SHORT COMMUNICATION

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

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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, \$\overline{\infty}\$ D2S1338, D19S433 and D3S1358 in the Fang population

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	59									0.0043		0.1557				

	HumVWA D8S1179 HumTPOX HumFGA HumCSF1PO D21S11 D18S51 D2S1338 D19S433 D3S1358	0.2295	0.0287	0.0861	0.0574	0.0246	0.0410	0.0041	0.0205	0.0164	0.0164	0.0041		
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Table 1 (continued)

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.

 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.

CE Chance of exclusion.

PD Power of discrimination.

p Hardy-Weinberg equilibrium.

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