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An investigation of 10 Y-STR loci and the detection of specific haplotype frequencies in Turkish population

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ABSTRACT

This study is to survey 10 Y-STR loci in 241 males from Turkey.

In this study, the 241 healthy and unrelated males living in different parts of Turkey for at least three generations were included. Genomic DNAs were isolated from peripheral blood samples by standard phenol-chloroform extraction method. 10 Y-STR loci including DYS19, DYS385a/b, DYS388, DYS389I/II, DYS390, DYS391, DYS392, DYS393, and YCAIIa/b were analyzed by using PCR and denaturing PAGE.

Allele frequencies, gene diversities and haplotype frequencies were analyzed. Gene diversity per locus varied from 0.5788 (DYS388) to 0.8903 (DYS385a/b). The numbers of haplotypes in *minHt* recommended by YCC and *Ht*10 have been 208 and 186, respectively. When our *minHt* haplotypes frequencies compared with the other seven populations, we have found statistically significant differences between our results and other populations (p < 0.01) except that Czech population (p > 0.05). We suggest that an alternative haplotype designated as *aHt* maybe alternative to *minHt* in respect of its Y-STR content with the highest gene diversity value. The *aHt* haplotype has found a higher discriminatory potential than *minHt* haplotype with a better $P_{d\ combined}$ value (0.9999936 vs 0.9999836) and has higher average gene diversity per locus (0.7834 vs 0.7518) in Turkish population.

***aHt* haplotype can be proposed as an alternative to *minHt* in paternity testing and forensic medicine applications involving Turkish male population. This study has also provided additional information to the framework of variation involving 10 Y-STR loci as well as a further contribution to the Y-STR database for Turkish male population.**

Keywords: Y Chromosome; Y-STR; Polymorphism; Haplotype; Turkey

1. INTRODUCTION

Human Y chromosome has been known to display comparatively low levels of polymorphisms in contrast with autosomal chromosomes. Nonetheless, there are many types of Y-chromosome specific polymorphisms identified in the non-recombining region of Y (NRY) including RFLPs, Y *Alu* and microsatellite polymorphisms [1, 2]. Microsatellites or short tandem repeats (STRs) are dispersed throughout the genome and are known to be highly polymorphic; hence, each microsatellite locus generally has many alleles due to variable number of repeat units [3,4].

Allelic genotyping of STRs does not require the use of complex molecular techniques, since amplifications and visualization of PCR products make it easy. Y-chromosome specific STRs (Y-STRs) are chosen as more informative in paternity testing, forensic applications and the study of population histories due to the haploid state of Y chromosome which ensures both the transmittance by the paternal lineages and the lack of recombination in NRY, excluding pseudoautosomal regions (PARs) [5−11].

Allelic and haplotypic distributions of Y-STRs have shown significant differences in different geographical regions, ethnical groups and communities [12-18]. Therefore, allelic and haplotypic frequencies of Y-STRs should be determined in a male population prior to any interpretations of forensic analysis and paternity testing [6,8-11,19]. In this study, allelic and haplotypic frequentcies involving 10 Y-STR loci: 8 Y-STR loci as recommended by Y Chromosome Consortium (YCC) plus DYS388 and YCAIIa/b-have been determined with such a necessity in a representative group of Turkish population in order to make comparisons with other populations.

2. MATERIALS AND METHODS

10 Y-STR loci were analyzed which included eight loci recommended by YCC for minimal haplotype (*minHt*)-DYS19, DYS385a/b, DYS389I/II, DYS390, DYS391, DYS392, and DYS393 [20,21] and the additional two: DYS388 and YCAIIa/b.

Healthy and unrelated 241 males living in different parts of Turkey for at least three generations were included in this study. The written informed consents were obtained from the study subjects and the study protocol was approved by the ethics committee of Ankara University Medical Faculty.

