

Announcement of population data

Genetic data on 12 STRs (F13A01, F13B, FESFPS, LPL, CSF1PO, TPOX, TH01, vWA, D16S539, D7S820, D13S317, D5S818) from four ethnic groups of São Paulo, Brazil

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**Abstract**

Allelic frequencies for 12 short tandem repeats (STRs) (F13A01, F13B, FESFPS, LPL, CSF1PO, TPOX, TH01, vWA, D16S539, D7S820, D13S317 and D5S818) were estimated, also as forensic parameters, from a sample of 916 unrelated Brazilian subjects classified into four ethnic groups: European-derived, African-derived, Brazilian Mulattos and Asian-derived. © 2003 Elsevier Science Ireland Ltd. All rights reserved.

**Keywords:** STR; Genetic admixture; Human population; São Paulo; Brazil

**General information on the population of São Paulo, Brazil:** Brazil constitutes a melting-pot of populations and the similarities among these different groups (mainly from Caucasian and African origin) are much more impressive than the dissimilarities, when compared to other countries [1,2]. Several research groups have tried to better characterize the Brazilian genetic miscegenation in relation to various genetic systems [3–12]. The ethnic population structure for the São Paulo area, the biggest Brazilian city, is considered to be complex. Brazil was discovered and colonized by Portugal at the beginning of the 16th century. In the same century, the slavery of African individuals was introduced. After that, other ethnic–geographic populations have migrated to Brazil, mainly from Spain, Italy, Germany and Japan. At the end of the 20th century, Brazilian population was composed of 62.6% Caucasians, 5.8% African-derived,

30.8% Brazilian Mulattos, and 0.8% Asian descendents [13]. We describe here the results of a systematic study of the genotype polymorphism frequencies at 12 loci in four Brazilian subpopulations, following the guidelines for publication of population data requested by the journal [14].

**Population samples:** Nine hundred and sixteen unrelated healthy volunteer blood donors were studied after a written informed consent. Subjects were asked about their ethnic group and those of their parents and grand-parents, according to their own definition. Phenotype analysis (skin and axilla color and face characteristics) was performed by the interviewer. Subjects were then classified accordingly into four ethnic groups: European-derived, African-derived, Brazilian Mulattos and Asian-derived. For instance, subjects were classified as African-derived when the characteristic phenotype was present and subjects described themselves and their parents and all their grand-parents as African-derived (or blacks). The same procedure was followed for the classification of individuals into other groups.

**DNA extraction, PCR amplification, and genotyping:** DNA was extracted from 5 ml blood by standard procedure

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Table 1  
Allelic frequency distribution for European-derived Brazilians

Alleles	F13A01	F13B	FESFPS	LPL	CSF1PO	TH01	TPOX	vWA	D16S539	D7S820	D13S317	D5S818
3.2	0.041											
4	0.065											
5	0.221					0.010						
6	0.264	0.125			0.000	0.209	0.013		0.005	0.003		
7	0.248	0.034	0.004	0.008	0.012	0.214	0.008		0.007	0.044	0.002	0.010
8	0.101	0.229	0.022	0.000	0.017	0.149	0.450		0.041	0.117	0.118	0.005
9	0.013	0.248	0.038	0.041	0.030	0.170	0.131		0.122	0.182	0.091	0.043
9.3						0.222						
10	0.002	0.347	0.231	0.338	0.267	0.021	0.079		0.115	0.241	0.041	0.062
11	0.002	0.017	0.372	0.276	0.297	0.003	0.255	0.007	0.253	0.198	0.256	0.338
12	0.007	0.000	0.238	0.267	0.260		0.056	0.000	0.250	0.170	0.287	0.335
13	0.002		0.072	0.062	0.106		0.007	0.013	0.142	0.024	0.149	0.176
14	0.009		0.023	0.008	0.009			0.075	0.038	0.019	0.043	0.028
15	0.013				0.002			0.128	0.014	0.002	0.013	0.003
16	0.013							0.248				
17								0.277				
18								0.165				
19								0.068				
20								0.018				
21								0.000				
<i>N</i>	556	536	554	532	576	616	604	600	584	572	558	580
Ho	0.781	0.709	0.736	0.718	0.754	0.798	0.685	0.807	0.829	0.783	0.788	0.717
He	0.804	0.750	0.745	0.734	0.761	0.810	0.706	0.808	0.823	0.826	0.805	0.737
PD	0.933	0.894	0.894	0.881	0.902	0.935	0.872	0.936	0.945	0.945	0.935	0.887
PE	0.564	0.442	0.487	0.457	0.516	0.597	0.406	0.611	0.653	0.568	0.578	0.455
<i>P</i>	0.867	0.950	0.670	0.750	0.678	0.714	0.840	0.570	0.426	0.976	0.806	0.818

*N*: number of chromosomes; Ho: observed heterozygosity; He: expected heterozygosity; PD: power of discrimination; PE: a priori power of exclusion; *P*: Hardy–Weinberg equilibrium. Fisher exact test based on 4800 shufflings, for standard error <0.01.

