

Announcement of population data  
STR data from S. Tomé e Príncipe  
(Gulf of Guinea, West Africa)

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**Abstract**

Allele frequencies for eight STRs (CD4, FES/FPS, MBPB, TH01, TP53, TPO, F13A1, VWA) were estimated from samples (sized between 279 and 328) of unrelated individuals born in S. Tomé e Príncipe (Gulf of Guinea, West Africa). © 2001 Elsevier Science Ireland Ltd. All rights reserved.

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Population	Unrelated healthy individuals from S. Tomé e Príncipe
Extraction	Chelex extraction according to Lareu et al. [1]
PCR	Target DNA (5 ng) following the conditions described by Silva et al. [2]
Typing	Polyacrylamide gel electrophoresis, visualization by silver staining and typing using home-made reference sequenced ladders
Quality control	Proficiency testing of the GEP-ISFG WG ( <a href="http://www.gep.usc.es">http://www.gep.usc.es</a> )
Results	See Table 1
Analysis of data	GENEPOP [3]; expected heterozygosity according to Nei [4]
Access to the data	<a href="http://www.ipatimup.pt/STR">http://www.ipatimup.pt/STR</a>
Other remarks	Comparisons between allele frequencies estimated in our sample and those reported for USA African Americans [5,6] revealed significant differences for all STRs except for VWA (MBPB and TP53 were not tested since no published data were available)

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Table 1  
Allele frequencies for eight STR loci in S. Tomé e Príncipe

Allele <sup>a</sup>	CD4 N: 324	FES/FPS N: 321	MBPB N: 321	TH01 N: 327	TP53 N: 325	TPO N: 328	F13A1 N: 279	VWA N: 328
3.2							0.109	
4					0.004		0.054	
5	0.253				0.078		0.389	
6	0.136			0.098	0.034	0.064	0.120	
7	0.020	0.039	0.040	0.349	0.340	0.040	0.170	
8	0.142	0.107	0.005	0.332	0.300	0.354	0.051	
9	0.031	0.045	0.100	0.157	0.140	0.216	0.002	
9.3				0.053				
10	0.107	0.226	0.229	0.011	0.032	0.087		
11	0.193	0.360	0.523		0.031	0.212	0.006	0.002
12	0.049	0.187	0.070		0.037	0.027	0.007	
13	0.049	0.030	0.033		0.002		0.059	0.017
14	0.015	0.006			0.002		0.023	0.060
15	0.005						0.006	0.204
16							0.004	0.285
17								0.186
18								0.175
19								0.050
20								0.021
Ho	0.886	0.754	0.651	0.749	0.765	0.726	0.771	0.805
He	0.844	0.770	0.657	0.732	0.765	0.770	0.785	0.806
PD	0.957	0.914	0.842	0.883	0.911	0.913	0.931	0.935
CE	0.670	0.542	0.416	0.477	0.539	0.542	0.588	0.596
P <sup>b</sup>	0.343	0.500	0.536	0.777	0.549	0.176	0.046	0.677

<sup>a</sup> Ho: observed heterozygosity; He: expected heterozygosity; PD: power of discrimination; CE: a priori chance of exclusion.

<sup>b</sup> Hardy–Weinberg equilibrium, exact test probability based on 2000 shufflings standard error <0.01.

Genetic diversity parameters for all loci were consistently higher than the registered for Caucasian populations.

In contrast with the findings in Cabo Verde [7] no evidence of significant Caucasian admixture was detected in S. Tomé e Príncipe.

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