Genomic DNAs were isolated from peripheral blood samples by standard phenol-chloroform extraction method [22]. Four multiplex PCR analyses were carried out with locus specific primers in a total volume of 25 µl reaction mixture, containing; 50 - 150 ng genomic DNA, 10 mM Tris-HCl, 50 mM KCl, 1.5 mM $MgCl_2$, 0.1 - 0.8 µM of each primer, 200 µM of each dNTP (**Sigma**), 5 µg BSA and 1 unit Taq DNA polymerase (**Invitrogen**) [23]. Y-STRs amplified in combination in multiplex PCR are as follows: DYS389I, DYS389 II and DYS390 in multiplex I; DYS392 and DYS393 in multiplex II; DYS19 and DYS388 in multiplex III; DYS385a/b and DYS391 in multiplex IV; while YCAIIa/b loci were amplified separately. Cycling conditions were as follows: 32 cycles of 94˚C - 1 min, 54˚C - 1 min, 72˚C - 1 min for multiplex I, II, IV and YCAIIa/b; 35 cycles of 94˚C - 1 min, 55˚C - 1 min, 72˚C - 60 min for multiplex III. An initial denaturation at 94˚C - 2.5 min and a final extension at 72˚C - 10 min were performed before and after each cycling reactions. Female DNA was used as a negative control in every run.

Amplified products were separated by 6% denaturing polyacrylamide gel electrophoresis (PAGE) for 3 h at 1500 V. Visualization of PCR products was carried out by a modification of the silver staining method of Santos, *et al.* [23]. Gels were fixed for 15 min at room temperature in 10% (v/v) ethanol which were treated with 1% (v/v) nitric acid for 3 min with agitation thereafter. Gels were then rinsed in deionized water for 1 min and treated with 0.2% (w/v) silver nitrate and 0.1% (v/v) formaldehyde solution for 25 min with agitation. Gels were rinsed for a few seconds in deionized water, and developed in an aqueous solution of 3% Na_2CO_3 (w/v), 100 µl/L 2% (w/v) $Na_2S_2O_3$ and 0.1% formaldehyde until the bands were well visualized. Staining was ended with a fixative solution.

Allelic genotyping were carried out by using the defined DNA size markers (**Fermentase**, pUC Mix Marker, 8; ΦX174 RF DNA/BsuRI [HaeIII] Marker, 9) and self-made ladders as standards.

Allele frequencies, gene diversities (H), haplotype frequencies and genetic differentiation between populations were computed using Arlequin 3.1.1 software. Allele frequencies were calculated by gene counting, while H was computed for each locus according to the by formula (1), where n is the number of samples, k is the number of haplotypes, and p_i is the frequency of i-th haplotype [24].

$$H = \frac{n}{n-1}\left(1-\sum_{1}^{k} p_i^2\right) \tag{1}$$

The Combined Power of Discrimination ($P_{d\ combined}$) for haplotypes was calculated using the by formula (2), where P_{di} is Power of Discrimination of i-th locus [25].

$$P_{d\ combined} = 1-\prod_{i=1}^{n}\left(1-P_{di}\right) \tag{2}$$

3. RESULTS AND DISCUSSION

10 Y-STRs have been analyzed for diversity in 241 healthy and unrelated male individuals from Turkey. Observed allele or genotype frequencies of the 10 Y-STR loci have been given in **Table 1.** Variations in the number of individuals for certain loci have been brought about by some technical problems not anticipated.

Gene diversity values for each 10 Y-STR loci have been given in **Table 1**. The lowest gene diversity (0.5788) has been found in DYS388 locus, wherein the most frequent allele has been allele 13 with a frequency of 62.08%. This result has been in accord with the data reported by YCC [21]. The highest gene diversity (0.8903) has been found in DYS385 locus, wherein the most frequent allele has been allele 14 with a frequency of 17.62% (**Table 1**).

