TECHNICAL NOTE

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Population Genetics of Nine STR Loci in Two Populations from Brazil*

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ABSTRACT: The Short Tandem Repeats (STRs) D3S1358, HUMvWA31/A, HUMFIBRA/FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, and D7S820 were studied in two Brazilian populations (from Amazonia and S. Paulo) using the "AmpFl STR Profiler Plus PCR Amplification Kit." The nine loci showed a combined discrimination power greater than 0.9999999999 and a chance of exclusion of 0.9999.

KEYWORDS: forensic science, DNA typing, population genetics, D3S1358, VWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, Brazil

The polymorphisms D3S1358 (1), HUMvWA31/A (2,3), HUMFIBRA/FGA (4), D8S1179 (5), D21S11 (6), D18S51 (7), D5S818 (8), D13S317 (8), and D7S820 (9), have recently become available in the multiplex "AmpFl STR Profiler Plus PCR Amplification Kit" (10). The gene frequencies for these loci were determined in two populations from Brazil.

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Materials and Methods

DNA was extracted (11) using "Chelex 100" (Sigma, St. Louis, USA) from 3 mm^2 of cotton fabric blood stains obtained by venipuncture of peripheral blood from unrelated individuals born in two Brazilian states: Amazonia and S. Paulo.

Multiplex PCR amplification of the D3S1358, HUMvWA31/A, HUMFIBRA/FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, and D7S820 loci used per sample, approximately 2.5 ng of DNA, 21 μL of AmpF/STR PCR reaction mix, 1 μL of AmpliTaq Gold DNA polymerase and 11 μL of AmpF/STR Profiler Plus primer set, following the protocol (10) described in the AmpF/STR Profiler Plus™ PCR Amplification Kit (Perkin Elmer, Roche Molecular Systems, Branchburg, New Jersey, USA).

The Perkin-Elmer 9600 cycling parameters were as follows: initial incubation at 95°C-11 m; 28 cycles of 94°C-1 m; 59°C-1 m; 72°C-1 m; extension at 60°C-45 m; final step at 25°C $<$ 18 h.

Electrophoresis was carried out in a 4% polyacrylamide denaturing sequencing gel on an ABI 377 DNA sequencer using the internal standard Genescan ROX 2500 (Foster City, Ca, USA), for 2 h at constant power (3000 V, 60 mA, 200 W) and 51°C.

Hardy-Weinberg equilibrium was tested with the exact test proposed by Guo and Thompson (12). An unbiased estimate of heterozygosity was computed according to Nei (13), discrimination power according to Jones (14) and chance of exclusion according to Ohno (15).

Results and Discussion

The allelic frequencies of the D3S1358, HUMvWA31/A, HUMFIBRA/FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, and D7S820 systems and the evaluation of the Hardy-Weinberg equilibrium in the two populations from the Brazil are presented in Tables 1 and 2. There is agreement between the observed genotype values and those expected under the Hardy-Weinberg equilibrium ($p > 0.05$) except with the D18S51 system in the Amazonian population.

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TABLE 1—*Gene frequencies and the Hardy-Weinberg equilibrium test for the nine STRs in the Amazonian population.*

Allele	(*n*)	Prop.
D3S1358 (*n* = 100)		
13	(1)	0.005
14	(11)	0.055
15	(68)	0.340
16	(72)	0.360
17	(31)	0.155
18	(16)	0.080
19	(1)	0.005
$P = 0.1443 \pm 0.0015$		
D8S1179 (*n* = 100)		
8	(1)	0.005
9	(2)	0.010
10	(21)	0.105
11	(12)	0.060
12	(37)	0.185
13	(51)	0.255
14	(50)	0.250
15	(22)	0.110
16	(4)	0.020
$P = 0.3107 \pm 0.0022$		
D21S11 (*n* = 100)		
24.2	(1)	0.005
27	(3)	0.015
28	(20)	0.100
29	(51)	0.255
30	(40)	0.200
30.2	(6)	0.030
31	(19)	0.095
31.2	(27)	0.135
32	(1)	0.005
32.2	(20)	0.100
33.2	(8)	0.040
34	(2)	0.010
34.2	(2)	0.010
$P = 0.5431 \pm 0.0035$		
vWA31/A (*n* = 100)		
13	(1)	0.005
14	(18)	0.090
15	(19)	0.095
16	(61)	0.305
17	(48)	0.240
18	(36)	0.180
19	(16)	0.080
20	(1)	0.005
$P = 0.6038 \pm 0.0020$		
D18S51 (*n* = 100)		
11	(2)	0.010
12	(22)	0.110
13	(31)	0.155
14	(43)	0.215
15	(24)	0.120
16	(25)	0.125
17	(18)	0.090
18	(16)	0.080
19	(6)	0.030
20	(9)	0.045
21	(2)	0.010
22	(1)	0.005
26	(1)	0.005
$P = 0.0366 \pm 0.0010$		
D13S317 (*n* = 100)		
8	(13)	0.065
9	(32)	0.160
10	(21)	0.105
11	(53)	0.265
12	(41)	0.205
13	(27)	0.135
14	(13)	0.065
$P = 0.5904 \pm 0.0013$		
FGA (*n* = 100)		
17	(1)	0.005
18	(2)	0.010
19	(13)	0.065
20	(17)	0.085
21	(24)	0.120
22	(33)	0.165
22.2	(1)	0.005
23	(24)	0.120
24	(37)	0.185
25	(25)	0.125
26	(16)	0.080
27	(6)	0.030
28	(1)	0.005
$P = 0.9003 \pm 0.0016$		
D5S818 (*n* = 100)		
7	(14)	0.070
8	(4)	0.020
9	(10)	0.050
10	(10)	0.050
11	(77)	0.385
12	(55)	0.275
13	(28)	0.140
14	(2)	0.010
$P = 0.3711 \pm 0.0020$		
D7S820 (*n* = 100)		
7	(2)	0.010
8	(31)	0.155
9	(13)	0.065
10	(51)	0.255
11	(54)	0.270
12	(40)	0.200
13	(7)	0.035
14	(2)	0.010
$P = 0.5699 \pm 0.0018$		

