

FOR THE RECORD

Juan José Builes,^{1,2} M.Sc.; Jorge Rodríguez,^{1,2} Biol; Alba Montoya,^{2,3} Biol; M Luisa Bravo,² M.Sc.; Felix Izarra,³ Biol; Oscar Ochoa,³ Biol; Lizandrina Pérez,³ M.Sc.; and Jorge Hau,³ M.Sc.

A Peruvian Population Study of Eight Y-Chromosome STR Loci

POPULATION: We have analyzed the distribution of the allele frequencies and haplotypes at eight Y-chromosomal short tandem repeat (STR) loci (DYS437, DYS438, DYS439, DYS460, DYS461, GATA A10, GATA C4 and GATA H4) in a sample population of 87 unrelated individuals from Perú.

KEYWORDS: forensic science, DNA typing, population genetics, Y-chromosome, STR, DYS437, DYS438, DYS439, DYS460, DYS461, GATA A10, GATA C4 and GATA H4, Perú

Blood samples from 87 unrelated individuals from Perú were collected. DNA was extracted of FTA Cards using FTA purification reagent. The primer sequences of loci and cycling conditions were as recommended (1–3). The eight loci were amplified in two multiplexes. Multiplex I includes four STR: GATA-C4, DYS438, DYS437 and DYS461. Multiplex II includes: GATA-H4, DYS439, GATA-A10 and DYS460. PCR conditions were as follows: 5 ng DNA in 15 µl total reaction volume containing 2 mM MgCl₂, 1X PCR Taq DNA Polimerasa buffer, 0.5 U Taq DNA Polymerase (Promega), 200 µM of each dNTP, 0.53 µM GATA-C4 primers, 1.6 µM DYS438 primers, 0.8 µM DYS437 primers, 1.6 µM DYS461 primers, 0.8 µM GATA-H4 primers, 0.67 µM DYS439 primers, 0.53 µM GATA-A10 primers and 1.06 µM DYS460 primers. After a 3 min a 95°C pre-incubation, a total of 35 cycles were carried out in a PTC-100 (MJ-Research) PCR System, denaturation for 30 s at 94°C, annealing for 20 s at 60°C and extension for 30 s at 70°C, followed by a 45 min final extension at 70°C. The PCR products were analyzed using denaturing 4% acrylamide-bis-acrilamide gel electrophoresis and detected by silver staining. Alleles were identified based on the number of repeats and their attribution was made by comparison with an in-house constructed allelic ladder and following the published nomenclature (3) and ISFG guidelines for STR analysis (4). Correct allele calling was additionally assured by successful participation in the quality control test of the GEP-ISFG. The gene frequencies and gene or haplotype diversity values were calculated using the software ARLEQUIN version 2000 (5) and Nei formulation (6), the discrimination capacity was the percentage proportion of the different haplotypes.

Table 1 summarizes the allele frequency distribution and gene diversity for each locus. The most frequent haplotypes observed, the haplotype diversity and discrimination capacity are presented in Table 2. Complete data are available at the e-mail address of the corresponding author upon request.

Acknowledgments

This work was partially supported by GENES Ltda.

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Additional information and reprint requests:
Juan José Builes G., M.Sc.
GENES Ltda. Lab. de Genética Forense y
Huellas Digitales del DNA
Cra. 48 No. 10-45. Cons. 612
Medellín—Colombia
E-mail: genforense@epm.net.co

¹ GENES Ltda., Laboratorio de Genética Forense y Huellas Digitales del DNA. Medellín—Colombia.

² Instituto de Biología, Universidad de Antioquia. Medellín—Colombia.

³ Laboratorio de Biología Molecular-ADN Forense, Dirección de Criminalística de la Policía Nacional de Perú, Lima, Perú.

TABLE 1—Allele frequencies, number of alleles and gene diversities of eight Y-chromosome STR loci in a Peruvian population sample.

Allele	GATA C4	DYS438	DYS437	DYS461	GATA H4	DYS439	GATA A10	DYS460
7								0,011
8								0,023
9								0,506
10		0,115				0,034		0,402
11		0,494		0,069		0,241		0,057
12		0,379		0,713		0,540	0,011	
13		0,011	0,011	0,172		0,161	0,057	
14			0,667	0,046		0,011	0,195	
15			0,276			0,011	0,506	
16			0,046				0,172	
17							0,046	
18							0,011	
20	0,023							
21	0,080							
22	0,471							
23	0,345							
24	0,069							
25	0,011				0,011			
26					0,034			
27					0,333			
28					0,586			
29					0,034			
NA	6	4	4	4	5	6	7	5
GD	0,6556	0,6067	0,483	0,4610	0,5502	0,631	0,6793	0,5859

NA: Number alleles; GD: Gene diversity.

