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FOR THE RECORD

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Y-Chromosomal STR Haplotypes at the Loci DYS19, DYS385, DYS389II, DYS390, DYS391, and DYS393 in Marmara Region of Turkey

POPULATION: Ninety-two unrelated healthy males from Marmara Region in Turkey (İstanbul not included).

KEYWORDS: forensic science, short tandem repeats (STR); Y-chromosome, haplotype, population data, forensics, Marmara Region, Turkey

Genomic DNA was isolated from either blood samples or hair samples using Chelex extraction procedure (1).

The extracted DNA was quantified according to the quantification procedure (2). Slot-blot hybridization was done using the Quantiblot® Human DNA Quantification Kit (Perkin-Elmer, Foster City, CA).

PCR amplification: The six Y-chromosome STR loci (namely, DYS19, DYS385, DYS389II, DYS390, DYS391, and DYS393) were co-amplified (3) using approximately 2 ng of genomic DNA in a total reaction volume of 25 μL following the method of the Y-PLEX™ 6 kit user's manual (ReliaGene Technologies, Inc., New Orleans, LA). The primers for DYS19, DYS389II, and DYS393 are labeled with 5-FAM and the primers for DYS385, DYS390, and DYS391 are labeled with TAMRA. All loci were amplified in a GeneAmp PCR System 9700 (PE Applied Biosystems).

The amplified products (4) were detected with the ABI PRISM® 310 Genetic Analyzer using the separation medium Performance Optimized Polymer 4 (POP-4), 47 cm capillaries, filter set A, and an injection time of 5 s as described in the ABI PRISM® 310 Genetic Analyzer User's Manual (PE Applied Biosystems). The results were analyzed using Gene Scan analysis software v.3.1.2 and genotypes were determined by comparison with allelic ladder using Genotyper DNA fragment analysis software v.2.5 (PE Applied Biosystems) with the Y-Typer 310 Macro v.3.0 (ReliaGene Technologies, Inc., New Orleans, LA). Allele designations (5–7) were determined by comparison of the sample fragments with those of allelic ladders provided with kit.

See Tables 1 and 2 for results.

Analysis of data: Frequencies were calculated through the gene counting method. Haplotype and gene diversity was calculated according to Nei (8).

In the population object of study, we observed 78/84 different haplotypes. A list of the 78 haplotypes is in Table 2. The most common haplotypes are H12, H22, H23, H46, H57, H73 (2 in 84, 2.38% of individuals). The overall haplotype diversity is 98.94%, with 78 unique assets out of 84 test samples.

The complete dataset can be accessed at http://hadicakir.medyatext.gen.tr.

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TABLE 1—*Allele/genotype-frequencies of the six Y-STR loci in Marmara Region of Turkey.*

Allele	DYS19 (*n* = 92)	DYS389II (*n* = 92)	DYS390 (*n* = 92)	DYS391 (*n* = 92)	DYS393 (*n* = 92)	Genotype	DYS385 (*n* = 84)
9				0.0652		11–12	0.0119
10				0.7609		11–13	0.0357
11				0.1739	0.0109	11–14	0.0952
12					0.3478	11–15	0.0476
13	0.0869				0.4891	11–16	0.0357
14	0.2935				0.1196	12–12	0.0119
15	0.4348				0.0326	12–13	0.0357
16	0.1739					12–14	0.0238
17	0.0109					12–15	0.0357
21			0.0435			12–17	0.0476
22			0.1195			12–19	0.0119
23			0.3804			13–14	0.0357
24			0.2283			13–15	0.0595
25			0.2174			13–16	0.0714
26			0.0109			13–17	0.0357
28		0.1304				13–18	0.0595
29		0.2826				14–15	0.0238
30		0.3914				14–16	0.0476
31		0.1304				14–17	0.0476
32		0.0652				14–20	0.0119
						15–16	0.0119
						15–17	0.0595
						15–18	0.0119
						15–19	0.0119
						16–17	0.0357
						16–18	0.0119
						17–17	0.0357
						17–18	0.0119
						17–19	0.0119
						18–19	0.0119
Total	1.0000	1.0000	1.0000	1.0000	1.0000		1.0000
h*	0.6871	0.7286	0.7396	0.3866	0.6244		0.9524

* h: gene diversity value.

