



A genetic population study of six Y chromosomal STRs in Central-West African immigrants in Spain and Southwest Spain populations

J.J. Gamero^{a,*}, J.L. Romero^a, J.L. González^a,
M.I. Cuesta^a, M. Carvalho^b, M.J. Anjos^b, F. Corte-Real^b,
D.N. Vieira^b, Ma.C. Vide^b

^a*Faculty of Medicine, Department of Legal Medicine, University of Cádiz, Fragela s/n, Cádiz 11003, Spain*

^b*Institute of Legal Medicine of Coimbra, 3000 Coimbra, Portugal*

Keywords: STRs; Y-chromosome; Population study; Forensic genetics

1. Introduction

STRs on the Y chromosome are very useful for sex identification as well as for individual identification and paternity testing [1]. Likewise, these markers can be particularly helpful to detect male DNA fractions in stains involving male/female mixtures, the most common biological material found in sexual crimes [2].

In the present study, the allele distributions of the polymorphic loci DYS19, DYS385, DYS389I, DYS389II, DYS390 and DYS393 were examined in Southwest Spain and the black West African immigrant population.

2. Materials and methods

Whole EDTA blood was obtained by venipuncture from 111 unrelated Spaniards from the southwest of Spain (S. Spain), and 103 unrelated black West African immigrants (C.

* Corresponding author. Fax: +34-56-223-139.

E-mail address: joaquin.gamero@uca.es (J.J. Gamero).

African I.S.) from different countries situated to the south of the Sahara desert who use the south of Spain as a point of entry into the European Community (EC).

The DNA was extracted using a Chelex 100 protocol as described by Walsh et al. [3]. The quantity of recovered DNA was determined using QuantiBlot® Human DNA Quantitation Kit (Perkin Elmer).

DYS19, DYS389I, DYS389II, DYS390 and DYS393 were amplified as described by Gusmão et al. [4] and Carracedo et al. [2]. DYS385 was amplified using conditions described by Schneider et al. [5,6]. The DYS385 amplification conditions complied with the methodology described by Schneider et al. The PCR was performed in a Perkin Elmer 9600 thermocycler.

Table 1

Y STR haplotypes in a black Central-West African immigrant population in Spain (C. African I.S.)

Haplotype	DYS19	DYS389I	DYS389II	DYS390	DYS393	DYS385	Haplotype	DYS19	DYS389I
h1	15	9	26	22	13	14, 15	h34	17	9
h2	15	10	28	21	10	17, 19	h35	17	9
h3	14	11	27	21	14	16, 16	h36	15	11
h4	15	10	28	21	13	17, 17	h37	16	10
h5	16	10	28	22	13	16, 27	h38	15	10
h6	14	10	27	21	13	14, 17	h39	16	11
h7	13	11	28	23	12	15, 16	h40	17	10
h8	16	10	28	22	13	16, 17	h41	16	10
h9	14	10	28	21	13	16, 19	h42	15	9
h10	15	10	28	21	13	16, 18	h43	15	9
h11	15	10	27	21	14	18, 18	h44	15	10
h12	16	8	25	21	13	14, 14	h45	15	9
h13	15	10	27	21	13	17, 17	h46	16	10
h14	15	10	28	21	14	15, 15	h47	15	10
h15	16	10	29	21	14	14, 16	h48	14	9
h16	15	10	28	21	14	14, 16	h49	16	10
h17	16	9	26	21	14	16, 18	h50	15	9
h18	14	9	26	22	14	16, 20	h51	16	10
h19	15	10	28	21	13	14, 18	h52	15	18
h20	16	10	28	21	14	13, 16	h53	15	10
h21	15	10	27	21	14	16, 17	h54	17	10
h22	16	10	27	21	14	15, 16	h55	15	10
h23	16	10	28	21	13	17, 17	h56	15	10
h24	15	10	26	25	13	13, 16	h57	16	10
h25	15	10	27	21	13	17, 19	h58	15	11
h26	15	10	27	21	13	13, 15	h59	16	10
h27	15	10	29	21	13	16, 17	h60	16	10
h28	15	10	27	20	13	14, 16	h61	15	9
h29	15	10	27	21	14	14, 16	h62	15	8
h30	15	10	27	21	14	16, 16	h63	15	10
h31	15	8	26	21	13	16, 16	h64	16	10
h32	15	10	26	24	13	13, 15	h65	13	10
h33	15	10	27	21	14	15, 20	h66	15	11

