FOR THE RECORD

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Genetic Variation for 15 Short Tandem Repeat Loci in an El Salvadoran (Central America) Population

POPULATION: El Salvador ($n = 294$–296).

Blood samples were obtained from 294 to 296 unrelated El Salvadoran individuals in whom previous informed consent was obtained. Genomic DNA was extracted using the organic phenol–chloroform–isoamyl alcohol method. Amplification was performed using the commercial kit 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).

The statistical evaluation was carried out with the aid of GDA and PowerStats software packages (2,3). Statistical parameters such as power of discrimination (PD) and *a priori* chance of exclusion (CE) for each loci were estimated as described by Huston (4). Also, we calculated the polymorphic information content (PIC) according to Botstein et al (5). Minimum allele frequencies (MAF) for polymerase chain reaction (PCR)-based loci, based on statistical and population genetics theory (6) were determined. Thus, a greater confidence of the DNA profile frequency estimates can be attained with current size databases. 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. There is a little evidence for departures from independence in the population analyzed (data not shown) (Table 1).

TABLE 1—*Allele frequencies for 15 STR loci in an El Salvadoran population.*

Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	D16S539	TH01	TPOX	CSF1PO	Penta D	Penta E
2.2														0.0085	
5														0.0034	0.0287
6											0.4088	0.0084			0.0017
7							0.0574		0.0169		0.2601	0.0051	0.0135	0.0085	0.0642
8				0.0034			0.0017	0.0676	0.0878	0.0101	0.0760	0.4814	0.0034	0.0186	0.0270
9				0.0051			0.0642	0.1976	0.0608	0.1284	0.0963	0.0625	0.0236	0.2288	0.0051
9.3											0.1520				
10				0.0557		0.0068	0.0591	0.1081	0.2872	0.2196	0.0068	0.0372	0.2213	0.2288	0.0338
11				0.0608		0.0051	0.4747	0.1993	0.2787	0.2720		0.2314	0.2821	0.1475	0.0591
12	0.0034			0.1385		0.1047	0.2551	0.1959	0.2196	0.2652		0.1672	0.3767	0.1288	0.2111
13	0.0051	0.0017		0.3243		0.0946	0.0794	0.1182	0.0389	0.0895		0.0051	0.0743	0.1525	0.0760
14	0.0765	0.0492		0.2635		0.1622	0.0084	0.1115	0.0101	0.0118		0.0017	0.0051	0.0542	0.0878
15	0.4286	0.0847		0.1166		0.1486		0.0017		0.0034				0.0169	0.1132
16	0.2568	0.3695		0.0304		0.1554								0.0034	0.0845
17	0.1412	0.3034	0.0034	0.0017		0.1368									0.0422
18	0.0850	0.1407	0.0068			0.0861									0.0338
19	0.0034	0.0339	0.0895			0.0541									0.0338
20		0.0169	0.0625			0.0236									0.0422
21			0.0845			0.0068									0.0422

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TABLE 1— *Continued.*

Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	D16S539	TH01	TPOX	CSF1PO	Penta D	Penta E
22			0.1250			0.0101									0.0034
22.2			0.0017												
23			0.1351			0.0017									0.0084
23.2			0.0017												
24			0.1655			0.0034									0.0017
24.2					0.0017										
25			0.1706												
25.2					0.0017										
26			0.1081		0.0017										
27			0.0321		0.0167										
28			0.0101		0.0861										
29			0.0017		0.2365										
29.2					0.0034										
30			0.0017		0.2500										
30.2					0.0068										
31					0.0456										
31.2					0.1047										
32					0.0118										
32.2					0.1368										
33					0.0017										
33.2					0.0676										
34					0.0017										
34.2					0.0118										
35					0.0051										
35.2					0.0051										
36					0.0034										
n	294	295	296	296	296	296	296	296	296	296	296	296	296	295	296
MAF	0.0095	0.0094	0.0107	0.0098	0.0100	0.0110	0.0095	0.0103	0.0100	0.0103	0.0096	0.0089	0.0093	0.0104	0.0111
H	0.7177	0.7051	0.8682	0.7669	0.7939	0.8885	0.7264	0.8277	0.7939	0.8277	0.7399	0.6115	0.6892	0.8339	0.8986
PD	0.8723	0.8923	0.9701	0.9253	0.9565	0.9690	0.8568	0.9539	0.9123	0.9115	0.8840	0.8571	0.8767	0.9452	0.9812
CE	0.4562	0.4362	0.7311	0.5391	0.5878	0.7720	0.4702	0.6514	0.5878	0.6514	0.4926	0.3049	0.4117	0.6634	0.7927
PIC	0.6760	0.7009	0.8651	0.7550	0.8182	0.8651	0.6528	0.8197	0.7444	0.7486	0.6857	0.6371	0.6756	0.8078	0.8970
p	0.4740	0.9595	0.0805	0.4775	0.8390	0.4455	0.5860	0.5955	0.2055	0.4635	0.9745	0.0905	0.1385	0.0995	0.2735

n, sample size; MAF, minimum allele frequency; *H*, observed heterozigosity; PD, power of discrimination; CE, probability of paternity exclusion; PIC, polymorphic information content; *p*, Hardy–Weinberg equilibrium, χ^2 exact test based on 2,000 shufflings; STR, short tandem repeat.

The complete data set is available to any interested researcher upon request from the corresponding author.

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