

FOR THE RECORD

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Y-Chromosome STR Haplotypes in Central-West African Immigrant in Spain Population Sample

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Blood samples were obtained from 103 healthy unrelated black West African immigrant population in Spain from different countries situated to the south of the Sahara desert. The DNA was extracted using Chelex 100 protocol as described by Walsh et al. (1). 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. (2). The DYS385 amplification conditions complied with the methodology described by Schneider et al. (3). The PCR was performed in a Perkin Elmer 9600 thermocycler.

Allele nomenclature was proposed by Kayser et al. (4) and de Knijff (5) with the exception of the DYS389 locus. The nomenclature of this locus was according Gusmão et al. (2).

Electrophoresis was carried out on 4% polyacrylamide denaturing sequencing gels in a 377 automated system (Applied Biosystems Division/Perkin Elmer). Genotype classification was done using Genescan PCR analysis software with 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), Dr. P.M. Schneider (Institut für Rechtsmedizin, Mainz, Germany). Haplotype diversity was calculated according to Nei (6). Analysis of Molecular Variance (AMOVA) was performed by Markov test using the Arlequin software 1.1 (7). Genetic distance matrix between populations were obtained by using the pairwise difference genetic distance.

A total of 98 different haplotypes were observed (Table 1), 93 of them being unique. The most common haplotype (DYS19: 15, DYS385: 16/16, DYS389I: 10, DYS389II: 28, DYS390: 21, and DYS393: 13) had frequency of 1.94% (h16, h21, h22, h38, and h54). Haplotype diversity for each of the markers is shown in Table 1. Haplotype diversity for all seven Y-specific STR loci in Central-

West African Immigrant in Spain population was calculated to be 0.9990 (standard error: 0.0015).

Pairwise haplotype analysis using the population studied and other Iberian and African populations (8,9) shows the valencian ($p = 0.000$) population distant from the rest of the populations.

The complete data are available to any interested researcher upon request.

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TABLE 1—Y STR haplotypes in a black Central-West African immigrant population in Spain.

Haplotype	n	F	DYS19	DYS389I	DYS389II	DYS390	DYS393	DYS385
h1	1	0,0097	15	9	26	22	13	14,15
h2	1	0,0097	15	10	28	21	10	17,19
h3	1	0,0097	14	11	27	21	14	16,16
h4	1	0,0097	15	10	28	21	13	17,17
h5	1	0,0097	16	10	28	22	13	16,27
h6	1	0,0097	14	10	27	21	13	14,17
h7	1	0,0097	13	11	28	23	12	15,16
h8	1	0,0097	16	10	28	22	13	16,17
h9	1	0,0097	14	10	28	21	13	16,19
h10	1	0,0097	15	10	28	21	13	16,18
h11	1	0,0097	15	10	27	21	14	18,18
h12	1	0,0097	16	8	25	21	13	14,14
h13	1	0,0097	15	10	27	21	13	17,17
h14	1	0,0097	15	10	28	21	14	15,15
h15	1	0,0097	16	10	29	21	14	14,16
h16	2	0,0194	15	10	28	21	14	14,16
h17	1	0,0097	16	9	26	21	14	16,18
h18	1	0,0097	14	9	26	22	14	16,20
h19	1	0,0097	15	10	28	21	13	14,18
h20	1	0,0097	16	10	28	21	14	13,16
h21	2	0,0194	15	10	27	21	14	16,17
h22	2	0,0194	16	10	27	21	14	15,16
h23	1	0,0097	16	10	28	21	13	17,17
h24	1	0,0097	15	10	26	25	13	13,16
h25	1	0,0097	15	10	27	21	13	17,19
h26	1	0,0097	15	10	27	21	13	13,15
h27	1	0,0097	15	10	29	21	13	16,17
h28	1	0,0097	15	10	27	20	13	14,16
h29	1	0,0097	15	10	27	21	14	14,16
h30	1	0,0097	15	10	27	21	14	16,16
h31	1	0,0097	15	8	26	21	13	16,16
h32	1	0,0097	15	10	26	24	13	13,15
h33	1	0,0097	15	10	27	21	14	15,20
h34	1	0,0097	17	9	26	23	13	14,14
h35	1	0,0097	17	9	27	21	15	17,17
h36	1	0,0097	15	11	28	21	15	18,21
h37	1	0,0097	16	10	27	21	13	15,17
h38	2	0,0194	15	10	28	21	13	16,17
h39	1	0,0097	16	11	29	21	14	15,16
h40	1	0,0097	17	10	28	22	15	15,16
h41	1	0,0097	16	10	28	21	14	17,18
h42	1	0,0097	15	9	26	21	14	16,16
h43	1	0,0097	15	9	26	21	16	17,18
h44	1	0,0097	15	10	29	21	13	15,16
h45	1	0,0097	15	9	26	22	13	15,16
h46	1	0,0097	16	10	27	21	15	16,18
h47	1	0,0097	15	10	27	22	14	17,18
h48	1	0,0097	14	9	25	25	13	19,19
h49	1	0,0097	16	10	28	21	13	17,18
h50	1	0,0097	15	9	27	21	13	15,16
h51	1	0,0097	16	10	28	21	14	16,16
h52	1	0,0097	15	18	28	23	15	16,16
h53	1	0,0097	15	10	29	21	13	15,18
h54	2	0,0194	17	10	27	21	14	16,16
h55	1	0,0097	15	10	28	21	14	15,16
h56	1	0,0097	15	10	28	21	13	17,18
h57	1	0,0097	16	10	27	20	14	15,15
h58	1	0,0097	15	11	28	21	14	15,17
h59	1	0,0097	16	10	29	21	14	16,16
h60	1	0,0097	16	10	28	21	13	14,15
h61	1	0,0097	15	9	27	22	13	13,15
h62	1	0,0097	15	8	25	21	13	16,16
h63	1	0,0097	15	10	27	21	14	16,18
h64	1	0,0097	16	10	29	21	14	16,17
h65	1	0,0097	13	10	28	24	12	15,16
h66	1	0,0097	15	11	27	21	14	18,18
h67	1	0,0097	15	10	27	21	13	15,18
h68	1	0,0097	15	11	28	21	14	17,17
h69	1	0,0097	14	9	25	22	14	16,18