The allele nomenclature used, followed the guidelines proposed by Kayser et al. [7] and De Knijff [8] with the exception of the DYS389 locus, where the nomenclature used was according to Roewer et al. [9], Rolf et al. [10], Gusmão et al. [4] and Carracedo et al. [2].

Electrophoresis was carried out on 4% polyacrylamide denaturing sequencing gels in a 377 automated system (Applied Biosystems). Genotype classification was done using Genescan PCR analysis software with the Local Southern Method and by side-to-side comparison with allelic ladders. These ladders were kindly provided by Dr. Carracedo (Institute of Legal Medicine of Santiago de Compostela) and Dr. P.M. Schneider (Institut für Rechtsmedizin, Mainz). Haplotype diversity was calculated according to Nei [11].

DYS389II	DYS390	DYS393	DYS385	Haplotype	DYS19	DYS389I	DYS389II	DYS390	DYS393	DYS385
26	23	13	14, 14	h67	15	10	27	21	13	15, 18
27	21	15	17, 17	h68	15	11	28	21	14	17, 17
28	21	15	18, 21	h69	14	9	25	22	14	16, 18
27	21	13	15, 17	h70	15	9	27	21	14	14, 15
28	21	13	16, 17	h71	16	9	27	22	12	14, 14
29	21	14	15, 16	h72	13	10	28	24	14	16, 17
28	22	15	15, 16	h73	14	10	27	23	14	15, 17
28	21	14	17, 18	h74	15	10	27	22	13	27, 19
26	21	14	16, 16	h75	15	10	28	21	13	15, 17
26	21	16	17, 18	h76	15	10	29	21	14	15, 16
29	21	13	15, 16	h77	15	10	29	21	14	14, 15
26	22	13	15, 16	h78	15	11	27	21	14	16, 16
27	21	15	16, 18	h79	15	11	28	21	14	16, 16
27	22	14	17, 18	h80	15	11	28	21	14	15, 16
25	25	13	19, 19	h81	15	11	29	23	13	13, 15
28	21	13	17, 18	h82	15	12	29	22	14	16, 18
27	21	13	15, 16	h83	15	12	29	22	13	12, 15
28	21	14	16, 16	h84	16	9	27	22	13	13, 16
28	23	15	16, 16	h85	16	10	27	21	13	16, 17
29	21	13	15, 18	h86	16	10	27	21	15	14, 18
27	21	14	16, 16	h87	16	11	27	21	14	16, 16
28	21	14	15, 16	h88	15	9	26	22	13	17, 17
28	21	13	17, 18	h89	16	11	27	22	13	16, 17
27	20	14	15, 15	h90	16	11	28	21	15	17, 17
28	21	14	15, 17	h91	17	9	26	22	13	17, 19
29	21	14	16, 16	h92	17	10	27	20	14	15, 16
28	21	13	14, 15	h93	17	10	28	20	15	16, 16
27	22	13	13, 15	h94	17	11	28	22	13	16, 16
25	21	13	16, 16	h95	17	11	28	22	13	15, 16
27	21	14	16, 18	h96	17	11	28	22	13	15, 18
29	21	14	16, 17	h97	17	11	28	22	13	16, 15
28	24	12	15, 16	h98	17	11	28	22	13	17, 17
27	21	14	18, 18							

Analysis of molecular variance (AMOVA) was performed by Markov test using the Arlequin software 1.1 [12]. Genetic distance matrix between populations was obtained by using the pairwise difference genetic distance.

