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Haplotype frequencies of DYS19, DYS389 I/II, DYS390, DYS391, DYS393 and DYS385 STR loci in Barcelona (North-East Spain)

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Abstract

We report a Y-chromosome haplotype frequency database obtained from a Barcelona population study. Samples were typed according to the published nomenclature and the ISFG guidelines for short tandem repeat (STR) analyses.

Keywords: Y-chromosome; STR; Population genetics; Barcelona; Haplotype

1. Introduction

The aim of this study is to report the haplotype frequency database for DYS19, DYS389 (I and II), DYS390, DYS391, DYS393 and DYS385 STR loci in Barcelona. The establishment of well-defined local databases is essential for using Y-chromosome, short tandem repeats (STR) in routine practice [1].

2. Material and methods

DNA was extracted from blood samples ($n = 163$) from healthy unrelated individuals (males), living in the metropolitan area of Barcelona, by using the phenol–chloroform–isoamyl alcohol method [2]. Hot-start PCR triplex (Triplex I: DYS19 and DYS389 I/II;

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Table 1
Haplotypes of the DYS19, DYS385, DYS389 I, and II, DYS390, DYS391, DYS392, and DYS393 in population from Barcelona

	n	Haplotypes									n	Haplotypes							
1	1	13	11–14	13	29	24	11	13	13	66	1	14	12–14	12	28	23	11	14	13
2	1	13	11–14	13	29	25	9	14	13	67	1	14	12–14	13	29	24	11	13	13
3	1	13	11–14	14	30	25	11	13	13	68	1	14	12–14	13	29	24	11	14	13
4	1	13	11–16	14	30	25	10	13	13	69	1	14	12–14	13	30	23	11	13	13
5	2	13	12–14	13	29	24	11	13	13	70	1	14	12–14	14	30	23	11	13	13
6	1	13	13–14	14	30	23	9	12	13	71	1	14	12–14	14	30	25	11	13	13
7	1	13	13–14	14	30	24	9	11	13	72	1	14	12–15	12	29	24	11	13	13
8	1	13	13–14	14	30	25	9	11	13	73	1	14	12–15	13	29	24	10	13	13
9	1	13	13–14	15	32	25	9	11	13	74	1	14	12–15	14	30	24	11	14	13
10	1	13	13–15	14	30	24	9	11	13	75	1	14	13–14	13	29	24	11	13	13
11	1	13	15–15	13	31	24	10	11	13	76	1	14	13–16	13	29	23	10	11	12
12	1	13	16–16	13	30	23	10	11	13	77	1	14	13–17	12	29	24	10	11	13
13	1	13	16–16	13	30	24	10	11	13	78	1	14	13–17	13	29	23	10	11	12
14	1	13	16–16	13	33	26	10	11	13	79	1	14	13–18	13	31	23	10	11	12
15	1	13	16–17	13	31	24	10	11	13	80	1	14	13–18	14	31	23	11	11	12
16	1	13	16–18	13	30	24	11	11	13	81	1	14	14–14	12	28	22	10	11	13
17	1	13	16–18	13	32	23	10	11	13	82	1	14	14–15	12	28	22	10	11	13
18	1	13	16–18	14	31	25	10	11	13	83	1	14	14–15	12	28	24	11	13	13
19	1	13	17–18	12	30	25	10	11	13	84	1	14	14–16	13	29	23	10	11	12
20	1	13	17–20	12	31	24	10	14	13	85	1	14	14–16	13	31	24	10	12	14
21	1	14	9–14	13	31	26	11	13	13	86	1	14	14–16	14	31	23	10	13	13
22	1	14	10–13	14	30	23	11	13	13	87	1	14	14–18	13	28	23	10	13	12
23	1	14	10–14	13	31	24	10	13	13	88	1	14	15–16	12	30	22	10	14	14
24	1	14	11–11	13	28	24	11	13	13	89	1	14	16–18	13	30	24	10	11	13
25	2	14	11–11	13	29	24	11	13	13	90	1	14	17–18	14	30	23	10	14	13
26	1	14	11–11	14	29	23	10	13	13	91	1	14	17–19	13	30	24	10	11	13
27	2	14	11–11	14	30	23	10	13	13	92	1	15	9–16	13	29	22	10	14	12
28	1	14	11–14	12	28	25	11	13	13	93	1	15	10–12	13	29	22	11	11	13
29	1	14	11–14	12	31	24	10	13	13	94	1	15	10–14	13	29	25	11	13	13
30	1	14	11–14	13	27	23	11	13	13	95	1	15	11–11	13	29	23	11	13	13
31	1	14	11–14	13	29	23	10	13	13	96	1	15	11–12	13	29	24	11	13	12
32	2	14	11–14	13	29	23	11	13	13	97	1	15	11–14	13	29	24	11	13	13
33	1	14	11–14	13	29	23	11	14	13	98	1	15	11–14	13	30	24	11	13	13
34	5	14	11–14	13	29	24	10	13	13	99	1	15	11–14	14	30	24	11	13	13
35	1	14	11–14	13	29	24	10	13	14	100	1	15	11–14	14	30	25	11	13	13
36	1	14	11–14	13	29	24	10	14	13	101	1	15	11–15	13	29	23	11	13	13
37	1	14	11–14	13	29	24	11	12	13	102	1	15	11–15	14	30	24	10	13	13
38	1	14	11–14	13	29	24	11	13	12	103	1	15	11–15	14	31	24	11	13	13
39	15	14	11–14	13	29	24	11	13	13	104	1	15	12–12	13	28	23	10	11	13
40	1	14	11–14	13	29	24	12	13	13	105	1	15	12–15	12	29	22	10	11	12
41	1	14	11–14	13	29	25	11	13	13	106	1	15	13–14	12	28	22	10	11	13
42	3	14	11–14	13	30	24	11	13	13	107	1	15	13–15	12	30	23	10	11	14
43	1	14	11–14	13	30	24	11	14	13	108	1	15	13–16	13	29	23	10	11	12
44	1	14	11–14	14	29	23	10	13	13	109	1	15	13–16	14	28	23	9	11	12
45	2	14	11–14	14	29	24	11	13	13	110	1	15	14–14	13	27	22	10	11	15
46	2	14	11–14	14	30	24	10	13	13	111	1	15	14–15	12	27	22	10	11	14
47	4	14	11–14	14	30	24	11	13	13	112	1	15	14–16	12	29	23	10	14	13
48	1	14	11–14	14	31	23	10	13	14	113	1	15	14–16	13	30	23	10	15	13
49	1	14	11–14	14	31	24	10	13	13	114	1	15	14–17	13	29	23	10	13	13