The observed number of haplotypes and their frequencies involving *minHt* and *Ht*10 haplotypes in this current survey have been tabulated in **Table 2**. The number of haplotypes detected for *minHt* is 208 and 186 for *Ht*10. Each haplotype belonging to *Ht*10 have been found to be unique while the same holds for *minHt* with the exception of H15 which has been detected in two individuals. Gene diversity, average gene diversity per locus and Combined Power of Discrimination ($P_{d\ combined}$) values for *Ht*10 and *minHt* haplotypes have been given in **Table 3**.

minHt haplotypes detected in this study group have been compared with seven other populations: Croatian

Table 1. Detected allele frequencies and gene diversities of the Y-STR loci in Turkish population.

Allele	DYS19 (n = 228)	DYS385* (n = 454)	DYS388 (n = 234)	DYS389I (n = 239)	DYS389II (n = 234)	DYS390 (n = 241)	DYS391 (n = 224)	DYS392 (n = 237)	DYS393 (n = 241)	YCAII* (n = 392)
7		0.0022								
8		0.0176						0.0042		
9		0.0330					0.0130	0.0042	0.0124	
10		0.0969					0.1732	0.0633	0.0166	
11		0.0903	0.0083	0.0167			0.5541	0.4262	0.0747	
12		0.1189	0.0083	0.0628			0.2338	0.2321	0.3942	
13	0.0342	0.1608	0.6208	0.2929			0.0260	0.1941	0.3361	
14	0.2222	0.1762	0.0458	0.4059				0.0422	0.1162	0.0025
15	0.4145	0.1057	0.0958	0.1590				0.0295	0.0498	0.0
16	0.2863	0.0815	0.1542	0.0628				0.0042		0.0
16.3		0.0066								
17	0.0385	0.0441	0.0542							0.0228
17.2		0.0022								
17.3		0.0396								
18	0.0043	0.0022	0.0083							0.0533
19		0.0132	0.0042							0.3173
20		0.0066				0.0041				0.1675
21		0.0022				0.0083				0.1066
22						0.0581				0.1878
23						0.2116				0.1193
24						0.3361				0.0203
25						0.2739				0.0
26					0.0085	0.0913				0.0025
27					0.0427	0.0166				
28					0.1667					
29					0.1838					
30					0.2564					
31					0.1453					
32					0.1410					
33					0.0556					
H	**0.6971**	**0.8903**	**0.5788**	**0.7191**	**0.8293**	**0.7583**	**0.6101**	**0.7232**	**0.7126**	**0.8087**

*Allele frequencies was calculated including two genomic copies.

Table 2. Detected number of haplotypes and their frequencies in *minHt* and *Ht*10 haplotypes surveyed in Turkish population in this study.

Haplotypes	*Ht*10*											
	*minHt***											
	DYS19	DYS385a/b	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	*N***	YCAIIa/b	DYS388	*N****
HPT1	15	11, 11	13	29	23	10	11	12	*1*	24/24	16	*1*
HPT2	15	10, 10	14	31	23	11	11	12	*1*	26/21	15	*1*
HPT3	15	13, 9	13	29	25	11	13	12	*1*	20/20	15	*1*
HPT4	15	13, 12	13	29	24	12	11	13	*1*	23/20	13	*1*
HPT5	15	13, 9	13	29	25	12	13	12	*1*	23/20	13	*1*
HPT6	15	15, 14	13	30	24	10	11	13	*1*	23/20	12	*1*
HPT7	15	15, 10	13	29	24	12	13	12	*1*	24/20	13	*1*
HPT8	14	13, 9	14	32	23	11	12	12	*1*	22/20	16	*1*
HPT9	15	12, 8	12	29	24	11	14	12	*1*	21/19	15	*1*
HPT10	15	12, 10	14	32	25	11	11	12	*1*	22/19	16	*1*
HPT11	15	14, 12	15	33	24	11	11	12	*1*	22/17	16	*1*
HPT12	16	15, 12	15	33	24	11	11	12	*1*	22/22	16	*1*
HPT13	15	17.3, 11	13	28	24	10	12	13	*1*	22/19	13	*1*
HPT14	15	17, 17	14	31	25	11	11	13	*1*	20/19	13	*1*
HPT15	14	14, 10	14	30	24	11	11	12	*2*	22/19	16	*1*
HPT16	16	17.3, 11	15	31	24	11	11	12	*1*	22/19	17	*1*
HPT17	14	17.3, 14	13	31	23	11	11	13	*1*	22/19	13	*1*
HPT18	16	13, 12	13	31	23	12	11	13	*1*	21/19	16	*1*
HPT19	16	13, 9	15	33	25	11	11	12	*1*	22/21	17	*1*
HPT20	15	14, 11	14	31	24	11	11	12	*1*	22/20	13	*1*
HPT21	15	12, 12	14	31	25	11	12	13	*1*	23/19	13	*1*
HPT22	14	13, 11	14	30	24	12	11	12	*1*	22/19	16	*1*
HPT23	16	16, 11	14	30	26	12	11	12	*1*	23/19	13	*1*
HPT24	13	17.3, 12	14	32	24	12	12	13	*1*	22/19	17	*1*
HPT25	14	16, 15	14	31	24	11	12	13	*1*	20/20	13	*1*

