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Announcement of population data

Y-chromosome STR haplotypes in a southwest Spain population sample

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Abstract

The Y-chromosome polymorphism of eight STRs (DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392; DYS393, DYS385) were studied in 111 unrelated individuals from the population of southwest Spain. The most common haplotype was shared by 3.6% of the sample, while 99 haplotypes were unique. The gene diversity was 0.9977. © 2002 Elsevier Science Ireland Ltd. All rights reserved.

Keywords: Y-chromosome STRs; PCR multiplex; Forensic genetics; Population genetics

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Population: Blood samples were obtained from 111 healthy unrelated males from the southwest of Spain.

Extraction: The DNA was extracted using the 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).

PCR: 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] and multiplex amplification of DYS391 DYS392, DYS393 was carried out according to Kloosterman et al. [4]. The PCR was performed in a Perkin-Elmer 9600 thermocycler.

Allele nomenclature was proposed by Kayser et al. [5] and de Knijff [6] with the exception of the DYS389 locus. The nomenclature of this locus was in accordance with that of Roewer et al. [7], Rolf et al. [8], Gusmão et al. [2].

Typing: 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 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), Dr. P.M. Schneider (Institut für Rechtsmedizin, Mainz, Germany) and Dr. Kloosterman (The Forensic Science Laboratory, Rijswijk, The Netherlands).

Results: The results are shown in Table 1

Quality control: Proficiency testing of the GEP-ISFH WG (http://www.usc.es/gep-isfh).

Data analysis: The haplotype diversity was calculated according to Nei. [9]. Analysis of molecular variance (AMOVA) was performed with the Markov test using the Arlequin software 1.1 [10]. The genetic distance matrix between populations was obtained by using the pairwise difference genetic distance. A unweighted pair group method with arithmetic means (UPGMA) tree was built from the distance matrix using the options NEIGHBOUR and DRAWTREE in the PHYLIP package [11] employing Nei [12] genetic distances.

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Other remarks: A total of 103 different haplotypes were observed (Table 1), 99 of them being unique. The most common haplotypes (DYS19:14, DYS385:11/14, DYS389I:10, DYS389II:26, DYS390:24, DYS391:10, DYS392:13; DYS393:13) had a frequency of 3.60% (h5 and h14). The haplotype diversity for each of the markers is shown in Table 1. The haplotype diversity for all nine Y-specific STR loci in the southwest of Spain population was calculated to be 0.9977 (S.E. 0.0019).

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Table 1
Y-STR haplotypes in a southwest of Spain population[a]

Haplotype	*n*	*F*	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS385
h1	1	0.0090	15	9	25	22	10	13	14	12.15
h2	1	0.0090	15	10	27	24	9	11	14	11.15
h3	1	0.0090	15	10	27	23	10	13	12	13.15
h4	1	0.0090	14	11	27	24	9	13	13	11.15
h5	4	0.0360	14	10	26	24	11	11	13	11.14
h6	1	0.0090	14	10	25	24	11	13	13	11.14
h7	1	0.0090	15	10	26	23	12	11	13	14.16
h8	1	0.0090	14	10	26	24	10	14	13	11.14
h9	1	0.0090	14	10	26	23	10	13	13	13.14
h10	1	0.0090	13	11	27	24	11	13	13	13.14
h11	2	0.0180	14	10	26	24	10	11	13	11.14
h12	1	0.0090	14	10	26	24	9	11	13	11.14
h13	1	0.0090	14	10	26	25	10	12	13	11.14
h14	4	0.0360	14	10	26	24	11	13	13	11.14
h15	1	0.0090	14	10	25	24	10	13	13	11.14
h16	1	0.0090	14	9	25	24	10	13	14	11.14
h17	1	0.0090	16	10	26	23	9	11	12	15.18
h18	1	0.0090	15	10	26	24	10	13	13	11.14
h19	1	0.0090	14	10	26	23	11	13	13	11.14
h20	1	0.0090	16	10	25	23	11	11	13	12.13
h21	1	0.0090	14	10	27	23	10	13	13	19.20
h22	1	0.0090	17	10	25	23	10	14	13	11.12
h23	1	0.0090	15	11	26	24	11	11	12	10.14
h24	1	0.0090	15	10	27	25	10	11	13	11.14
h25	1	0.0090	13	11	26	23	10	13	13	13.14
h26	1	0.0090	14	10	25	24	9	13	13	11.15
h27	1	0.0090	14	10	25	24	10	11	13	12.14
h28	1	0.0090	14	11	25	24	11	13	13	11.15
h29	1	0.0090	15	10	26	24	10	13	13	12.13
h30	1	0.0090	15	9	26	22	10	11	14	15.15
h31	1	0.0090	14	10	26	23	11	11	13	14.14
h32	1	0.0090	14	11	27	24	10	13	13	11.15
h33	1	0.0090	14	9	25	25	10	11	13	11.13
h34	1	0.0090	14	9	25	24	9	13	13	11.14
h35	1	0.0090	15	10	26	23	10	14	12	13.16
h36	1	0.0090	14	11	27	24	10	11	13	11.14
h37	1	0.0090	13	10	27	23	10	13	13	16.16
h38	1	0.0090	14	10	26	23	10	13	12	16.17
h39	1	0.0090	14	9	25	24	10	11	13	11.14
h40	1	0.0090	14	11	26	25	10	13	13	11.14
h41	1	0.0090	14	11	28	23	10	11	12	11.14
h42	2	0.0180	14	9	25	23	10	13	13	11.14
h43	1	0.0090	13	11	28	22	10	13	13	12.16
h44	1	0.0090	13	9	27	25	9	11	13	16.18
h45	1	0.0090	15	11	27	23	10	11	14	12.14
h46	1	0.0090	14	12	28	24	10	13	13	11.15
h47	1	0.0090	15	10	26	24	10	13	12	13.17
h48	1	0.0090	14	11	27	24	11	13	13	11.15
h49	1	0.0090	14	10	26	24	10	11	13	10.13
h50	1	0.0090	13	10	27	24	10	13	14	16.16
h51	1	0.0090	14	9	26	22	10	11	13	13.16
h52	1	0.0090	14	11	28	23	11	13	12	17.17
h53	1	0.0090	14	11	28	23	11	13	12	15.15
h54	1	0.0090	15	10	26	25	10	11	13	11.14
h55	1	0.0090	14	11	27	24	10	11	13	10.14
h56	1	0.0090	16	11	26	25	9	13	14	11.14
h57	1	0.0090	13	10	27	24	9	11	13	16.18

