540	0.2080	0.0212	0.0943		0.0127	0.1047			0.0539		0.0392		0.2520	
13.2												0.0049		0.0840	
14	0.0198	0.0600		0.0082		0.0720	0.3992			0.0147		0.0637		0.1960	0.0661
14.2												0.0049		0.0400	
15	0.0079					0.2288	0.2248					0.1225	0.0083	0.0480	0.3099
15.2														0.0640	
16						0.2500	0.0620					0.1961	0.0792	0.0080	0.3347
16.2														0.0600	
17						0.2415	0.0194		0.0085			0.2059	0.0708		0.2521
17.2														0.0040	
18						0.0975						0.1471	0.0208		0.0372
18.2									0.0171						
19						0.0636			0.0598			0.1275	0.1292		
19.2									0.0085						
20						0.0212			0.0470			0.0441	0.0958		
20.2									0.0043						
21									0.1325			0.0245	0.1375		
21.2									0.0043						
22									0.1752				0.1583		
22.2									0.0128						
23									0.1581				0.0625		
24									0.1581				0.0958		
25									0.0940				0.1250		
26									0.0385		0.0123		0.0125		
27									0.0427		0.0328				
28									0.0085		0.2705				
29									0.0043		0.1557				

Table 1 (continued)

Allele	D5S818	D13S317	D7S820	D16S539	HumTH01	HumVWA	D8S1179	HumTPOX	HumFGA	HumCSF1PO	D21S11	D18S51	D2S1338	D19S433	D3S1358
30											0.2295				
30.2									0.0085		0.0287				
31											0.0861				
31.2									0.0085		0.0574				
32											0.0246				
32.2											0.0410				
33											0.0041				
33.2											0.0205				
34											0.0164				
35											0.0164				
35.2											0.0041				
44.2									0.0043						
45.2									0.0043						

Table 2 Statistical parameters of forensic interest

Locus	h	PD	CE	p
D5S818	0.762	0.874	0.530	0.187
D13S317	0.696	0.840	0.422	0.311
D7S820	0.746	0.900	0.503	0.875
D16S539	0.803	0.914	0.605	0.306
HUMCSF1PO	0.745	0.917	0.501	0.095
HUMTPOX	0.786	0.902	0.574	0.979
HUMTH01	0.744	0.889	0.500	0.304
HUMVWA	0.807	0.930	0.612	0.097
D8S1179	0.760	0.901	0.526	0.356
HUMFGA	0.846	0.968	0.687	0.672
D3S1358	0.736	0.865	0.485	0.392
D21S11	0.787	0.953	0.575	0.580
D18S51	0.824	0.958	0.643	0.909
D2S1338	0.868	0.968	0.730	0.134
D19S433	0.800	0.961	0.599	0.218
Combined		>0.999	>0.999	

h heterozygosity index.
CE Chance of exclusion.
PD Power of discrimination.
p Hardy-Weinberg equilibrium.

Table 3 Comparison between Fang and other populations of Bantu speakers

Locus	Bubi	Hutu	Ovambos	Ugandans
HUMCSF1PO	0.8183	0.0001		
HUMTPOX	0.0946	0.1160		
HUMTH01	0.9064	0.1257	0.0032	0.0540
HUMVWA	0.3552	4.48×10^{-7}	0.1110	0.0198
D8S1179	0.0228	0.2596		
D3S1358	0.5704	0.7417		
D18S51	0.2393	0.2540		
D5S818		0.7545		
D7S820		0.0587		
D13S317		0.0496		
HUMFGA		0.0197		
D16S539		0.0393		
D21S11		0.9106	0.1250	0.0115

The results were compared with other Bantu groups: Bubis (Bioko Island) [7], Hutus (Rwandans) [8], Ovambos (S-W Bantu group) and Ugandans (Namibians) [9]. The comparison between Fangs and Bubis shows no statistically significant differences for all loci, except for D8S1179 system (p=0.0228), which suggests some genetic affinities between the two groups.

The comparison between Fangs and other Bantu speaking groups revealed significant differences for some loci (Table 3). These results confirm that in Africa, as we suggested previously [7], there is a certain degree of genetic heterogeneity.

Acknowledgements The authors are very grateful to the Fang population for generously collaborating in the present study.

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