TABLE 2—The haplotype of eight Y-chromosome STR loci in a Peruvian population sample (H haplotype n number of individuals observed for each haplotype).

Haplotypes	GATA C4	DYS438	DYS437	DYS461	GATA H4	DYS439	GATA A10	DYS460	n
H1	23	12	14	13	27	12	16	11	1
H2	23	12	15	12	28	12	15	11	3
H3	22	11	14	12	28	12	15	10	1
H4	23	12	14	12	28	13	14	11	1
H5	22	11	14	13	28	12	18	12	1
H6	23	12	15	12	28	12	13	12	1
H7	23	12	15	12	28	13	15	11	1
H8	22	11	14	12	28	11	16	10	2
H9	24	11	15	14	27	12	15	10	1
H10	22	12	14	13	26	12	15	12	1
H11	22	11	14	14	28	12	16	10	1
H12	23	12	14	12	28	12	15	11	2
H13	22	12	14	12	28	12	15	9	1
H14	23	12	14	13	28	11	15	10	1
H15	22	11	14	12	28	12	14	11	2
H16	22	11	14	12	26	11	16	10	1
H17	22	12	14	12	27	11	15	11	1
H18	23	12	15	13	27	12	14	11	1
H19	22	10	16	11	27	12	13	10	1
H20	23	12	15	12	28	11	15	11	1
H21	22	11	14	14	28	12	15	10	1
H22	24	11	14	11	28	10	17	11	1
H23	23	11	14	12	27	13	14	11	1
H24	22	10	14	12	28	13	14	10	1
H25	22	12	14	12	28	12	14	10	1
H26	21	10	15	12	29	12	15	10	1
H27	22	11	14	12	28	13	14	11	1
H28	22	11	14	12	27	12	15	10	1
H29	22	11	14	12	27	13	14	11	1
H30	20	11	14	12	27	12	15	10	1
H31	22	11	14	12	27	13	16	11	1
H32	24	11	14	12	28	10	14	11	1
H33	25	12	15	12	28	11	15	11	1
H34	21	10	14	12	27	11	15	11	1
H35	22	11	14	12	27	12	16	10	5
H36	23	11	14	12	28	13	15	10	1
H37	20	11	14	12	28	12	15	10	1
H38	23	12	15	14	28	11	13	11	1

TABLE 2—Continued.

Haplotypes	GATA C4	DYS438	DYS437	DYS461	GATA H4	DYS439	GATA A10	DYS460	<i>n</i>
H39	21	10	14	13	28	10	14	11	1
H40	24	11	16	13	28	12	15	10	1
H41	22	11	14	13	28	11	17	11	1
H42	23	12	15	12	29	12	15	10	1
H43	22	11	15	12	28	12	15	10	1
H44	21	10	14	12	28	11	14	11	1
H45	23	12	14	12	28	12	15	10	1
H46	22	11	14	13	27	11	15	10	1
H47	23	12	15	12	28	12	16	11	2
H48	23	12	15	11	28	11	15	12	1
H49	21	10	16	11	27	11	13	10	1
H50	22	11	14	13	28	11	15	10	1
H51	24	12	15	12	28	12	14	11	1
H52	22	11	14	12	28	13	15	10	1
H53	22	11	14	13	27	12	14	10	1
H54	23	11	14	11	27	13	16	10	1
H55	22	12	14	12	28	12	13	10	1
H56	22	11	14	13	27	12	12	11	1
H57	23	12	15	12	28	12	15	12	1
H58	22	12	14	12	27	12	15	10	1
H59	22	11	14	12	27	13	15	10	1
H60	23	11	14	12	27	11	15	10	1
H61	23	12	14	12	28	11	15	11	1
H62	22	10	13	12	27	12	15	10	1
H63	22	11	14	12	28	11	17	10	1
H64	22	11	14	12	27	11	15	10	1
H65	22	11	14	12	28	12	14	7	1
H66	23	11	14	13	28	11	15	10	1
H67	22	11	14	12	29	13	15	10	1
H68	23	12	15	12	28	13	15	10	1
H69	21	10	14	13	28	16	14	11	1
H70	23	12	15	12	27	11	15	11	1
H71	23	12	15	12	28	12	17	11	1
H72	22	13	14	12	27	12	14	10	1
H73	22	11	15	13	28	13	15	10	1
H74	24	12	16	12	25	12	15	11	1
H75	23	10	15	11	28	12	15	10	1
H76	23	12	14	12	27	14	16	11	1
H77	21	11	15	12	26	12	15	9	1

Haplotype diversity: 0.9955; Discrimination capacity: 0.8736.