Table 1 (*Continued*)

Haplotype	*n*	*F*	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS385
h58	1	0.0090	15	9	25	24	9	11	13	13.16
h59	1	0.0090	13	9	26	25	9	11	13	17.18
h60	1	0.0090	14	10	26	24	10	13	13	10.14
h61	1	0.0090	14	10	26	24	10	11	14	11.14
h62	1	0.0090	14	10	26	24	10	13	14	11.14
h63	1	0.0090	13	10	28	25	11	11	14	15.16
h64	1	0.0090	15	11	28	23	10	13	15	14.15
h65	1	0.0090	16	10	25	23	10	13	13	12.12
h66	1	0.0090	15	11	28	24	12	14	13	11.14
h67	1	0.0090	15	11	27	24	12	13	13	11.12
h68	1	0.0090	14	11	27	25	10	13	13	11.14
h69	1	0.0090	14	11	27	23	10	11	13	11.13
h70	1	0.0090	15	9	25	24	10	13	11	11.15
h71	1	0.0090	16	10	26	25	11	13	13	10.14
h72	1	0.0090	16	10	26	25	10	13	13	12.14
h73	1	0.0090	14	10	26	24	11	11	13	11.16
h74	1	0.0090	14	11	27	24	10	11	13	11.15
h75	1	0.0090	14	11	26	24	10	14	13	11.14
h76	1	0.0090	14	10	26	23	10	13	12	11.14
h77	1	0.0090	14	10	26	24	10	11	13	12.14
h78	1	0.0090	15	10	26	25	10	13	12	12.13
h79	1	0.0090	14	11	27	24	11	13	13	13.15
h80	1	0.0090	13	10	28	25	10	13	14	11.14
h81	1	0.0090	14	11	27	25	11	11	13	11.15
h82	1	0.0090	16	10	26	25	10	11	13	11.14
h83	1	0.0090	14	11	27	24	11	14	13	10.14
h84	1	0.0090	14	10	26	24	10	13	13	10.13
h85	1	0.0090	15	10	26	24	10	11	13	11.14
h86	1	0.0090	13	10	27	24	10	13	13	16.17
h87	1	0.0090	14	11	27	24	9	14	13	11.14
h88	1	0.0090	13	11	27	24	9	11	13	13.14
h89	1	0.0090	15	10	27	24	9	11	13	11.15
h90	1	0.0090	15	9	27	25	9	11	12	14.17
h91	1	0.0090	15	10	27	24	11	12	13	11.14
h92	1	0.0090	14	10	26	24	11	11	13	11.15
h93	1	0.0090	14	9	25	23	10	14	13	14.14
h94	1	0.0090	15	10	26	24	11	13	13	11.15
h95	1	0.0090	13	10	25	24	10	14	12	14.18
h96	1	0.0090	15	11	27	24	11	11	13	11.14
h97	1	0.0090	13	10	26	22	10	11	13	13.14
h98	1	0.0090	14	11	27	22	11	13	12	12.17
h99	1	0.0090	14	11	28	24	10	11	13	11.14
h100	1	0.0090	14	11	27	24	10	14	13	11.14
h101	1	0.0090	14	11	27	24	11	11	13	11.14
h102	1	0.0090	15	11	29	24	10	13	13	11.13
h103	1	0.0090	15	10	26	24	11	11	14	11.14
HVD			0.614	0.5912	0.6908	0.6101	0.5963	0.5982	0.4169	0.8252

[a] *N*: number of haplotypes; *n*: individuals observed for each haplotype; HVD: haplotype diversity value; *F*: frequency for each haplotype in 111 individuals.

AMOVA analysis using the population studied and other Iberian and African populations [13–15] in all the analysed systems except DYS385 shows the southwest Spain population distant from the rest of the populations ($P < 0.05$), except for the Basque ($P = 0.077$) and Valencian ($P = 0.079$) populations [11]. When the population differentiation test was carried out at each STR [13,14], it showed a complex description. No significant population differentiation was found at DYS19, DYS390, DYS391 and DYS393. The highest population differentiation is at DYS389I ($P = 0.000$), DYS389II ($P = 0.000$) and barely significant values appear ($P = 0.02$) at DYS392.

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