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SHORT COMMUNICATION

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Gabon black population data on the ten short tandem repeat loci D3S1358, VWA, D16S539, D2S1338, D8S1179, D21S11, D18S51, D19S433, TH01 and FGA

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Abstract Allele frequencies for ten short tandem repeat (STR) loci D3S1358, VWA, D16S539, D2S1338, D8S1179, D21S11, D18S51, D19S433, TH01 and FGA were determined in a Black African sample population from Gabon. All loci were highly polymorphic and except for TH01, D21S11 and D16S539, all met Hardy-Weinberg expectations. There was little evidence of association of alleles between the loci in this database. The combined power of exclusion for the ten STR loci was 0.999981. While significant differences between the Gabon population and the Austrian Caucasian population were found at all loci, significant differences were found between the Gabon population and Zimbabweans only for D3S1358 and between the Gabon population and African Americans only for TH01 and D8S1179.

Keywords Gabon · DNA · Short tandem repeats · Population study · Forensic science

Introduction

A population study was carried out on unrelated Black African individuals from Gabon to determine allele and genotype frequencies for forensic purposes. In the current study, population data were obtained for the ten STR loci included in the AmpF*l*STR SGM Plus kit (Perkin Elmer, Foster City, Calif.). A subset of these loci are the PCR-based markers recommended as DNA databasing standards by Interpol (ISSOL – Interpol standard set of loci), FBI (CODIS – Combined DNA Index System) and ENFSI (ESS – European standard set of loci). This paper presents allele frequency data in Black Africans from Gabon for the STR loci D3S1358, VWA, D16S539, D2S1338, D8S1179, D21S11, D18S51, D19S433, TH01 and FGA. The data can be employed to provide estimates of the frequency of a DNA profile in human identity testing, particularly in Gabon.

Material and methods

Blood samples were taken from Gabon Black Africans. The population sample had previously been collected for other investigations and 108 unrelated individuals were included in this study. Genomic DNA was extracted as described by Kraft et al. [1] and amplification was carried out using 2 ng of template DNA applying the AmpF*l*STR SGM plus systems kit (Perkin Elmer) in a Perkin Elmer 9600 thermal cycler, according to the manufacturer's recommendations and products were loaded on the CE310 Genetic Analyser (ABI) using Genescan-500 ROX (Perkin Elmer) as internal lane standard. GeneScan analysis was performed on the raw data and alleles were labelled according to the international nomenclature [2] using the Genotyper Software package (Perkin Elmer).

Allele frequencies were calculated from the numbers of each genotype obtained in the sample set. Statistical evaluations (Unbiased estimates of expected heterozygosity, unbiased estimate of the expected homozygote and heterozygote frequencies, exact test, interclass criterion for detecting disequilibrium between loci, power of exclusion, power of discrimination, R × C contingency table test) were facilitated using a computer program kindly provided by Bruce Budowle (FBI Academy, Quantico, Va.) and DNAVIEW software designed by Charles Brenner (Berkeley, Calif.) as described previously [3].

Results and discussion

Allele frequencies of the ten STR loci investigated are shown in Table 1. All loci are highly polymorphic. The observed heterozygosities range from 66.3% for the D3S1358 locus to 93.1% for the FGA locus.

Based on the results of the exact test, the loci D21S11, TH01 and D16S539 showed departures from Hardy-Weinberg expectations (Table 1). After employing a Bonferroni correction [4] for the number of loci analysed, these observations are not likely to be significant.

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Table 1 Observed allele frequencies and summary of statistical analysis for the 10 STR loci in 108 unrelated Gabon black individuals (*HO* observed homozygosity, *HE* expected homozygosity, *E* exact test probability values, *PD* power of discrimination, *PE* probability of exclusion)