HPT26	14	17.3, 13	13	30	25	11	13	13	*1*	20/19	13	*1*
HPT27	15	17.3, 15	14	31	23	11	11	12	*1*	22/19	16	*1*
HPT28	15	14, 10	14	30	25	12	13	12	*1*	23/19	13	*1*
HPT29	14	14, 10	13	30	25	11	11	13	*1*	23/19	16	*1*
HPT30	15	16, 14	14	30	24	11	13	13	*1*	23/23	13	*1*
HPT31	15	15, 13	14	30	26	11	11	12	*1*	22/19	13	*1*
HPT32	16	14, 10	14	32	25	10	11	13	*1*	23/19	13	*1*
HPT33	15	21, 12	14	33	24	12	11	12	*1*	22/19	15	*1*
HPT34	15	14, 10	15	30	25	12	11	13	*1*	22/19	13	*1*
HPT35	15	17.3, 13	14	30	24	11	12	11	*1*	22/18	16	*1*
HPT36	14	16, 12	13	30	26	11	11	12	*1*	23/19	13	*1*
HPT37	15	11, 9	14	30	26	11	8	13	*1*	22/19	15	*1*
HPT38	16	14, 14	12	29	23	11	10	14	*1*	22/19	13	*1*
HPT39	15	17.2, 15	13	30	25	11	10	14	*1*	22/18	16	*1*
HPT40	16	14, 14	13	30	23	11	10	13	*1*	23/19	13	*1*
HPT41	15	14, 10	14	30	24	12	11	13	*1*	22/19	15	*1*
HPT42	15	20, 9	13	30	24	12	10	12	*1*	22/19	13	*1*
HPT43	15	19, 17	13	29	25	11	10	13	*1*	22/18	16	*1*
HPT44	15	15, 10	14	31	25	12	11	12	*1*	23/19	13	*1*
HPT45	15	16, 12	14	31	24	12	10	12	*1*	22/19	15	*1*
HPT46	15	9, 9	14	31	25	12	11	13	*1*	22/19	13	*1*
HPT47	15	16, 12	14	33	23	10	11	12	*1*	22/18	16	*1*
HPT48	16	11, 10	14	32	24	11	10	12	*1*	23/19	13	*1*
HPT49	15	13, 11	13	30	24	11	12	13	*1*	22/19	15	*1*
HPT50	13	14, 12	13	32	22	11	11	15	*1*	22/19	13	*1*
HPT51	14	15, 12	15	33	24	11	12	12	*1*	22/18	16	*1*
HPT52	14	17, 11	12	29	24	10	11	12	*1*	23/19	13	*1*
HPT53	14	15, 14	12	30	23	10	11	13	*1*	22/19	15	*1*
HPT54	14	17, 13	14	32	24	10	11	12	*1*	22/19	13	*1*
HPT55	14	17, 14	14	32	25	10	13	13	*1*	22/18	16	*1*
HPT56	14	17, 12	14	32	23	10	12	12	*1*	23/19	13	*1*
HPT57	16	12, 9	13	31	26	11	11	13	*1*	22/19	15	*1*
HPT58	14	10, 10	14	32	24	11	11	12	*1*	22/19	13	*1*
HPT59	14	14, 11	13	31	26	10	13	12	*1*	22/18	16	*1*
HPT60	15	17, 13	14	32	24	10	12	11	*1*	23/19	13	*1*
HPT61	16	14, 14	14	31	24	10	12	13	*1*	22/19	15	*1*
HPT62	14	13, 11	15	32	25	11	13	12	*1*	22/19	13	*1*
HPT63	15	15, 12	13	31	22	12	11	15	*1*	22/18	16	*1*
HPT64	15	19, 12	14	32	26	12	13	13	*1*	23/19	13	*1*
HPT65	16	13, 11	14	29	25	11	10	14	*1*	22/19	15	*1*
HPT66	14	14, 12	14	31	25	11	11	12	*1*	22/19	13	*1*
HPT67	15	14, 12	14	33	25	11	12	14	*1*	22/18	16	*1*
HPT68	14	13, 10	14	31	26	12	13	12	*1*	23/19	13	*1*
HPT69	13	15, 15	14	32	25	12	11	13	*1*	21/19	13	*1*
HPT70	14	16, 13	14	32	24	11	12	12	*1*	22/17	16	*1*
HPT71	14	19, 13	14	33	24	11	12	11	*1*	22/19	19	*1*
HPT72	16	14, 10	15	33	25	12	12	13	*1*	23/19	13	*1*
HPT73	15	16, 13	13	30	25	10	10	12	*1*	20/19	16	*1*
HPT74	14	13, 12	15	29	26	9	11	12	*1*	22/20	16	*1*
HPT75	14	14, 12	15	28	24	10	12	12	*1*	22/19	16	*1*
HPT76	16	14, 13	16	29	24	11	12	14	*1*	20/19	13	*1*
HPT77	15	14, 10	13	27	22	10	13	15	*1*	20/19	13	*1*
HPT78	15	15, 12	14	28	24	10	13	11	*1*	22/19	16	*1*
HPT79	14	13, 10	15	29	23	12	13	11	*1*	21/19	17	*1*
HPT80	13	14, 12	14	30	25	10	12	12	*1*	22/20	13	*1*
HPT81	15	14, 7	15	28	23	10	13	10	*1*	21/20	13	*1*
HPT82	15	11, 10	14	27	23	10	11	14	*1*	20/19	13	*1*
HPT83	13	15, 13	15	28	25	10	11	11	*1*	20/19	13	*1*
HPT84	14	12, 12	15	29	25	12	12	9	*1*	24/19	13	*1*
HPT85	14	15, 14	16	29	24	11	11	13	*1*	21/19	13	*1*
HPT86	14	14, 11	14	28	23	10	10	13	*1*	21/19	13	*1*
HPT87	15	16, 16	14	27	25	11	11	11	*1*	22/21	13	*1*
HPT88	13	17.3, 17	14	28	25	11	11	11	*1*	22/18	13	*1*
HPT89	16	14, 14	13	26	24	11	11	13	*1*	20/20	13	*1*
HPT90	16	13, 11	14	28	26	11	11	11	*1*	21/19	13	*1*
HPT91	15	14, 14	13	27	23	11	11	15	*1*	19/18	13	*1*
HPT92	13	17.3, 12	14	28	25	11	11	9	*1*	22/19	16	*1*
HPT93	15	15, 12	14	28	23	11	11	15	*1*	19/17	13	*1*
HPT94	14	15, 12	14	27	25	12	12	11	*1*	23/19	13	*1*