TABLE 2—*Gene frequencies and the Hardy-Weinberg equilibrium test for the nine STRs in the S. Paulo population.*

Allele	(*n*)	Prop.
D3S1358 (*n* = 93)		
14	(19)	0.102
15	(59)	0.317
16	(47)	0.253
17	(40)	0.215
18	(19)	0.102
19	(2)	0.011
P = 0.8751 ± 0.0007		
D8S1179 (*n* = 91)		
8	(1)	0.006
9	(4)	0.022
10	(21)	0.115
11	(13)	0.071
12	(34)	0.187
13	(48)	0.264
14	(31)	0.170
15	(23)	0.126
16	(6)	0.033
17	(1)	0.006
P = 0.1598 ± 0.0018		
D21S11 (*n* = 91)		
27	(2)	0.011
28	(40)	0.220
29	(35)	0.192
30	(40)	0.220
30.2	(6)	0.033
31	(15)	0.082
31.2	(18)	0.099
32	(2)	0.011
32.2	(15)	0.082
33	(1)	0.006
33.2	(8)	0.044
P = 0.7932 ± 0.0020		
vWA31/A (*n* = 93)		
14	(24)	0.129
15	(26)	0.140
16	(43)	0.231
17	(39)	0.210
18	(40)	0.215
19	(12)	0.065
20	(1)	0.005
21	(1)	0.005
P = 0.6270 ± 0.0018		
D18S51 (*n* = 89)		
10	(5)	0.028
11	(2)	0.011
12	(23)	0.129
13	(26)	0.146
14	(22)	0.124
15	(21)	0.118
16	(33)	0.185
17	(22)	0.124
18	(12)	0.067
19	(6)	0.034
20	(3)	0.017
21	(3)	0.017
P = 0.5159 ± 0.0025		
D13S317 (*n* = 91)		
8	(16)	0.088
9	(10)	0.055
10	(11)	0.060
11	(60)	0.330
12	(55)	0.302
13	(23)	0.126
14	(6)	0.033
15	(1)	0.006
P = 0.8270 ± 0.0012		
FGA (*n* = 92)		
17	(1)	0.005
18	(2)	0.011
18.2	(1)	0.005
19	(13)	0.071
20	(24)	0.130
21	(21)	0.114
22	(38)	0.207
23	(21)	0.114
24	(29)	0.158
25	(22)	0.120
26	(6)	0.033
27	(5)	0.027
29	(1)	0.005
P = 0.9231 ± 0.0013		
D5S818 (*n* = 89)		
7	(2)	0.011
8	(1)	0.006
9	(9)	0.051
10	(8)	0.045
11	(68)	0.382
12	(64)	0.360
13	(20)	0.112
14	(5)	0.028
15	(1)	0.006
P = 0.0850 ± 0.0016		
D7S820 (*n* = 91)		
7	(5)	0.028
8	(28)	0.154
9	(19)	0.104
10	(57)	0.313
11	(36)	0.198
12	(33)	0.181
13	(3)	0.017
14	(1)	0.006
P = 0.3417 ± 0.0018		

TABLE 3—*Statistical parameters of forensic interest for the nine STRs in the Amazonian and S. Paulo populations.*

System	h ± se		DP		CE	
	Amaz	SP	Amaz	SP	Amaz	SP
D3S1358	0.700 ± 0.046	0.720 ± 0.046	0.860	0.909	0.483	0.550
vWA31/A	0.760 ± 0.043	0.807 ± 0.041	0.924	0.936	0.598	0.631
FGA	0.940 ± 0.024	0.848 ± 0.038	0.964	0.964	0.748	0.734
D8S1179	0.800 ± 0.040	0.813 ± 0.041	0.934	0.937	0.628	0.665
D21S11	0.840 ± 0.036	0.835 ± 0.039	0.953	0.950	0.694	0.682
D18S51	0.840 ± 0.036	0.910 ± 0.030	0.961	0.964	0.739	0.749
D5S818	0.750 ± 0.043	0.719 ± 0.048	0.876	0.850	0.532	0.471
D13S317	0.840 ± 0.036	0.802 ± 0.042	0.939	0.909	0.652	0.564
D7S820	0.810 ± 0.039	0.769 ± 0.044	0.918	0.923	0.592	0.600

Mean heterozygosity	Amazonian	0.809
	S. Paulo	0.803
Combined DP	Amazonian	0.99999999997
	S. Paulo	0.99999999998
Combined CE	Amazonian	0.999896
	S. Paulo	0.999891

The nine loci showed a combined chance of exclusion (CE) of 0.9999 and a combined discrimination power (DP) greater than 0.9999999999, the systems HUMFIBRA/FGA, D21S11, and D18S51 being the most informative (Table 3).

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