continues

TABLE 1—Continued.

Haplotype	n	F	DYS19	DYS389I	DYS389II	DYS390	DYS393	DYS385
h70	1	0,0097	15	9	27	21	14	14,15
h71	1	0,0097	16	9	27	22	12	14,14
h72	1	0,0097	13	10	28	24	14	16,17
h73	1	0,0097	14	10	27	23	14	15,17
h74	1	0,0097	15	10	27	22	13	27,19
h75	1	0,0097	15	10	28	21	13	15,17
h76	1	0,0097	15	10	29	21	14	15,16
h77	1	0,0097	15	10	29	21	14	14,15
h78	1	0,0097	15	11	27	21	14	16,16
h79	1	0,0097	15	11	28	21	14	16,16
h80	1	0,0097	15	11	28	21	14	15,16
h81	1	0,0097	15	11	29	23	13	13,15
h82	1	0,0097	15	12	29	22	14	16,18
h83	1	0,0097	15	12	29	22	13	12,15
h84	1	0,0097	16	9	27	22	13	13,16
h85	1	0,0097	16	10	27	21	13	16,17
h86	1	0,0097	16	10	27	21	15	14,18
h87	1	0,0097	16	11	27	21	14	16,16
h88	1	0,0097	15	9	26	22	13	17,17
h89	1	0,0097	16	11	27	22	13	16,17
h90	1	0,0097	16	11	28	21	15	17,17
h91	1	0,0097	17	9	26	22	13	17,19
h92	1	0,0097	17	10	27	20	14	15,16
h93	1	0,0097	17	10	28	20	15	16,16
h94	1	0,0097	17	11	28	22	13	16,16
h95	1	0,0097	17	11	28	22	13	15,16
h96	1	0,0097	17	11	28	22	13	15,18
h97	1	0,0097	17	11	28	22	13	16,15
h98	1	0,0097	17	1	28	22	13	17,17
HVD			0,6463	0,5888	0,7132	0,5313	0,6164	0,9359

* N: number of haplotype; n: individuals observed for each haplotype; HVD: haplotype diversity value; F: frequency for each haplotype in 103 individuals.