

Announcement of population data

Brazilian population database for the 13 STR loci of the AmpF/STR[®] Profiler Plus[™] and Cofiler[™] multiplex kits

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Abstract

Allele frequencies for the 13 STR core loci (D3S1358, VWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, CSF1PO, TPOX, THO1 and D16S539) included in the AmpF/STR[®] Profiler Plus[™] and AmpF/STR[®] Cofiler[™] kits were obtained for a sample of 700–800 genetically unrelated Brazilians. The expected performance of these loci for personal identification and paternity testing in the Brazilian population was estimated. © 2001 Elsevier Science Ireland Ltd. All rights reserved.

Keywords: STR; AmpF/STR[®] Profiler Plus[™]; AmpF/STR[®] Cofiler[™]; Population database; Brazil

Population	Unrelated healthy individuals mainly from the central, southeastern and southern regions of Brazil and to a lesser extent from the northern and northeastern region. These individuals constituted a representative sample of the typically mixed ethnicity in Brazil
Extraction	DNA was extracted and purified using the GFX Genomic Blood Kit (Amersham-Pharmacia, Uppsala, Sweden) and quantitated in agarose minigels
PCR	According to the manufacturer's instructions (AmpF/STR [®] Profiler Plus [™] and AmpF/STR [®] Cofiler [™] PCR amplification kits — PE Biosystems) using between 1 and 2 ng of template DNA
Typing	ABI377XL and reference ladders (PE Biosystems)
Results	See Table 1
Quality control	Proficiency testing of the GEP-ISFG-year 2000
Analysis of data	Genetic data analysis (GDA) [1] and GENEPOP [2] packages
Access to the data	Upon request by contacting dna@hereditas.com.br
Other remarks	Deviation from independence between loci was deemed significant ($P < 0.05$) for pairwise comparisons D8S1179/THO1, D5S818/D16S539, D13S317/FGA, FGA/VWA, D16S539/TPOX, D21S11/FGA and FGA/D16S539

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32			0.001		0.012								
32.2					0.100								
33					0.002								
33.2					0.033								
34					0.001								
34.2					0.002								
35					0.004								
36					0.001								
H_{obs}	0.762	0.795	0.859	0.831	0.836	0.897	0.709	0.786	0.802	0.783	0.797	0.671	0.722
H_{exp}	0.779	0.805	0.867	0.814	0.842	0.881	0.723	0.797	0.799	0.793	0.796	0.693	0.725
P	0.715	0.442	0.202	0.573	0.968	0.451	0.007	0.997	0.762	0.053	0.124	0.127	0.888
PD	0.916	0.934	0.967	0.941	0.957	0.973	0.877	0.931	0.929	0.926	0.926	0.858	0.874
PE	0.589	0.634	0.741	0.653	0.702	0.766	0.511	0.626	0.622	0.614	0.613	0.477	0.508

^a H_{obs} — observed heterozygosity, H_{exp} — expected heterozygosity, P — Hardy–Weinberg equilibrium exact test based on 1000 shufflings, PD — power of discrimination, PE — probability of exclusion, N — number of individuals typed.

References

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- [2] M. Raymond, F. Rousset, GENEPOP (version 1.2): population genetics software for exact tests and ecumenicism, *J. Heredity* 86 (1995) 248–249.