

FOR THE RECORD

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Allele Frequencies of Y-Chromosome STR Loci DYS385 and DYS392 in Three Eastern Spanish Populations*

POPULATION: 109 males from three Spanish populations: Valencia ($N = 20$) and the islands of Majorca ($N = 51$) and Minorca ($N = 38$) (Spain).

KEYWORDS: forensic science, Y-chromosome, short tandem repeats, population data, Eastern Spain

Blood samples were collected from healthy autochthonous unrelated males from Valencia and the islands of Majorca and Minorca (Spain). DNA was extracted by means of a standard phenol/ chloroform DNA protocol (1). Coamplification of the loci DYS385 and DYS392 was performed in a duplex reaction, using approximately 20 ng of genomic DNA in a total reaction volume of 25 μ L. The primers used are described in Kayser et al. (2) and de Knijff et al. (3). PCR cycling conditions were as described in Füredi et al. (4), with minor modifications. A GeneAmp PCR System 2400 (PE Applied Biosystems) was used for amplification. Detection of the amplified products was carried out using an ABI 310 automatic sequencer (Perkin-Elmer) along with the GENESCAN 2.1 Analysis software. Our own allele ladders were used for allele designations. Allele nomenclature was as proposed by Kayser et al. (2) and de Knijff et al. (3). Gene diversity was estimated according to Nei (5). Allele frequencies, as well as pairwise analysis, were calculated using the ARLEQUIN package (6). Data on Iberian populations were used for comparisons (7–11). DYS392 gene diversities (0.448–0.640) were within the range of those observed in the other Y-chromosome STRs studied in these samples (12), whereas DYS385 had the highest gene diversities (0.615–0.755). Comparisons between all of the three populations studied showed no significant differences. When comparisons were carried out with other Iberian populations, significant differences were observed at DYS385. With respect to Catalonia and Andalusia, we found differences at DYS392.

This dataset can be accessed at <http://www.uib.es/depart/dba/Genetics/web/pagininvestigacio.htm>.

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TABLE 1—Allele frequencies and gene diversities at the STR loci *DYS385* and *DYS392* in the populations studied. Number of individuals in parenthesis.

Locus	Allele	Majorca (51)	Minorca (38)	Valencia (20)	Pooled (109)
DYS385	9–13	0.020	0.009
	10–14	0.039	0.018
	11–11	0.020	0.009
	11–13	...	0.053	0.050	0.028
	11–14	0.608	0.500	0.450	0.541
	11–15	0.078	0.079	...	0.064
	12–12	0.020	0.026	...	0.018
	12–13	...	0.026	...	0.009
	12–14	...	0.079	0.050	0.037
	12–15	0.039	0.026	...	0.028
	12–16	0.020	0.009
	12–17	0.020	0.009
	13–16	0.020	...	0.100	0.028
	13–17	0.059	...	0.100	0.046
	14–14	...	0.026	...	0.009
	14–15	0.050	0.009
	14–16	...	0.053	...	0.018
	15–15	...	0.026	...	0.009
	15–16	...	0.026	0.100	0.028
	16–16	0.020	...	0.050	0.018
16–17	...	0.026	...	0.009	
16–18	0.039	0.018	
17–18	0.050	0.009	
17–19	...	0.053	...	0.018	
	Gene diversity	0.615	0.725	0.755	0.694
DYS392	10	0.020	0.009
	11	0.157	0.211	0.300	0.202
	12	0.059	0.053	0.100	0.064
	13	0.706	0.711	0.500	0.670
	14	0.059	0.026	0.100	0.055
	Gene diversity	0.472	0.448	0.640	0.505

TABLE 2—Observed haplotypes distribution in the populations studied. (MA = Majorca, MI = Minorca, VA = Valencia, PO = Pooled).

Haplotypes	DYS392	DYS385	MA	MI	VA	PO	%
1	10	16, 16	1			1	(0.009)
2	11	11, 14	1			1	(0.009)
3	11	12, 12	1	1		2	(0.018)
4	11	12, 17	1			1	(0.009)
5	11	13, 16	1		2	3	(0.028)
6	11	13, 17	2		1	3	(0.028)
7	11	14, 14		1		1	(0.009)
8	11	14, 15			1	1	(0.009)
9	11	14, 16		1		1	(0.009)
10	11	15, 15		1		1	(0.009)
11	11	15, 16		1		1	(0.009)
12	11	16, 16			1	1	(0.009)
13	11	16, 17		1		1	(0.009)
14	11	16, 18	2			2	(0.018)
15	11	17, 18			1	1	(0.009)
16	11	17, 19		2		2	(0.018)
17	12	11, 14	3	1		4	(0.037)
18	12	14, 16		1		1	(0.009)
19	12	15, 16			2	2	(0.018)
20	13	9, 13	1			1	(0.009)
21	13	10, 14	2			2	(0.018)
22	13	11, 11	1			1	(0.009)
23	13	11, 13		2	1	3	(0.028)
24	13	11, 14	25	17	8	50	(0.459)
25	13	11, 15	4	3		7	(0.064)
26	13	12, 13		1		1	(0.009)
27	13	12, 14		3	1	4	(0.037)
28	13	12, 15	1	1		2	(0.018)
29	13	12, 16	1			1	(0.009)
30	13	13, 17	1			1	(0.009)
31	14	11, 14	2	1	1	4	(0.037)
32	14	12, 15	1			1	(0.009)
33	14	13, 17			1	1	(0.009)
Number of individuals			51	38	20		109
Number of haplotypes			18	16	11		33
Discriminatory capacity			35.3	42.1	55.0		30.3
Haplotype diversity			0.755 ± 0.064	0.795 ± 0.066	0.842 ± 0.077		0.783 ± 0.042