

FOR THE RECORD

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Paraguayan Population Data on the Fifteen STR Loci Included in the POWERPLEX 16™ Kit

POPULATION: Paraguay, South America

KEYWORDS: forensic science, DNA typing, population genetics, Paraguay, South America

Blood samples were obtained by venipuncture from unrelated individuals ($n = 168$) living in Paraguay.

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 FGA and Penta E, and the least discriminating are TPOX and D5S818 (Table 2). The 15 loci meet Hardy-Weinberg expectations. There is little evidence for association of alleles between pairs of the 15 loci. Only five (FGA/D18S51; $p = 0.033$; D8S1179/D13S317; $p = 0.006$; D5S818/CSF1PO; $p = 0.010$; TH01/PentaE; $p = 0.028$; CSF1PO/PentaD; $p = 0.004$) 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 >0.99999999 , and the combined power of exclusion is 0.99999944. The complete data are available by accessing <http://www.gitad.org/poblaciones>.

Acknowledgments

This study was supported by the “Fundacion M. Botin, Santander, Spain). We thank Promega Corp. for kindly providing the PowerPlex16 kit.

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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					0.03869		
6		0.28274					
7		0.27083			0.08631	0.05952	
8		0.06845			0.02083	0.00298	0.10714
9		0.12500			0.02083	0.02083	0.13393
9.3		0.24405					
10		0.00893		0.00595	0.05952	0.05655	0.06250
11				0.01786	0.10417	0.43750	0.22321
12	0.00298			0.11905	0.15179	0.30357	0.28274
13	0.00595			0.11905	0.12202	0.10714	0.11310
14	0.06250			0.26190	0.09226	0.00893	0.07738
15	0.36905			0.11607	0.12798	0.00298	
16	0.27381			0.11905	0.06845		
17	0.16964			0.13393	0.04762		
18	0.11607			0.05060	0.01488		
19				0.02381	0.00595		
20				0.02381	0.01488		
21					0.01190		
22				0.00893	0.00298		
23					0.00893		
24							
25							
26			0.00298				
27			0.00893				
28			0.11012				
29			0.19643				
29.2			0.00298				
30			0.27381				
30.2			0.03869				
31			0.03869				
31.2			0.11905				
32			0.01190				
32.2			0.12202				
33.2			0.05357				
34.2			0.00893				
35			0.00893				
35.2			0.00298				
Homozygosity test*	0.464	0.288	0.938	0.963	0.225	0.349	0.301
Exact test**	0.252	0.562	0.740	0.561	0.759	0.184	0.289
PD	0.89151077	0.89817177	0.95351474	0.95897109	0.97966270	0.86323696	0.93594104
PE	0.51483624	0.54415416	0.68506984	0.71032591	0.80853391	0.46343428	0.64294426

PD = Power discrimination.

PE = Power of exclusion.

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

** Exact test based on 2000 shufflings.

TABLE 2—Population sample in Paraguay, South America.

Allele	D7S820	D16S539	CSF1PO	PENTA D	vWA	D8S1179	TPOX	FGA
2.2				0.01190				
5								
6							0.00595	
7	0.02083		0.00298	0.00298				
8	0.12202	0.02679	0.00298	0.00298		0.01190	0.41369	
9	0.11607	0.15476	0.02679	0.18452		0.00893	0.06548	
9.3								
10	0.22619	0.11310	0.24107	0.17262		0.04167	0.03869	
11	0.25595	0.25893	0.23810	0.14583	0.00595	0.07738	0.38690	
12	0.20833	0.30655	0.41071	0.20238		0.11905	0.08929	
13	0.05060	0.11607	0.05655	0.19048		0.31845		
14		0.01786	0.02083	0.06845	0.05655	0.26190		
15		0.00595		0.01786	0.07143	0.12798		
16					0.32440	0.02976		
17					0.24405	0.00298		
18					0.22917			0.02083
19					0.06250			0.07440
20					0.00595			0.07738
21								0.17857
21.2								0.00298
22								0.15179
22.2								0.00893
23								0.10417
24								0.17560
25								0.12798
26								0.05357
27								0.02083
28								0.00298
29								
30								
30.2								
31								
31.2								
32								
32.2								
33.2								
Homozygosity test*	0.257	0.143	0.306	0.192	0.604	0.471	0.729	0.467
Exact test**	0.728	0.373	0.791	0.277	0.900	0.559	0.308	0.585
PD	0.92906746	0.92410714	0.87337018	0.94720805	0.91546202	0.92368197	0.82667234	0.96598639
PE	0.62024462	0.58835125	0.46963725	0.66195898	0.55883360	0.59971637	0.40801803	0.74098142

PD = Power discrimination.

PE = Power of exclusion.

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

** Exact test based on 2000 shufflings.