HPT95	14	12, 11	15	28	25	11	12	11	*1*	20/19	13	*1*
HPT96	15	14, 12	14	28	25	12	12	9	*1*	23/19	13	*1*
HPT97	16	14, 13	14	28	24	11	12	13	*1*	20/19	15	*1*
HPT98	17	15, 13	15	30	25	11	11	13	*1*	20/20	13	*1*
HPT99	14	17, 16	16	32	26	11	10	13	*1*	21/18	13	*1*
HPT100	15	14, 13	15	30	27	10	10	12	*1*	23/20	16	*1*
HPT101	16	16, 15	16	30	25	11	13	13	*1*	23/23	13	*1*
HPT102	16	16, 13	14	29	23	11	11	15	*1*	20/19	13	*1*
HPT103	16	15, 14	15	28	24	11	12	10	*1*	21/19	13	*1*
HPT104	15	14, 10	14	28	27	12	13	11	*1*	23/19	13	*1*
HPT105	15	17,13	15	29	25	11	12	10	*1*	22/19	16	*1*
HPT106	14	17, 15	14	29	23	10	11	11	*1*	20/18	13	*1*
HPT107	15	13, 12	15	29	26	11	13	10	*1*	23/19	13	*1*
HPT108	16	15, 13	14	28	22	11	13	15	*1*	20/19	13	*1*
HPT109	17	17.3, 17	16	31	23	11	12	15	*1*	21/19	13	*1*
HPT110	17	14, 13	14	28	23	12	11	14	*1*	20/19	13	*1*
HPT111	15	17.3, 14	16	30	25	11	12	12	*1*	22/19	14	*1*
HPT112	15	16, 15	14	28	24	11	12	13	*1*	21/19	15	*1*
HPT113	16	17.3, 13	15	29	24	11	13	12	*1*	22/19	16	*1*
HPT114	16	17, 11	15	29	25	11	11	12	*1*	22/19	16	*1*
HPT115	15	16, 15	16	30	26	10	12	14	*1*	22/19	13	*1*
HPT116	18	19, 13	16	29	25	11	11	13	*1*	21/19	13	*1*
HPT117	15	15, 14	15	28	25	12	12	12	*1*	22/19	13	*1*
HPT118	17	14, 10	16	31	27	11	11	13	*1*	23/19	13	*1*
HPT119	16	14, 10	15	29	25	13	12	13	*1*	22/19	13	*1*
HPT120	17	13, 13	14	29	25	10	11	13	*1*	23/22	14	*1*
HPT121	15	15, 13	15	29	24	11	11	12	*1*	22/19	16	*1*
HPT122	16	16, 13	14	28	23	10	11	14	*1*	20/20	13	*1*
HPT123	15	14, 10	16	30	24	12	12	11	*1*	22/19	13	*1*
HPT124	15	13, 12	14	28	24	11	13	13	*1*	19/14	13	*1*
HPT125	14	16, 10	13	29	23	11	11	13	*1*	22/19	13	*1*
HPT126	16	16.3, 13	14	29	23	11	11	13	*1*	22/19	16	*1*
HPT127	15	17.3, 13	14	28	24	11	11	12	*1*	22/19	16	*1*
HPT128	15	15, 13	14	29	24	12	11	12	*1*	22/22	18	*1*
HPT129	14	16.3, 14	14	29	23	13	13	13	*1*	19/19	13	*1*
