

FOR THE RECORD

Laura M. Cainé,¹ M.S.; Lurdes Pontes,¹ M.S.; David Abrantes,¹ M.S.; Gabriela Lima,¹ M.S.; and Fátima Pinheiro,¹ Ph.D.

Genetic Data of Eight Y-Chromosome STRs in Males from Santa Catarina, Brazil

POPULATION: 113 unrelated, autochthonous healthy males from Santa Catarina, Brazil

KEYWORDS: forensic science, DNA typing, Y-chromosome, population genetics, short tandem repeats, haplotype, DYS460 (GATA-A7.1), DYS461 (GATA-A7.2), GATA-A10, GATA-C4, GATA-H4, DYS437, DYS438, DYS439, Santa Catarina, Brazil

Extraction—DNA was extracted from blood stains using the Chelex® method (1). **PCR**: The co-amplification of DYS460 (GATA-A7.1), DYS461 (GATA-A7.2), GATA-A10, GATA-C4, GATA-H4, DYS437, DYS438, DYS439, Y-chromosome STRs was performed using an octoplex reaction, obtained by the modification of the protocol established for GEP-ISFG collaborative study on two Y-STRs tetraplexes (2). About 5–50 ng of genomic DNA was used in a 25 µL reaction volume containing 2 mM MgCl₂, 200 µM of dNTPs, 1 × ImmoBuffer (Bioline) and 0.5 U of Immolase™ DNA polymerase (Bioline). Primers concentrations and cycling

conditions were the same as described in (2) and carried out using a thermocycler GeneAmp® PCR System 9700 (Applied Biosystems).

Typing—The amplified products were detected and separated by capillary electrophoresis using an ABI PRISM® 310 Genetic Analyzer (Applied Biosystems). Fragment sizes were determined automatically using the Genescan® Analysis Software v.3.7 and by comparison with allelic ladders. Allele nomenclature was proposed by (3).

Results and analysis—Allele frequencies for the eight Y-chromosome STRs were estimated by the direct counting method (Table 1); haplotype (Table 2) and gene diversities (Table 1) were calculated according to Nei (4) using the Arlequin software package (5).

TABLE 1—Allele frequencies and gene diversity value at the eight Y-chromosome STRs in the Santa Catarina population (*n* = 113).

Allele	DYS461 (GATA-A7.2)	DYS437	DYS438	GATA-C4	DYS460 (GATA-A7.1)	GATA-A10	DYS439	GATA-H4
9	0.0796	...	0.0708	...	0.0088	...
10	0.0354	...	0.3540	...	0.3717	...	0.0531	...
11	0.3009	...	0.0708	...	0.5487	...	0.2920	...
12	0.5398	0.0088	0.4690	...	0.0088	...	0.5221	...
13	0.1239	...	0.0088	0.0973	0.1150	...
14	...	0.3717	0.0088	0.2301
15	...	0.4602	0.0088	0.6106	0.0088	...
16	...	0.1416	0.0619
17	...	0.0177
20	0.0796
21	0.2035
22	0.0973
23	0.5664
24	0.0442
25	0.0088
26	0.0088	0.0796
27	0.3097
28	0.5487
29	0.0531
h ^a	0.6068	0.6353	0.6489	0.6255	0.5607	0.5659	0.6315	0.5991

^a h^a: gene diversity value.

TABLE 2—*Distribution of the Y-chromosome STRs haplotypes in the Santa Catarina population (n=113).*

Ha	DYS461 (GATA-A7.2)	DYS437	DYS438	GATA-C4	DYS460 (GATA-A7.1)	GATA-A10	DYS439	GATA-H4	n ^b
1	10	14	10	21	10	13	11	26	2
2	10	15	12	23	11	16	11	28	1
3	10	16	10	21	11	15	13	28	1
4	11	14	9	21	10	15	12	27	1
5	11	14	10	21	10	14	12	26	1
6	11	14	10	23	9	15	12	28	1
7	11	14	10	21	10	15	11	27	1
8	11	14	10	23	10	15	11	27	1
9	11	14	10	23	10	15	11	28	1
10	11	14	10	21	11	13	12	28	1
11	11	14	10	23	11	15	12	28	1
12	11	14	10	22	11	14	11	27	1
13	11	14	10	23	11	15	11	28	1
14	11	14	11	22	10	15	11	27	2
15	11	14	11	23	11	15	11	27	1
16	11	14	11	23	10	15	10	28	1
17	11	14	11	23	11	13	13	27	1
18	11	14	12	23	10	15	12	28	1
19	11	14	14	20	10	14	11	28	1
20	11	15	9	22	9	14	11	28	1
21	11	15	9	22	11	15	12	27	1
22	11	15	10	22	10	13	12	27	1
23	11	15	12	23	9	15	12	27	1
24	11	15	12	24	10	14	12	28	1
25	11	15	12	23	11	14	15	27	1
26	11	15	12	23	11	15	13	27	1
27	11	15	12	23	11	15	12	28	1
28	11	15	12	24	11	15	12	29	1
29	11	15	12	23	11	14	12	28	1
30	11	15	12	23	11	15	11	28	1
31	11	16	10	23	10	13	11	27	1
32	11	16	10	20	10	14	11	28	1
33	11	16	10	20	10	14	11	29	1
34	11	16	10	23	11	13	11	26	1
35	11	16	12	23	11	15	12	28	1
36	11	17	10	21	11	13	11	28	1
37	12	12	15	23	11	16	12	27	1
38	12	14	9	23	10	15	12	27	1
39	12	14	9	22	10	16	12	29	1
40	12	14	9	21	10	16	12	29	1
41	12	14	10	21	11	14	11	26	1
42	12	14	10	22	11	13	10	28	1
43	12	14	10	20	11	15	11	28	1
44	12	14	10	21	9	15	12	28	1
45	12	14	10	21	9	16	12	28	1
46	12	14	10	23	11	15	11	28	1
47	12	14	10	22	11	15	12	28	1
48	12	14	11	23	11	16	10	29	1
49	12	14	11	23	9	15	9	28	1
50	12	14	12	23	11	15	12	28	1
51	12	14	12	23	11	15	12	27	1
52	12	14	12	23	10	15	12	27	1
53	12	15	10	23	10	15	13	28	1
54	12	15	10	24	10	14	12	28	1
55	12	15	12	23	11	15	12	28	13
56	12	15	12	23	12	15	12	28	1
57	12	15	12	24	10	15	10	27	1
58	12	15	12	23	11	15	13	28	2
59	12	15	12	23	11	15	12	26	1
60	12	15	12	23	10	14	12	27	1
61	12	15	12	23	10	15	13	28	1
62	12	15	12	23	11	16	12	28	1
63	12	15	12	23	11	15	12	27	1
64	12	15	12	23	10	14	12	29	1
65	12	15	12	23	11	15	10	28	1
66	12	15	12	20	11	15	12	28	2
67	12	15	12	23	11	14	12	28	2
68	12	15	12	23	10	15	12	27	1
69	12	15	12	23	11	14	11	28	1
70	13	15	12	23	11	15	12	28	1
71	12	15	12	23	10	15	12	28	1

