

## FOR THE RECORD

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# Angola Population Data with AmpF $\ell$ STR™ Profiler Plus

**POPULATION:** West Africa population sample ( $n = 116$ ) from Angola

**KEYWORDS:** forensic science, DNA typing, population genetics, West Africa, short tandem repeats, polymerase chain reaction, Profiler Plus, D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820

Blood stains from 116 unrelated individuals from Angola (West Africa) were stored using bloodstain card and extracted with the standard Chelex method. PCR amplification was performed in a GeneAmp® PCR System 9600, using the AmpF $\ell$ STR® Profiler Plus™ Amplification Kit, according to the manufacturer's recommendations. Electrophoresis of the PCR products was carried out in an ABI Prism™ 377 DNA Sequencer, using 5% denaturing Long Ranger® gels. Sample genotypes were determined with Genotyper® (version 2.0), by comparison with supplied allelic ladders and an internal size standard (GS-500Rox).

*Analysis of data*—Allele frequency distribution data for this West African population from Angola is presented in Table 1. Based on  $\chi^2$  test, the nine loci meet HWE expectations ( $p > 0.05$ ). Statistical forensic parameters were calculated—minimum allele frequency, heterozygosity, power of discrimination and probability of exclusion (1–4). Genetic diversity parameters for almost all loci were consistently higher than those reported for Portuguese Caucasian population (5). The combined values for power of discrimination and probability of exclusion were, respectively, PD = 0.999999999942 and PE = 0.999905.

High genetic variability was observed in this West Africa population due to high polymorphism and rare alleles. Several uncommon alleles have been detected: allele 11 in vWA; allele 8 in D8S1179; alleles 33.1, 37 and 38 in D21S11; allele 14.2 in D18S51 and allele 7 in D5S818 and D7S820. In all loci alleles with lower frequency than minimum allele frequency was observed. Rare alleles have also been noticed in several loci: FGA-allele 31.2 and D21S11-allele 29.1.

Comparing with other reported data of African populations (6–8), significant differences were detected in D3S1358, vWA and D21S11, namely the non-presence of small alleles in D3S1358 and the highest prevalence of allele 17 and allele 30 in vWA and D21S11, respectively.

Quality control: Proficiency testings of GEP-ISFG and ESWG-ISFG.

*Access to data*—Data can be accessed from the correspondent author at biblioteca.dlinml@oninet.pt.

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TABLE 1—Allele frequency distribution data for AmpF $\ell$ STR Profiler Plus loci in a West Africa population from Angola (n=116).

	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820
7							0.0043		0.0129
8				0.0043			0.0474	0.0690	0.2198
9				0.0086		0.0043	0.0129	0.0216	0.1164
10				0.0560		0.0043	0.0474	0.0560	0.2802
11		0.0086		0.0991		0.0043	0.2586	0.3319	0.2198
12		...		0.1336		0.0690	0.3578	0.3362	0.1250
13	0.0043	0.0086		0.2285		0.0862	0.2543	0.1509	0.0216
14	0.0948	0.1250		0.2759		0.1078	0.0172	0.0345	0.0043
14.2						0.0043			
15	0.2716	0.1422		0.1466		0.1379			
16	0.2802	0.1983		0.0388		0.1724			
17	0.2371	0.2328		0.0086		0.1380			
18	0.1077	0.1897	0.0086			0.1207			
18.2			0.0216						
19	0.0043	0.0776	0.0690			0.0862			
19.2			0.0043						
20		0.0172	0.0733			0.0388			
21			0.1164			0.0216			
21.2			0.0043						
22			0.1983			0.0043			
23			0.1509						
23.2			0.0086						
24			0.1724						
24.2			...		0.0043				
25			0.0991		...				
26			0.0474		...				
27			0.0172		0.0620				
28			0.0043		0.1293				
29					0.1767				
29.1					0.0043				
30					0.2371				
30.2					0.0388				
31					0.0560				
31.2			0.0043		0.1035				
32					0.0216				
32.2					0.0812				
33.1					0.0043				
33.2					0.0345				
34					0.0129				
35					0.0086				
36					0.0086				
37					0.0043				
38					0.0043				
Mfreq	0.0235	0.0251	0.0265	0.0248	0.0264	0.0271	0.0227	0.0229	0.0241
H	0.7742	0.8317	0.8752	0.8212	0.8707	0.8881	0.7386	0.7477	0.7984
PD	0.9099	0.9474	0.9678	0.9429	0.9692	0.9753	0.8850	0.8948	0.9272
PE	0.5518	0.6566	0.7421	0.6421	0.7374	0.7656	0.4998	0.5230	0.5467

Mfreq: minimum allele frequency; H: heterozygosity; PD: power of discrimination; PE: probability of exclusion.