TABLE 2—*Haplotype frequencies of the six Y-STR loci in Marmara Region of Turkey.*

							Observed Value	
H*	DYS19	DYS385	DYS389II	DYS390	DYS391	DYS393	n†	%
1	13	11–15	29	25	10	12	1	0.0119
2	13	15–17	31	24	10	13	1	0.0119
3	13	16–17	30	24	10	13	1	0.0119
4	13	16–17	31	23	10	13	1	0.0119
5	13	16–18	30	24	10	13	1	0.0119
6	13	17–17	32	24	10	13	1	0.0119
7	13	17–19	30	23	10	13	1	0.0119
8	13	18–19	31	24	10	13	1	0.0119
9	14	11–14	29	24	10	13	1	0.0119
10	14	11–16	29	24	11	13	1	0.0119
11	14	11–16	30	25	10	12	1	0.0119
12	14	12–13	29	23	10	13	2	0.0238
13	14	12–13	29	23	11	13	1	0.0119
14	14	12–14	29	24	11	12	1	0.0119
15	14	12–14	29	25	11	12	1	0.0119
16	14	12–15	28	24	10	12	1	0.0119
17	14	12–15	30	24	11	12	1	0.0119
18	14	12–17	28	23	10	12	1	0.0119
19	14	12–19	32	23	10	12	1	0.0119
20	14	13–14	28	24	10	13	1	0.0119
21	14	13–15	30	25	9	12	1	0.0119
22	14	13–15	30	25	10	12	2	0.0238
23	14	13–18	30	23	10	12	2	0.0238
24	14	14–15	28	23	10	12	1	0.0119
25	14	14–16	28	22	10	13	1	0.0119

TABLE 2—*Continued.*

							Observed Value	
H*	DYS19	DYS385	DYS389II	DYS390	DYS391	DYS393	n†	%
26	14	14–16	30	23	10	13	1	0.0119
27	14	14–17	31	23	10	13	1	0.0119
28	14	14–20	30	23	10	13	1	0.0119
29	14	15–17	31	22	10	13	1	0.0119
30	14	15–19	30	23	10	12	1	0.0119
31	15	11–14	30	24	11	13	1	0.0119
32	15	11–14	30	25	11	13	1	0.0119
33	15	11–15	30	25	11	13	1	0.0119
34	15	11–15	32	25	11	13	1	0.0119
35	15	11–16	28	23	10	13	1	0.0119
36	15	12–12	30	22	10	14	1	0.0119
37	15	12–15	29	23	10	12	1	0.0119
38	15	12–17	28	21	10	14	1	0.0119
39	15	13–14	29	23	10	14	1	0.0119
40	15	13–14	30	23	10	14	1	0.0119
41	15	13–15	29	21	10	15	1	0.0119
42	15	13–15	31	23	10	14	1	0.0119
43	15	13–16	29	21	10	15	1	0.0119
44	15	13–16	29	22	10	15	1	0.0119
45	15	13–16	29	23	9	12	1	0.0119
46	15	13–16	30	23	9	12	2	0.0238
47	15	13–17	29	23	9	12	1	0.0119
48	15	13–17	29	25	11	13	1	0.0119
49	15	13–17	30	23	10	12	1	0.0119
50	15	13–18	29	23	10	11	1	0.0119
51	15	13–18	30	23	10	12	1	0.0119
52	15	13–18	32	24	10	14	1	0.0119
53	15	14–16	28	21	10	14	1	0.0119
54	15	14–17	28	24	10	12	1	0.0119
55	15	14–17	29	23	10	12	1	0.0119
56	15	14–17	29	23	10	13	1	0.0119
57	15	15–17	30	22	10	12	2	0.0238
58	15	15–17	30	22	10	13	1	0.0119
59	15	15–18	30	22	10	12	1	0.0119
60	15	16–17	28	22	10	13	1	0.0119
61	15	17–17	30	22	11	14	1	0.0119
62	15	17–18	32	24	10	13	1	0.0119
63	16	11–12	29	25	10	13	1	0.0119
64	16	11–13	29	25	10	13	1	0.0119
65	16	11–13	31	25	10	13	1	0.0119
66	16	11–13	31	25	10	14	1	0.0119
67	16	11–14	29	25	10	13	1	0.0119
68	16	11–14	29	26	10	13	1	0.0119
69	16	11–14	30	24	11	13	1	0.0119
70	16	11–14	30	25	10	13	1	0.0119
71	16	11–14	31	25	11	13	1	0.0119
72	16	11–15	28	25	10	14	1	0.0119
73	16	12–17	29	23	10	12	2	0.0238
74	16	13–16	32	25	11	13	1	0.0119
75	16	14–15	30	24	10	13	1	0.0119
76	16	14–16	28	22	10	13	1	0.0119
77	16	17–17	29	23	10	13	1	0.0119
78	17	15–16	30	24	10	13	1	0.0119

* H: haplotype.
† *n*: male individuals observed for each haplotype.