Table 2  
Allelic frequency distribution for Brazilian Mulattos

Alleles	F13A01	F13B	FESFPS	LPL	CSF1PO	TH01	TPOX	vWA	D16S539	D7S820	D13S317	D5S818
3.2	0.050											
4	0.078											
5	0.244											
6	0.208	0.173			0.000	0.205	0.021		0.000	0.005		
7	0.214	0.084	0.008	0.003	0.027	0.293	0.033		0.000	0.027	0.010	0.025
8	0.103	0.168	0.028	0.000	0.035	0.146	0.384		0.060	0.172	0.088	0.027
9	0.035	0.238	0.064	0.100	0.055	0.164	0.172		0.158	0.107	0.090	0.035
9.3						0.179						
10	0.000	0.306	0.213	0.398	0.234	0.004	0.088		0.134	0.253	0.058	0.058
11	0.007	0.031	0.327	0.209	0.264	0.000	0.242	0.005	0.258	0.206	0.309	0.332
12	0.018	0.000	0.241	0.251	0.261		0.049	0.000	0.199	0.182	0.254	0.358
13	0.020		0.086	0.034	0.099		0.011	0.019	0.151	0.034	0.146	0.155
14	0.005		0.033	0.005	0.017			0.057	0.026	0.012	0.040	0.010
15	0.013				0.008			0.172	0.002	0.002	0.005	0.000
16	0.005							0.250				
17								0.238				
18								0.184				
19								0.056				
20								0.019				
21								0.000				

Table 2 (Continued)

Alleles	F13A01	F13B	FESFPS	LPL	CSF1PO	TH01	TPOX	vWA	D16S539	D7S820	D13S317	D5S818
<i>N</i>	398	382	394	382	402	440	430	424	418	412	398	400
Ho	0.789	0.717	0.741	0.691	0.786	0.786	0.716	0.764	0.799	0.825	0.779	0.735
He	0.832	0.786	0.777	0.725	0.794	0.794	0.754	0.812	0.826	0.819	0.799	0.733
PD	0.998	0.920	0.917	0.878	0.926	0.925	0.904	0.951	0.966	0.998	0.951	0.885
PE	0.564	0.442	0.487	0.457	0.516	0.597	0.406	0.611	0.653	0.568	0.578	0.455
<i>P</i>	0.967	0.992	0.918	0.891	0.666	0.656	0.936	0.973	0.868	0.446	0.810	0.503

*N*: number of chromosomes; Ho: observed heterozygosity; He: expected heterozygosity; PD: power of discrimination; PE: a priori power of exclusion; *P*: Hardy–Weinberg equilibrium. Fisher exact test based on 4800 shufflings, for standard error <0.01.

[15]. PCR amplification and STR genotyping were performed using the GenePrint Fluorescent STR Multiplex systems kindly provided by Promega (Madison, WI, USA): CTTv Multiplex (CSF1PO, TPOX, TH01 and vWA), Gamma STR Multiplex (D16S539, D7S820, D13S317 and D5S818) and FFFL Multiplex (F13A01, F13B, FESFPS and LPL). Amplified products were detected in silver nitrate stained 7 M urea–polyacrylamide denaturing gels.

**Results:** See Tables 1–4.

**Population genetics analysis:** The data were analyzed using the FSTAT V2.9.3 [16]. As heterogeneity tests dealing with insufficiently large frequencies could lead to biased results when Chi-square analysis is used, the Fisher exact test was performed. The raw data are available at <http://www.biologia.ufjf.br/papers/12STR-SaoPaulo-Brasil.txt>.

