

FOR THE RECORD

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Allele Frequencies for Markers CSF1PO, TPOX, TH01, F13A01, FESFPS, vWA, D16S539, D7S820, D13S317 in the General Population of Nicaragua

POPULATION: General Hispanic-admixed individuals from Nicaragua

KEYWORDS: forensic science, DNA typing, polymerase chain reaction, short tandem repeats, Nicaragua

Blood samples were collected in vacutainer tubes containing EDTA from 111 unrelated healthy volunteer blood donors at the blood bank of the Red Cross in Nicaragua. DNA was extracted by Chelex 100 method (1) and stored at -20°C until analyzed.

DNA typing was carried out according to the manufacturer's recommendations using Promega Corporation GenePrint[®] STR Systems (i.e., Silver Stain Detection kits) to analyze the following loci: CSF1PO, TPOX, TH01, F13A01, FESFPS, vWA, D16S539, D7S820 and D13S317 (2). Five nanograms of DNA were used in each PCR. PAGE and silver staining for STRs were performed according to the manufacturer's recommendations.

Assignment of alleles was made by visual comparison with commercially supplied reference allelic ladders. The allele frequencies, power of discrimination, power of exclusion, and paternity index of the nine STR loci were calculated using the program Powerstats (3). Hardy-Weinberg equilibrium (4) and observed and expected heterozygosity were estimated using the program Genetic Data Analysis (5).

No deviation from Hardy-Weinberg equilibrium was observed, except for the F13A01 locus ($p = 0.002$). This deviation could be due to population substructure at this locus, chance departures, or to allele drop out of large sized alleles. The joint power of discrimination (PD) for the loci studied is 0.999, the joint power of exclusion (CE) is 0.996 and the combined paternity index (TPI) is 403.23. This collection will undergo future updates.

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The complete dataset is available to any interested party upon request to the corresponding author.

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TABLE 1—Allele frequencies for the loci CSF1PO, TPOX, TH01, F13A01, FESFPS, vWA, D16S539, D7S820, D13S317 in a Nicaraguan sample population*.

Allele	CSF1PO	TPOX	TH01	F13A01	FESFPS	vWA	D16S539	D7S820	D13S317
3.2				0.288					
4				0.090					
5				0.198					
6		0.005	0.351	0.140					
7	0.009	0.005	0.293	0.221				0.014	
8	0.005	0.459	0.068	0.059	0.018		0.036	0.072	0.063
9	0.023	0.122	0.095	0.005			0.171	0.068	0.198
9.3			0.113						
10	0.270	0.050	0.072		0.140		0.243	0.275	0.113
11	0.293	0.302	0.009		0.450		0.252	0.311	0.239
12	0.333	0.059			0.257	0.005	0.185	0.194	0.207
13	0.059				0.095	0.009	0.095	0.059	0.099
14	0.009				0.041	0.041	0.018	0.009	0.081
15						0.162			
16						0.405			
17						0.230			
18						0.108			
19						0.027			
20						0.009			
21						0.005			
Hex	0.729	0.677	0.762	0.798	0.703	0.746	0.806	0.781	0.831
Hob	0.720	0.711	0.792	0.684	0.684	0.783	0.747	0.729	0.810
PD	0.870	0.817	0.887	0.923	0.854	0.882	0.927	0.919	0.947
PE	0.461	0.432	0.586	0.419	0.405	0.553	0.506	0.476	0.619
p	0.119	0.051	0.146	0.002	0.120	0.325	0.071	0.361	0.704
PI	1.79	1.68	2.41	1.63	1.59	2.22	1.98	1.85	2.64

* Hex: expected heterozygosity; Hob: observed heterozygosity; PD: power of discrimination; PE: power of exclusion; p: Hardy-Weinberg equilibrium (exact test based on 3,200 shufflings); PI: paternity index.