

FOR THE RECORD

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

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—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.