

FOR THE RECORD

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Population Data of Ecuador for Fifteen STR Loci (POWERPLEX™ 16)

POPULATION: Ecuador, South America

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Blood samples were obtained by venipuncture from unrelated individuals ($n = 150$) living in Ecuador.

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 fifteen STR loci are shown in Table 1. The most informative loci are FGA and Penta E, 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 five (D3S1358/D21S11; $p = 0.032$; FGA/D8S1179; $p = 0.009$; FGA/D5S818; $p = 0.021$; D18S51/TH01; $p = 0.007$; TH01/CSF1PO; $p = 0.028$) of 105 pairwise comparisons demonstrated a departure from expectations of independence. This number of departures is within expectations of departure by chance and

these five departures are not significant after correction for sampling (i.e., Bonferroni (7)). The combined power of discrimination is >0.9999999 , and the combined power of exclusion is 0.99999937 . 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					0.01000		
6		0.30000					
7		0.34000			0.06667	0.09667	
8		0.06000			0.03000	0.02333	0.06333
9		0.07333			0.01333	0.06333	0.21333
9.3		0.21667					
10		0.01000		0.00333	0.05667	0.05667	0.10667
11	0.00333			0.01667	0.06333	0.47000	0.17333
12	0.00333			0.08333	0.15667	0.21000	0.20667
13	0.01000			0.13333	0.06667	0.07667	0.15667
14	0.08000			0.23667	0.07000		0.08000
15	0.44667			0.14000	0.14667	0.00333	
16	0.24333			0.11333	0.08000		
17	0.12667			0.14000	0.05333		
18	0.08000			0.07667	0.06333		
19	0.00667			0.03333	0.04000		
20				0.01333	0.03667		
21				0.00333	0.02333		
22				0.00333	0.01667		
23				0.00333	0.00333		
24							
25			0.00333		0.00333		
26							
27			0.00667				
28			0.06667				
29			0.18667				
29.2			0.00667				
30			0.23667				
30.2			0.03667				
31			0.07667				
31.2			0.15333				
32			0.00667				
32.2			0.13333				
33			0.00333				
33.2			0.07333				
34.2			0.00333				
35			0.00667				
35.2							
Homozygosity test*	0.612	0.834	0.820	0.014	0.092	0.879	0.872
Exact test**	0.911	0.155	0.393	0.580	0.332	0.498	0.278
PD	0.88053333	0.87813333	0.95600000	0.96311111	0.98204444	0.88800000	0.94382222
PE	0.48881837	0.50250889	0.70285973	0.71989860	0.82867494	0.50397428	0.66869408

PD = Power of discrimination.

PE = Power of exclusion.

* χ^2 Based on unbiased estimate with 2000 shufflings.

** Exact test based on 2000 shufflings.

TABLE 2—Population data of Ecuador.

Allele	D7S820	D16S539	CSF1PO	PENTA D	vWA	D8S1179	TPOX	FGA
2.2				0.01000				
5								
6	0.00333			0.00333			0.00333	
7	0.01333		0.00333	0.01000			0.00333	
8	0.06667	0.00333	0.00333	0.00667		0.01000	0.50667	
9	0.05333	0.19333	0.02667	0.18333		0.00667	0.04333	
9.3								
10	0.26333	0.20333	0.27000	0.24667		0.08333	0.04667	
11	0.34333	0.25333	0.33333	0.15333	0.00333	0.05333	0.25667	
12	0.22333	0.23333	0.30667	0.14000		0.17333	0.14000	
13	0.03000	0.10667	0.05000	0.19000	0.00333	0.32000		
14	0.00333	0.00667	0.00667	0.05000	0.04667	0.22000		
15				0.00667	0.08333	0.09667		
16					0.37000	0.03333		
17					0.32333	0.00333		0.01000
18					0.10667			0.00667
19					0.05000			0.08000
20					0.01333			0.05667
21								0.08667
21.2								
22								0.11667
22.2								
23								0.11000
23.2								0.00333
24								0.20667
25								0.18333
26								0.10000
27								0.02667
28								0.01000
29								0.00333
30								
30.2								
31								
31.2								
32								
32.2								
33.2								
Homozygosity test*	0.386	0.987	0.378	0.276	0.666	0.203	0.107	0.337
Exact test**	0.627	0.480	0.052	0.381	0.068	0.610	0.078	0.436
PD	0.90204444	0.91893333	0.84835556	0.93937778	0.87048889	0.93226667	0.82284444	0.96382222
PE	0.53330873	0.58330714	0.46531012	0.64719527	0.51403170	0.61280461	0.41087974	0.73911909

PD = Power of discrimination.

PE = Power of exclusion.

* χ^2 Based on unbiased estimate with 2000 shufflings.

** Exact test based on 2000 shufflings.