

FOR THE RECORD

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Population Data on 15 STR Loci (PowerPlex 16™ Kit) in a Costa Rica (Central America) Sample Population

POPULATION: Costa Rica, Central America

KEYWORDS: forensic science, DNA typing, population genetics, Costa Rica, Central America

Blood samples were obtained by venipuncture from unrelated individuals ($n = 253\text{--}279$) living in Costa Rica. Approximately 1 ng of DNA were used in each amplification. The samples were amplified using the Powerplex 16™ kit (Promega) and the alleles were separated and detected using an Applied Biosystems ABI310 genetic analyzer.

The frequency of each allele for each locus was calculated from the numbers of each genotype in the sample set (i.e., the gene count method). Unbiased estimates of expected heterozygosity were computed as described by Edwards et al. (1). Possible divergence from Hardy-Weinberg expectations (HWE) was tested by calculating the unbiased estimate of the expected homozygote/heterozygote frequencies (1–4) and the exact test (5), based on 2000 shufflings

experiments. An interclass correlation criterion (6) for two-locus associations was used for detecting disequilibrium between the STR loci. The program for this analysis was kindly provided by R. Chakraborty (University of Texas, School of Biomedical Sciences, Houston Texas).

The distributions of the observed allele frequencies for the 15 STR loci are shown in Table 1. The most informative loci are Penta E and D18S51, and the least discriminating are TPOX and CSF1PO. The 15 loci meet Hardy-Weinberg expectations. There is little evidence for association of alleles between pairs of the 15 loci. Only four (D8S1179/D5S818; $p = 0.028$; TPOX/FGA; $p = 0.045$; FGA/TH01; $p = 0.026$; D5S818/D16S539; $p = 0.010$) of 105 pairwise comparisons demonstrated a departure from expectations of independence. This number of departures is within expectations of departure by chance and these four departures are not significant after correction for sampling (i.e., Bonferroni (7)). The combined power of discrimination is >0.99999999 , and the combined power of exclusion is 0.99999967.

The complete data are available by accessing <http://www.gitad.org/poblaciones>.

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TABLE 1—Observed allele frequencies for the 15 PowerPlex™ loci.

Allele	D3S1358	TH01	D21S11	D18S51	PENTA E	D5S818	D13S317
2.2							
5		0.00368			0.03360		
6		0.30331					
7		0.22426			0.14032	0.02347	
8		0.09375			0.02569	0.01444	0.10252
9		0.16176			0.00791	0.09747	0.15647
9.3		0.20956					
10	0.00179	0.00368		0.01832	0.04743	0.03610	0.07374
11				0.01832	0.11462	0.38989	0.21403
12				0.08059	0.15810	0.31769	0.26978
13	0.00538			0.11905	0.09289	0.11372	0.11331
14	0.11290			0.16850	0.09881	0.00722	0.06835
15	0.30466			0.13370	0.10474		0.00180

TABLE 1—Continued.

Allele	D3S1358	TH01	D21S11	D18S51	PENTA E	D5S818	D13S317	
16	0.25627			0.13553	0.02569			
17	0.17921			0.13187	0.03360			
18	0.13262			0.08242	0.03162			
19	0.00717			0.04945	0.02964			
20				0.03114	0.02372			
21				0.01099	0.01581			
22				0.01282	0.01383			
23				0.00183	0.00198			
24			0.00183	0.00366				
24.2			0.00366					
25				0.00183				
25.2			0.00366					
26			0.00366					
27			0.02747					
28			0.08974					
29			0.19963					
29.2			0.00366					
30			0.29121					
30.2			0.00549					
31			0.06227					
31.2			0.08425					
32			0.01465					
32.2			0.14103					
33			0.00183					
33.2			0.05495					
34			0.00183					
35			0.00183					
35.2			0.00183					
36			0.00549					
Homozygosity Test*	0.495	0.290	0.584	0.404	0.184	0.383	0.833	
Exact Test**	0.370	0.559	0.822	0.384	0.057	0.905	0.450	
PD	0.91561003	0.91481942	0.95144172	0.97328557	0.97883110	0.88037118	0.94280834	
PE	0.56804391	0.56507345	0.67549430	0.76953324	0.80674228	0.49317995	0.65108883	
Allele	D7S820	D16S539	CSF1PO	PENTA D	vWA	D8S1179	TPOX	FGA
2.2				0.00735				
3.2				0.00184				
5				0.01287				
6				0.00551			0.01321	
7	0.00730		0.00538	0.00735			0.00189	
8	0.12226	0.03058	0.00896	0.02206		0.00903	0.48113	
9	0.08759	0.13849	0.01434	0.16912		0.01083	0.06792	
10	0.25000	0.19964	0.20968	0.20037		0.04693	0.03585	
11	0.30657	0.23022	0.30287	0.20037	0.00365	0.09747	0.32075	
12	0.18248	0.24640	0.38351	0.19118		0.11552	0.07736	
13	0.03832	0.12770	0.07168	0.12132	0.00182	0.31408	0.00189	
14	0.00547	0.02518	0.00358	0.04228	0.08029	0.23105		
15		0.00180		0.01471	0.15146	0.11191		
16				0.00368	0.33759	0.05957		
17					0.25000	0.00181		0.00197
18					0.11131	0.00181		0.00984
19					0.05474			0.08071
20					0.00912			0.05512
21								0.11614
22								0.11614
22.2								0.00591
23								0.15551
23.2								0.00197
24								0.21260
25								0.13976
26								0.07677
27								0.02559
28								0.00197
Homozygosity Test*	0.149	0.057	0.237	0.402	0.325	0.275	0.221	0.274
Exact Test**	0.288	0.308	0.215	0.033	0.200	0.169	0.332	0.646
PD	0.92042730	0.93685627	0.87013271	0.95204369	0.91344771	0.93232024	0.80894268	0.96717093
PE	0.58417474	0.62035246	0.46248157	0.67328325	0.57743034	0.62833192	0.40411711	0.73432389

PD = power of discrimination; PE = power of exclusion; * χ^2_{ldf} based on unbiased estimate with 2000 shufflings; ** Exact test based on 2000 shufflings.

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