Table 3

Allelic frequency distribution for African-derived Brazilians

Alleles	F13A01	F13B	FESFPS	LPL	CSF1PO	TH01	TPOX	vWA	D16S539	D7S820	D13S317	D5S818
3.2	0.035											
4	0.083											
5	0.230											
6	0.214	0.205	0.005		0.000	0.178	0.042		0.002	0.007		
7	0.184	0.102	0.050	0.007	0.006	0.305	0.026		0.002	0.032	0.000	0.018
8	0.128	0.155	0.057	0.002	0.053	0.189	0.321		0.052	0.155	0.069	0.031
9	0.049	0.228	0.181	0.132	0.056	0.163	0.181		0.161	0.144	0.062	0.033
9.3						0.128						
10	0.000	0.233	0.336	0.375	0.199	0.015	0.096		0.144	0.282	0.067	0.062
11	0.007	0.030	0.269	0.199	0.245	0.008	0.240	0.008	0.277	0.202	0.269	0.302
12	0.005	0.002	0.066	0.225	0.277		0.083	0.000	0.199	0.146	0.317	0.343
13	0.019		0.036	0.053	0.115		0.011	0.016	0.119	0.029	0.151	0.185
14	0.019			0.007	0.030			0.092	0.028	0.003	0.055	0.025
15	0.018				0.019			0.196	0.005	0.000	0.010	0.001
16	0.009							0.243				
17								0.251				
18								0.125				
19								0.049				
20								0.017				
21								0.003				
<i>N</i>	570	540	562	552	628	662	658	638	638	618	596	610
Ho	0.821	0.748	0.779	0.670	0.716	0.785	0.689	0.781	0.787	0.822	0.721	0.741
He	0.840	0.797	0.771	0.750	0.805	0.797	0.789	0.814	0.820	0.813	0.789	0.752
PD	0.999	0.927	0.914	0.898	0.952	0.955	0.937	0.998	0.990	0.963	0.929	0.910
PE	0.639	0.507	0.561	0.384	0.454	0.572	0.408	0.563	0.575	0.641	0.462	0.494
<i>P</i>	0.846	0.980	0.390	0.855	0.342	0.184	1.000	0.952	0.956	0.366	0.998	0.708

*N*: number of chromosomes; Ho: observed heterozygosity; He: expected heterozygosity; PD: power of discrimination; PE: a priori power of exclusion; *P*: Hardy–Weinberg equilibrium. Fisher exact test based on 4800 shufflings, for standard error <0.01.

Table 4  
Allelic frequency distribution for Asian-derived Brazilians

Alleles	F13A01	F13B	FESFPS	LPL	CSF1PO	TH01	TPOX	vWA	D16S539	D7S820	D13S317	D5S818
3.2	0.156											
4	0.067											
5	0.144											
6	0.256	0.025			0.009	0.237	0.009		0.000	0.018		
7	0.289	0.013	0.000	0.012	0.009	0.342	0.037		0.000	0.036	0.054	0.009
8	0.078	0.088	0.011	0.000	0.009	0.061	0.435		0.036	0.089	0.259	0.009
9	0.011	0.150	0.011	0.048	0.029	0.281	0.102		0.241	0.062	0.143	0.071
9.3						0.061						
10	0.000	0.687	0.125	0.559	0.179	0.018	0.046		0.205	0.366	0.071	0.214
11	0.000	0.037	0.318	0.107	0.283	0.000	0.250	0.000	0.205	0.277	0.214	0.286
12	0.000	0.000	0.296	0.238	0.245		0.102	0.000	0.188	0.125	0.223	0.277
13	0.000		0.193	0.024	0.189		0.019	0.010	0.071	0.027	0.018	0.125
14	0.000		0.046	0.012	0.019			0.202	0.027	0.000	0.018	0.009
15	0.000				0.029			0.058	0.000	0.000	0.000	0.000
16	0.000							0.240				
17								0.231				
18								0.154				
19								0.086				
20								0.019				
21								0.000				
<i>N</i>	90	80	88	84	106	114	108	104	112	112	112	112
Ho	0.689	0.425	0.795	0.571	0.830	0.807	0.556	0.750	0.839	0.696	0.821	0.803
He	0.805	0.501	0.765	0.623	0.797	0.747	0.730	0.821	0.822	0.766	0.815	0.781
PD	0.928	0.715	0.900	0.998	0.969	0.887	0.923	0.950	0.943	0.908	0.948	0.913
PE	0.411	0.130	0.591	0.258	0.656	0.612	0.241	0.510	0.674	0.423	0.639	0.606
<i>P</i>	0.981	0.954	0.390	0.855	0.342	0.184	0.999	0.935	0.439	0.935	0.539	0.421

*N*: number of chromosomes; Ho: observed heterozygosity; He: expected heterozygosity; PD: power of discrimination; PE: a priori power of exclusion; *P*: Hardy–Weinberg equilibrium. Fisher exact test based on 4800 shufflings, for standard error <0.01.

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