Allele	D21S11	D18S51	TH01	D8S1179	VWA	FGA	D3S1358	D16S539	D2S1338	D19S433
5	–	–	–	–	–	–	–	0.009	–	–
6	–	–	0.093	–	–	–	–	–	–	–
7	–	–	0.389	–	–	–	–	–	–	–
8	–	–	0.319	–	–	–	–	0.032	–	–
9	–	–	0.134	–	–	–	–	0.278	–	0.009
9.3	–	–	0.051	–	–	–	–	–	–	–
10	–	–	0.014	–	–	–	–	0.144	–	0.037
11	–	0.005	–	0.056	0.014	–	–	0.255	–	0.116
12	–	0.014	–	0.139	–	–	0.005	0.134	–	0.088
12.2	–	0.005	–	–	–	–	–	–	–	0.055
13	–	0.018	–	0.143	0.023	–	0.005	0.139	–	0.241
13.2	–	0.005	–	–	–	–	–	–	–	0.088
14	–	0.042	–	0.347	0.079	–	0.088	0.009	–	0.166
14.2	–	–	–	–	–	–	–	–	–	0.065
15	–	0.157	–	0.241	0.217	–	0.342	–	0.019	0.028
15.2	–	–	–	–	–	–	–	–	–	0.069
16	–	0.194	–	0.074	0.255	–	0.310	–	0.069	0.005
16.2	–	–	–	–	–	–	–	–	–	0.028
17	–	0.227	–	–	0.157	0.014	0.208	–	0.093	–
17.2	–	–	–	–	–	–	–	–	–	0.005
18	–	0.153	–	–	0.176	0.014	0.042	–	0.102	–
18.2	–	–	–	–	–	0.014	–	–	–	–
19	–	0.092	–	–	0.060	0.055	–	–	0.176	–
19.2	–	–	–	–	–	0.005	–	–	–	–
20	–	0.051	–	–	0.014	0.060	–	–	0.130	–
21	–	0.023	–	–	0.005	0.106	–	–	0.083	–
21.2	–	–	–	–	–	0.005	–	–	–	–
22	–	0.009	–	–	–	0.129	–	–	0.097	–
23	–	–	–	–	–	0.171	–	–	0.060	–
24	–	0.005	–	–	–	0.190	–	–	0.065	–
25	–	–	–	–	–	0.157	–	–	0.079	–
26	–	–	–	–	–	0.037	–	–	0.028	–
27	0.093	–	–	–	–	0.028	–	–	–	–
28	0.264	–	–	–	–	0.005	–	–	–	–
29	0.162	–	–	–	–	–	–	–	–	–
30	0.171	–	–	–	–	–	–	–	–	–
30.2	0.009	–	–	–	–	–	–	–	–	–
31	0.097	–	–	–	–	–	–	–	–	–
31.2	0.042	–	–	–	–	0.005	–	–	–	–
32	0.018	–	–	–	–	–	–	–	–	–
32.1	0.009	–	–	–	–	–	–	–	–	–
32.2	0.032	–	–	–	–	–	–	–	–	–
33	0.009	–	–	–	–	–	–	–	–	–
33.1	0.014	–	–	–	–	–	–	–	–	–
33.2	0.014	–	–	–	–	–	–	–	–	–
34	0.014	–	–	–	–	–	–	–	–	–
35	0.042	–	–	–	–	–	–	–	–	–
35.1	0.005	–	–	–	–	–	–	–	–	–
35.2	0.005	–	–	–	–	–	–	–	–	–
44	–	–	–	–	–	0.005	–	–	–	–
HO	0.130	0.176	0.269	0.241	0.148	0.074	0.324	0.287	0.083	0.083
HE	0.145	0.148	0.279	0.223	0.175	0.124	0.263	0.197	0.099	0.126
E	0.044	0.782	0.017	0.428	0.661	0.915	0.731	0.022	0.517	0.160
PD[a]	0.947	0.955	0.854	0.912	0.934	0.962	0.888	0.926	0.973	0.961
PD[b]	0.962	0.959	0.874	0.916	0.944	0.971	0.883	0.930	0.980	0.971
PE	0.709	0.699	0.481	0.567	0.646	0.744	0.495	0.605	0.791	0.744

[a] PD calculated using observed data

[b] PD calculated using expected data

Table 2 G statistic test (probability values) for homogeneity allele distributions at four (Gabon population – Zimbabwean black population[a]), eight (Gabon population – African Americans[b]) and ten (Gabon population – Austrian Caucasians[c]) STR loci between a Gabon population, Zimbabwean Blacks, African Americans and Austrian Caucasians, respectively

Populations compared	Locus									
	D21S11	D18S51	TH01	D8S1179	VWA	FGA	D3S1358	D16S539	D2S1338	D19S433
Gabon/Zimbabwean Blacks	–[d]	–[d]	0.589	–[d]	0.628	0.593	$< 10^{-3}$	–[d]	–[d]	–[d]
Gabon/African Americans	0.070	0.112	0.005	0.008	0.288	0.063	0.640	0.073	–[d]	–[d]
Gabon/Austrian Caucasians	$< 10^{-3}$	$< 10^{-3}$	$< 10^{-3}$	$< 10^{-3}$	$< 10^{-3}$	0.001	$< 10^{-3}$	$< 10^{-3}$	$< 10^{-3}$	$< 10^{-3}$

[a] Data from Budowle et al. [5]
[b] Data from Budowle et al. [6]
[c] Data from Steinlechner et al. [3]
[d] No data available

Pair-wise interclass correlation tests were performed for all possible two-locus combinations and 2 deviations were detected in 45 pair-wise comparisons (i.e. D18S51/VWA, $P = 0.015$ and D2S1338/D16S539, $P = 0.017$), which is well within expectations.

The PD and PE for this Gabon Black African population sample are listed in Table 1.

The Gabon population allele frequencies for the loci TH01, VWA, FGA and D3S1358 were compared with Zimbabwean Black population data [5], the population groups differed at the D3S1358 locus (Table 2).

The allele frequencies for each locus (except D2S1338 and D19S433) of the Black African population data from Gabon were compared with African American data [6] (Table 2). The population groups were statistically similar at six out of eight loci compared. The population groups differed at the TH01 and D8S1179 loci.

Significant differences between an Austrian Caucasian population sample [3] and the Gabon population sample were found at each of the ten STRs (Table 2).

In conclusion, the use of the AmpF*l*STR SGM plus PCR system offers a highly polymorphic tool for human identity testing in the Gabon Black population.

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