HPT130	15	17.3, 17.3	14	29	24	12	11	12	*1*	22/21	15	*1*
HPT131	16	16.3, 11	14	28	24	12	11	12	*1*	22/19	15	*1*
HPT132	16	13, 10	13	29	24	11	11	14	*1*	20/20	13	*1*
HPT133	15	16, 10	13	28	23	11	9	13	*1*	20/20	15	*1*
HPT134	15	17.3, 15	15	32	24	11	12	13	*1*	20/20	13	*1*
HPT135	16	15, 10	14	29	26	10	12	14	*1*	23/19	14	*1*
HPT136	16	15, 13	14	28	24	11	13	15	*1*	20/19	14	*1*
HPT137	16	16, 15	14	28	23	11	11	12	*1*	23/20	13	*1*
HPT138	16	13, 12	14	27	24	10	11	12	*1*	19/18	17	*1*
HPT139	16	17, 13	13	28	25	11	11	12	*1*	20/19	13	*1*
HPT140	15	14, 11	16	29	26	12	12	12	*1*	23/22	13	*1*
HPT141	16	14, 13	15	30	23	11	11	14	*1*	20/19	13	*1*
HPT142	15	17, 16	16	30	24	11	11	13	*1*	22/21	13	*1*
HPT143	16	16, 13	16	31	24	10	11	13	*1*	22/19	13	*1*
HPT144	16	13,12	16	31	24	11	10	13	*1*	20/19	13	*1*
HPT145	16	17, 16	16	32	22	11	11	12	*1*	21/20	13	*1*
HPT146	16	14, 13	15	30	25	12	11	13	*1*	22/21	14	*1*
HPT147	16	14, 13	13	29	23	11	11	14	*1*	20/19	13	*1*
HPT148	16	11, 11	15	32	24	12	12	13	*1*	22/18	13	*1*
HPT149	15	14, 11	14	30	25	11	12	12	*1*	22/18	13	*1*
HPT150	15	17.3, 13	14	30	24	11	11	12	*1*	22/21	17	*1*
HPT151	15	14, 13	13	30	24	12	12	13	*1*	18/17	16	*1*
HPT152	16	14, 12	13	32	25	11	11	12	*1*	19/18	15	*1*
HPT153	15	14, 11	15	31	25	12	12	12	*1*	18/18	15	*1*
HPT154	15	15, 10	11	29	25	11	11	13	*1*	20/18	15	*1*
HPT155	16	16, 15	15	32	23	11	11	14	*1*	20/19	13	*1*
HPT156	16	16, 13	14	32	25	11	11	12	*1*	21/18	15	*1*
HPT157	16	14, 12	13	30	24	11	12	12	*1*	21/18	18	*1*
HPT158	14	15, 14	13	30	25	11	11	13	*1*	21/19	13	*1*
HPT159	16	13, 11	14	29	24	11	11	12	*1*	20/19	15	*1*
HPT160	15	16, 12	13	30	23	11	11	12	*1*	21/20	14	*1*
HPT161	14	15, 13	13	30	24	11	11	14	*1*	22/19	14	*1*
HPT162	14	14, 14	13	30	25	10	11	13	*1*	22/19	13	*1*
HPT163	14	15, 13	13	28	23	11	15	13	*1*	19/19	13	*1*

