

FOR THE RECORD

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Brazilian Caucasian Population Data for 15 STR Loci (PowerPlex 16TM Kit)

POPULATION: Brazil, South America

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Blood samples were obtained by venipuncture from unrelated individuals ($n = 100$) living in Brazil. Approximately 1 ng of DNA were used in each amplification. The samples were amplified using the Powerplex 16TM 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 D5S818. The 15 loci meet Hardy-Weinberg expectations. There is little evidence for association of alleles between pairs of the 15 loci. Only six (D13S317/vWA; $p = 0.044$; D13S317/Penta D; $p = 0.016$; vWA/FGA; $p = 0.027$; TH01/D3S1358; $p = 0.035$; TPOX/CSF1PO; $p = 0.033$; D3S1358/Penta E $p = 0.033$) of 105 pairwise comparisons demonstrated a departure from expectations of independence. This number of departures is within expectations of departure by chance and these six departures are not significant after correction for sampling (i.e., Bonferroni (7)). The combined

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power of discrimination is >0.99999999 , and the combined power of exclusion is 0.9999967.

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				0.06000				
5		0.00500						
6		0.17000						
7		0.23000		0.10500	0.00500			
8		0.14000		0.03000	0.01000	0.11500		
9		0.19500		0.02000	0.03500	0.07500		
9.3		0.22500						
10		0.03500		0.02500	0.10000	0.05500	0.04000	
11				0.01000	0.17500	0.38500	0.30000	
12				0.08500	0.15500	0.34000	0.32500	
13	0.00500			0.09000	0.09500	0.14500	0.11000	
14	0.06500			0.18000	0.06500	0.02500	0.03500	
15	0.30500			0.15000	0.06500			
16	0.31000			0.13000	0.03000			
17	0.20500			0.14000	0.01000			
18	0.09500			0.05500	0.04000			
19	0.01500			0.05500	0.01500			
19.2				0.00500				
20				0.04000	0.02000			
21				0.02000	0.01000			
22				0.01000				
23				0.00500				
24					0.00500			
25								
26								
27			0.06500					
28			0.16500					
29			0.20000					
29.2								
30			0.20000					
30.2			0.04000					
31			0.05000					
31.2			0.10000					
32			0.01500					
32.2			0.09500					
33.2			0.03500					
34.2			0.01000					
35			0.01500					
35.1			0.01000					
Homozygosity test*	0.495	0.017	0.263	0.969	0.263	0.159	0.287	
Exact test**	0.362	0.041	0.715	0.473	0.764	0.017	0.630	
PD	0.89740000	0.92940000	0.96200000	0.96860000	0.97620000	0.85640000	0.91800000	
PE	0.53064161	0.61603724	0.72804410	0.76701342	0.79647518	0.47093924	0.56613593	
Allele	D7S820	D16S539	CSF1PO	PENTA D	vWA	D8S1179	TPOX	FGA
2.2				0.01500				
5								
6						0.00500		
7	0.01000		0.03000					
8	0.16500	0.02000	0.00500	0.05000		0.00500	0.51500	
9	0.11000	0.16000	0.02500	0.15000		0.00500	0.10500	
9.3								
10	0.26500	0.07000	0.21500	0.16000		0.10500	0.07000	
11	0.24500	0.32000	0.35000	0.19500		0.05500	0.25500	
12	0.17500	0.21500	0.30500	0.18500		0.13500	0.04500	
13	0.03000	0.19500	0.06500	0.16000	0.01000	0.25500	0.00500	
14		0.01500		0.06000	0.07000	0.25000		
15		0.00500	0.00500	0.02000	0.18500	0.17000		
16					0.25500	0.02000		
17					0.28000		0.00500	
18					0.14500			
18.2					0.05000		0.00500	
19					0.00500		0.07000	
20							0.14500	
21							0.14500	
21.2								
22							0.15500	
22.2							0.01000	
22.3							0.00500	
23							0.18000	
24							0.13000	

TABLE 1—Continued.

Allele	D7S820	D16S539	CSF1PO	PENTA D	vWA	D8S1179	TPOX	FGA
24.2								0.00500
25								0.10500
26								0.03000
27								0.01000
28								
29								
30								
30.2								
31								
31.2								
32								
32.2								
33.2								
Homozygosity test*	0.857	0.735	0.412	0.242	0.194	0.368	0.074	0.400
Exact test**	0.065	0.395	0.785	0.133	0.046	0.466	0.527	0.156
PD	0.91900000	0.91380000	0.88720000	0.94880000	0.90480000	0.93300000	0.81300000	0.95840000
PE	0.60128470	0.57664122	0.49523125	0.69194011	0.59566631	0.62637293	0.41488206	0.73148288

PD = power of discrimination.

PE = power of exclusion.

* χ^2_{df} based on unbiased estimate with 2000 shufflings.

** Exact test based on 2000 shufflings.