

For the Record

Allele Frequency Distributions for Twelve STR Loci in a Brazilian Population

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Populaton: Individuals from greater Rio de Janeiro and outskirts.

Keywords: forensic science, population genetics, short tandem repeats, DNA typing, F13A01, F13B, FESFPS, LPL, HPRTB, CSF1PO, TH01, TPOX, vWA, D16S539, D7S820, D13S317, Caucasian, Rio de Janeiro, Brazil

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Genomic DNA was isolated from peripheral blood samples collected in the presence of EDTA, or from bucal swabs. In either case, DNA was extracted using standard organic phenol/water partition methods, or directly purified using PHARMACIA GFX Genomic Blood DNA Purification Kit. The individuals taking part in this study were unrelated volunteers. PCR amplifications were carried out in a Perkin-Elmer 9600, or an MJ-Research PTC-100 thermal cycler, using the optimum conditions for each locus. Amplicons were fractionated on a polyacrylamide sequencing gel (GIBCO-BRL) and silver stained using the PROMEGA silver staining system. The data were tested using the Genepop program, version 3.1 (1).

The complete data are available to any interested researcher upon request or by accessing <http://meusite.osite.com.br/sonda>.

Acknowledgments

The authors wish to acknowledge the expert help of Mr. Cássio Alessandro Paganoti Sartório.

Reference

1. Raymond M, Rousset F. GENEPOP (version 1.2): population genetics software for exact tests and ecumenicism. *J Heredity* 1995;86:248–9.

TABLE 1—Observed allele frequencies.

Allele	F13A01	F13B	FESFPS	LPL	HPRTB	CSF1PO	TH01	TPOX	vWA	D16S539	D7S820	D13S317
3,2	0.142											
4	0.219					0.002				0.005		
5	0.210					0.007	0.002			0.040	0.002	
6	0.251	0.166		0.002		0.022	0.238	0.019				
7	0.112	0.052	0.007	0.039		0.036	0.236	0.010		0.003	0.019	
8	0.011	0.174	0.030			0.124	0.164	0.473		0.056	0.146	0.084
9		0.234	0.028	0.236	0.014	0.202	0.135	0.134		0.170	0.144	0.068
10	0.003	0.371	0.252	0.298	0.014	0.262	0.225	0.056		0.132	0.275	0.064
11		0.003	0.403	0.238	0.077	0.195		0.247	0.002	0.241	0.231	0.323
12			0.222	0.135	0.295	0.084		0.050	0.062	0.183	0.159	0.315
13	0.016		0.056	0.043	0.348	0.050		0.011	0.111	0.137	0.019	0.103
14	0.003		0.002	0.007	0.188	0.015			0.181	0.031	0.005	0.043
15	0.022			0.002	0.058	0.002			0.201	0.002		
16	0.011				0.005				0.226			
17									0.130			
18									0.055			
19									0.024			
20									0.007			
									0.002			
N =	183	310	216	292	140	302	307	310	274	311	309	311
P (Exact Test)*	0.0044	0.6629	0.0016	0.0000	0.6962	0.0000	0.8144	0.0067	0.0000	0.0000	0.3082	0.1082

* P (Exact Test) based on 5000 dememorization steps, 1000 batches and 2000 iterations per batch.