TABLE 2—Continued.

Ha	DYS461 (GATA-A7.2)	DYS437	DYS438	GATA-C4	DYS460 (GATA-A7.1)	GATA-A10	DYS439	GATA-H4	n ^b
72	12	15	12	23	11	15	13	27	1
73	12	15	13	23	10	15	11	28	1
74	12	16	10	23	10	15	12	28	1
75	12	16	10	20	10	13	11	27	1
76	12	16	10	20	10	14	11	27	1
77	12	16	10	21	10	15	13	27	1
78	12	16	10	21	10	14	11	27	1
79	12	16	10	21	10	15	11	28	1
80	12	16	10	21	10	15	11	27	1
81	12	16	12	23	11	15	13	28	2
82	12	16	12	26	11	15	13	27	1
83	13	15	12	23	11	15	12	25	1
84	13	14	9	22	9	14	12	27	2
85	13	14	9	21	10	14	12	28	1
86	13	17	10	21	10	14	12	27	1
87	13	14	10	21	10	14	11	27	1
88	13	14	10	21	11	13	10	28	1
89	13	14	10	21	10	14	11	26	1
90	13	14	10	21	10	15	11	26	1
91	13	14	11	21	11	15	12	27	1
92	13	15	10	20	11	14	11	27	1
93	13	15	12	24	11	14	13	28	1
94	13	15	12	23	11	15	12	26	1

H^a: haplotype; n^b: number of individuals observed for each haplotype.

A total of 94 different haplotypes were observed, 86 of them being unique. The most common haplotype was 12, 15, 12, 23, 11, 15, 12, 28 (DYS461 (GATA-A7.2), DYS437, DYS438, GATA-C4, DYS460 (GATA-A7.1), GATA-A10, DYS439, GATA-H4). The haplotype diversity for all eight Y-chromosome STRs was 0.9866 ± 0.0066 . The data generated show that the eight Y-chromosome haplotype (DYS461 (GATA-A7.2), DYS437, DYS438, GATA-C4, DYS460 (GATA-A7.1), GATA-A10, DYS439, GATA-H4) is highly polymorphic and discriminative in Santa Catarina, Brazil population.

The complete dataset is available upon request at biologia@dpinml.mj.pt.

References

- Walsh PS, Metzger DA, Higuchi R. CHELEX® 100 as a medium for simple extraction of DNA for PCR-based typing from forensic material. *BioTechniques* 1991;10:506–13.
- Sánchez-Diz P, Gusmão L, Beleza S, Benítez-Páez A, Castro A, García O,

et al. Results of the GEP-ISFG collaborative study on two Y-STRs tetraplexes: GEPY I (DYS461, GATA C4, DYS437 and DYS438) and GEPY II (DYS460, GATA A10, GATA H4 and DYAS439). *Forensic Sci Int* 2003;135:158–62.

- Gusmão L, González-Neira A, Lareu M, Costa S, Amorim A, Carracedo A. Chimpanzee homologous of human Y specific STRs: a comparative study and a proposal for nomenclature. *Forensic Sci Int* 2002;126:129–36.
- Nei M. Molecular evolutionary genetics. New York: Columbia University Press, 1973.
- Schneider S, Roessli D, Excoffier L. Arlequin version 2.000: A software for population genetics data analysis. Genetics and Biometry Laboratory, University of Geneva, Switzerland, 2000.

[PubMed]

[PubMed]

Additional information and reprint requests:

Laura Mendes Cainé, M.S.
Delegação do Porto do Instituto Nacional de Medicina Legal
Jardim Carrilho Videira
4050-167 Porto
Portugal
E-mail:laurakaine@hotmail.com

[PubMed]