3. Results

A total of 98 (Table 1) and 103 (Table 2) haplotypes were observed in Central-West African immigrants in Spain (C. African I.S.) and Southwest Spain (S. Spain)

Table 2
Y STR haplotypes in a southwest of Spain population (S. Spain)

Haplotype	DYS19	DYS389I	DYS389II	DYS390	DYS393	DYS385	Haplotype	DYS19	DYS389I
h1	15	9	25	22	14	12, 15	h36	14	11
h2	15	10	27	24	14	11, 15	h37	13	10
h3	15	10	27	23	12	13, 15	h38	14	10
h4	14	11	27	24	13	11, 15	h39	14	9
h5	14	10	26	24	13	11, 14	h40	14	11
h6	14	10	25	24	13	11, 14	h41	14	11
h7	15	10	26	23	13	14, 16	h42	14	9
h8	14	10	26	24	13	11, 14	h43	13	11
h9	14	10	26	23	13	13, 14	h44	13	9
h10	13	11	27	24	13	13, 14	h45	15	11
h11	14	10	26	24	13	11, 14	h46	14	12
h12	14	10	26	24	13	11, 14	h47	15	10
h13	14	10	26	25	13	11, 14	h48	14	11
h14	14	10	26	24	13	11, 14	h49	14	10
h15	14	10	25	24	13	11, 14	h50	13	10
h16	14	9	25	24	14	11, 14	h51	14	9
h17	16	10	26	23	12	15, 18	h52	14	11
h18	15	10	26	24	13	11, 14	h53	14	11
h19	14	10	26	23	13	11, 14	h54	15	10
h20	16	10	25	23	13	12, 13	h55	14	11
h21	14	10	27	23	13	19, 20	h56	16	11
h22	17	10	25	23	13	11, 12	h57	13	10
h23	15	11	26	24	12	10, 14	h58	15	9
h24	15	10	27	25	13	11, 14	h59	13	9
h25	13	11	26	23	13	13, 14	h60	14	10
h26	14	10	25	24	13	11, 15	h61	14	10
h27	14	10	25	24	13	12, 14	h62	14	10
h28	14	11	25	24	13	11, 15	h63	13	10
h29	15	10	26	24	13	12, 13	h64	15	11
h30	15	9	26	22	14	15, 15	h65	16	10
h31	14	10	26	23	13	14, 14	h66	15	11
h32	14	11	27	24	13	11, 15	h67	15	11
h33	14	9	25	25	13	11, 13	h68	14	11
h34	14	9	25	24	13	11, 14	h69	14	11
h35	15	10	26	23	12	13, 16	h70	15	9

populations, respectively. Of these, 93 (C. African I.S.) and 88 (S. Spain) were unique.

The most common haplotypes were h16, h21, h22, h38 and h54 (C. African I.S.) and h5 and h14 (S. Spain). Haplotype diversity for each of the markers is shown in Table 3. Haplotype diversity for all Y-specific STR loci studied were of 0.9990 (S.E.: 0.0015) in the Central-West African immigrants in Spain and 0.9977 (S.E.: 0.0019) in the Southwest Spain populations.

Pairwise haplotype analysis using the population studied and other Europe and Iberian populations [2,13] in all the analyzed systems except DYS385 shows the data for the

