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FOR THE RECORD

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Genetic Variation for 7 STR Loci in a Colombian Population (Department of Valle del Cauca)

POPULATION: Department of Valle del Cauca, Colombia (n = 81–461).

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

Whole blood samples were obtained from 81–461 unrelated Colombian individuals from the parentage testing routinely done at the Laboratory of Immunology and Immunogenetics, Hospital Universitario del Valle in Cali, Colombia, previous informed consent. Genomic DNA was extracted from 1 mL of EDTA anticoagulated peripheral blood using the salting-out methodology. After DNA quantitation by spectrophotometry, 1–2 ng of DNA were amplified using the commercial kits AmpFℓSTR Cofiler (PE Biosystems, Foster City, CA), Geneprint Fluorescent STR Multiplex F13A01, FES/FPS, F13B, LPL (FFFL) and PowerPlex 16 (Promega Corporation, Madison, WI), following the 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 using the GDA program (2). Statistical parameters such as power of discrimination (PD) and a priori chance of exclusion (CE) for each loci were estimated as described by Huston (3). Also we calculated the polymorphic information content (PIC) according to Botstein et al. (4). The Hardy-Weinberg equilibrium for each loci and linkage disequilibrium were verified using the GDA program. We did not find significant deviation from Hardy-Weinberg equilibrium at all loci. The complete data set is available to any interested researcher upon request from the corresponding author.

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TABLE 1—*Allelle frequencies for 7 STR loci in a Colombian population (Valle del Cauca).*

Allele	Penta E	Penta D	D16S539	LPL	F13A01	F13B	FES/FPS
2.2		0.0200					
3.2					0.2530		
4					0.0783		
5	0.0492	0.0108	0.0033		0.2470		
6	0.0015	0.0031			0.1506	0.0542	
7	0.0815	0.0046			0.2349	0.0482	
8	0.0538	0.0354	0.0119		0.0241	0.1265	0.0361
9	0.0169	0.1800	0.1540	0.0309		0.3072	0.0060
10	0.0569	0.2015	0.1584	0.5062	0.0060	0.4639	0.1807
11	0.0708	0.1908	0.2625	0.2407			0.4819
12	0.1692	0.1292	0.2679	0.1296			0.2289
13	0.0985	0.1385	0.1150	0.0864			0.0663
14	0.0769	0.0600	0.0271	0.0062	0.0060		
15	0.0954	0.0123					
16	0.0646	0.0077					
17	0.0415	0.0015					
18	0.0215	0.0046					
19	0.0308						
20	0.0354						
21	0.0231						
22	0.0077						
23	0.0046						
N	325	325	461	81	83	83	83
H	0.9231	0.8677	0.7722	0.6420	0.8193	0.6747	0.5783
PD	0.9837	0.9566	0.9293	0.8255	0.9160	0.8257	0.8454
CE	0.8428	0.7300	0.5486	0.3443	0.6353	0.3902	0.2657
PIC	0.9112	0.8310	0.7663	0.6147	0.7578	0.6152	0.6304
p	0.5428	0.9438	0.3306	0.4625	0.3897	0.1897	0.1816

N (sample size). H (observed heterozygosity). PD (power of discrimination). CE (probability of paternity exclusion). PIC (polymorphic information content). *p* (Hardy-Weinberg equilibrium. Fisher's exact test based on 2000 shufflings).