

FOR THE RECORD

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Allele Frequencies for the AmpF ℓ STR Profiler Loci in a Colombian Population (Department of Boyaca)

POPULATION: Department of Boyaca, Colombia ($n = 183$)

KEYWORDS: forensic science, DNA typing, short tandem repeat, population genetics, Colombia

Whole blood samples were obtained in the genetics laboratory of the UIS (Universidad Industrial de Santander) and Boyaca Regional ICBF (Instituto Colombiano de Bienestar Familiar) from 183 unrelated Colombian donors (Department of Boyaca). Genomic DNA was extracted using the salting out procedure. PCR amplification was performed using the AmpF ℓ STR Profiler amplification kit (PE-Biosystems, Foster City, CA) following manufacturer's instructions. The amplified products were separated and detected using the ABI 310 DNA sequencer (PE-Biosystems,

Foster City, CA). Alleles were classified according to the recommendations of the ISFH (1). Statistical analysis was performed as previously reported (2). The complete data set is available to any interested researcher upon request from the corresponding author, Oscar Garcia, Ph.D.

References

1. DNA recommendations. Report concerning further recommendations of the DNA Commission of the ISFH regarding PCR-based polymorphism in STR (short tandem repeat) system. Int J Legal Med 1994;107:159–60.
2. Yunis JJ, Garcia O, Baena A, Arboleda G, Uriarte I, Yunis E. Population frequency for the short tandem repeat loci D18S849, D3S1744, and D12S1090 in Caucasian-Mestizo and African descent populations of Colombia. J Forensic Sci 2000;45(2):429–31.

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TABLE 1—Allele frequencies for the AmpF ℓ STR Profiler loci in a Colombian population.

Allele	D3S1358	VWA	FGA	TH01	TPOX	CSF1PO	D5S818	D13S317	D7S820
6				0.4098	0.0027				
7				0.2322		0.0055	0.0464		0.0164
8				0.0683	0.5082	0.0055		0.0765	0.1120
9				0.1011	0.0301	0.0328	0.0956	0.1612	0.0546
9.3				0.1721					
10				0.0164	0.0628	0.2705	0.0437	0.0902	0.2678
11					0.2623	0.2869	0.4262	0.1858	0.2896
12					0.1175	0.3279	0.2377	0.2978	0.2131
13	0.0027	0.0082			0.0164	0.0683	0.1366	0.1066	0.0328
14	0.0820	0.0519				0.0027	0.0137	0.0820	0.0109
15	0.3552	0.0683							0.0027
16	0.2732	0.3279							
17	0.1448	0.3169	0.0082						
18	0.1311	0.1639	0.0055						
19	0.0109	0.0519	0.0574						
20		0.0082	0.1120						
20.2			0.0027						
21		0.0027	0.1066						
22			0.1148						
23			0.1120						
24			0.1230						
25			0.1721						
26			0.1448						
27			0.0328						
28			0.0082						
H	0.7213	0.7705	0.8962	0.7158	0.6393	0.7596	0.6995	0.8525	0.7650
PD	0.9015	0.8901	0.9678	0.8844	0.8252	0.8698	0.8835	0.9428	0.9225
CE	0.4620	0.5455	0.7876	0.4532	0.3408	0.5263	0.4274	0.6997	0.5358
P*	0.5200	0.0790	0.2495	0.8010	0.3305	0.1130	0.2855	0.4085	0.9825
P**	0.4680	0.1375	0.1525	0.7285	0.1150	0.1215	0.1745	0.6020	0.9780

H (observed heterozygosity), PD (Power of discrimination), CE (a priori chance of exclusion), P* (Hardy-Weinberg equilibrium, chi square test), P** (Hardy-Weinberg equilibrium, exact test based on 2000 shufflings).