DYS389II	DYS390	DYS393	DYS385	Haplotype	DYS19	DYS389I	DYS389II	DYS390	DYS393	DYS385
27	24	13	11, 14	h71	16	10	26	25	13	10, 14
27	23	13	16, 16	h72	16	10	26	25	13	12, 14
26	23	12	16, 17	h73	14	10	26	24	13	11, 16
25	24	13	11, 14	h74	14	11	27	24	13	11, 15
26	25	13	11, 14	h75	14	11	26	24	13	11, 14
28	23	12	11, 14	h76	14	10	26	23	12	11, 14
25	23	13	11, 14	h77	14	10	26	24	13	12, 14
28	22	13	12, 16	h78	15	10	26	25	12	12, 13
27	25	13	16, 18	h79	14	11	27	24	13	13, 15
27	23	14	12, 14	h80	13	10	28	25	14	11, 14
28	24	13	11, 15	h81	14	11	27	25	13	11, 15
26	24	12	13, 17	h82	16	10	26	25	13	11, 14
27	24	13	11, 15	h83	14	11	27	24	13	10, 14
26	24	13	10, 13	h84	14	10	26	24	13	10, 13
27	24	14	16, 16	h85	15	10	26	24	13	11, 14
26	22	13	13, 16	h86	13	10	27	24	13	16, 17
28	23	12	17, 17	h87	14	11	27	24	13	11, 14
28	23	12	15, 15	h88	13	11	27	24	13	13, 14
26	25	13	11, 14	h89	15	10	27	24	13	11, 15
27	24	13	10, 14	h90	15	9	27	25	12	14, 17
26	25	14	11, 14	h91	15	10	27	24	13	11, 14
27	24	13	16, 18	h92	14	10	26	24	13	11, 15
25	24	13	13, 16	h93	14	9	25	23	13	14, 14
26	25	13	17, 18	h94	15	10	26	24	13	11, 15
26	24	13	10, 14	h95	13	10	25	24	12	14, 18
26	24	14	11, 14	h96	15	11	27	24	13	11, 14
26	24	14	11, 14	h97	13	10	26	22	13	13, 14
28	25	14	15, 16	h98	14	11	27	22	12	12, 17
28	23	15	14, 15	h99	14	11	28	24	13	11, 14
25	23	13	12, 12	h100	14	11	27	24	13	11, 14
28	24	13	11, 14	h101	14	11	27	24	13	11, 14
27	24	13	11, 12	h102	15	11	29	24	13	11, 13
27	25	13	11, 14	h103	15	10	26	24	14	11, 14
27	23	13	11, 13							
25	24	11	11, 15							

Table 3
Haplotype diversity value

	DYS19	DYS389I	DYS389II	DYS390	DYS393	DYS385
(C. African I.S.)	0.6463	0.5888	0.7132	0.5313	0.6164	0.9359
(S. Spain)	0.6144	0.5912	0.6908	0.6101	0.4169	0.8252

Central-West African immigrant population in Spain ($p=0.000$) separating from the data for the rest of the populations.

References

- [1] M. Sasaki, H. Shiono, *J. Forensic Sci.* 41 (1996) 275–278.
- [2] A. Carracedo, et al., *Forensic Sci. Int.* 119 (2001) 28–41.
- [3] P.S. Walsh, et al., *BioTechniques* 10 (4) (1991) 506–513.
- [4] L. Gusmão, et al., *Forensic Sci. Int.* 106 (1999) 163–172.
- [5] P.M. Schneider, et al., *Forensic Sci. Int.* 102 (1999) 159–165.
- [6] P.M. Schneider, et al., *Forensic Sci. Int.* 97 (1998) 61–70.
- [7] M. Kayser, et al., *Int. J. Legal Med.* 110 (1997) 125–133.
- [8] P. De Knijff, et al., *Int. J. Legal Med.* 110 (1997) 134–140.
- [9] L. Roewer, et al., in: G. Sensabaugh, B. Olaisen, P. Lincoln (Eds.), *Advances in Forensic Genetics*, vol. 8, Elsevier Science, 2000.
- [10] B. Rolf, et al., *Eur. J. Genet.* 6 (6) (1998) 558–583.
- [11] M. Nei, *Proc. Natl. Acad. Sci. U. S. A.* 70 (1973) 3321–3323.
- [12] S. Schneider, et al., *Arlequin ver. 1.1*, University of Geneva, 1977.
- [13] A. González-Neira, et al., *Forensic Sci. Int.* 110 (2000) 117–126.