Table 1 (*continued*)

	n	Haplotypes									*n*	Haplotypes							
50	1	14	11–14	14	31	24	11	11	13	115	1	15	15–17	14	30	22	10	12	12
51	1	14	11–14	14	31	24	11	13	13	116	1	15	15–17	14	30	23	10	11	12
52	1	14	11–14	14	32	24	10	13	13	117	1	15	16–17	13	30	22	10	12	14
53	1	14	11–15	12	28	24	10	13	13	118	1	16	11–14	13	31	24	10	13	13
54	2	14	11–15	13	29	24	10	13	13	119	1	16	11–14	14	31	25	10	11	13
55	2	14	11–15	13	29	24	11	13	13	120	1	16	12–12	13	28	23	10	11	13
56	1	14	11–15	13	29	24	11	13	14	121	1	16	13–16	13	29	24	11	11	13
57	1	14	11–15	13	29	24	12	13	13	122	1	16	13–17	12	28	26	10	11	13
58	1	14	11–15	13	29	24	13	13	13	123	2	16	14–14	12	29	22	10	11	14
59	1	14	11–15	13	30	23	11	13	13	124	1	16	14–14	13	31	23	10	13	13
60	1	14	11–15	13	30	24	10	11	12	125	1	17	15–16	13	28	23	10	11	13
61	1	14	11–15	14	30	23	11	13	13	126	1	17	12–12	13	28	23	10	11	13
62	3	14	11–15	14	30	24	11	13	13	127	1	17	12–12	14	29	25	9	11	12
63	1	14	11–15	14	31	24	10	13	14	128	1	17	12–14	14	31	25	10	12	14
64	1	14	11–15	14	32	24	10	13	14	129	1	17	15–17	13	29	23	10	13	14
65	1	14	12–13	13	29	24	11	13	13										

Triplex II: DYS390, DYS391 and DYS393) and singleplex (DYS385 and DYS392) amplifications were accomplished with fluorescein labelled primers by the method described by Gené et al. [3]. The primers used were those described by Kayser et al. [1] and de Knijff et al. [4]. Genotypes were analyzed in denaturing 6% polyacrylamide gel electrophoresis, using a monochrome automated laser fluorescence sequencer. Our group has participated in the Y-STR Haplotyping Quality Assurance Exercise, 2000–2001. The alleles from all loci reported were typed according to the published nomenclatures and the ISFG guidelines for STR analyses.

Gene diversity value (*D*) was calculated with the equation $D = 1 - \Sigma q_i^2$, where q_i is the frequency of the *i*th haplotype [5,6]. The power of exclusion for Y-linked systems is identical to the gene diversity value. The discrimination capacity was calculated as a percentage of the different haplotype frequencies. The program ARLEQUIN 1.1 was used for all calculations [7].

3. Results and discussion

The allele distribution and gene diversities for each locus were similar to previously reported European data [1]. As shown in Table 1, complete eight Y-chromosomal STR haplotypes could be obtained for 163 individuals, among which 129 different haplotypes were observed, 115 of them being unique (Discrimination Capacity: 0.79%). Gene diversity was 0.9897. From a forensic point of view, the theoretical values obtained revealed that the eight combined systems have a high diagnostic efficiency.

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