HPT164	16	14, 12	13	30	25	10	11	13	*1*	20/20	13	*1*
HPT165	17	13, 12	14	30	26	11	11	13	*1*	23/19	13	*1*
HPT166	14	16, 13	14	30	25	11	11	13	*1*	22/19	13	*1*
HPT167	16	15, 8	13	28	23	11	14	12	*1*	21/19	13	*1*
HPT168	17	13, 13	13	29	24	9	12	11	*1*	22/20	13	*1*
HPT169	15	13, 11	14	30	24	13	11	12	*1*	21/19	13	*1*
HPT170	15	16, 12	13	32	24	13	11	12	*1*	23/19	15	*1*
HPT171	17	11, 10	13	28	27	12	13	13	*1*	23/19	13	*1*
HPT172	16	13, 13	11	28	25	12	13	13	*1*	22/20	13	*1*
HPT173	15	15, 11	14	33	26	12	13	12	*1*	22/19	13	*1*
HPT174	16	14, 8	13	28	23	12	15	12	*1*	21/20	13	*1*
HPT175	14	15, 14	11	28	25	11	13	12	*1*	22/19	13	*1*
HPT176	13	14, 12	13	31	23	11	13	12	*1*	22/19	16	*1*
HPT177	14	13, 10	13	28	26	11	14	12	*1*	23/19	13	*1*
HPT178	15	20, 15	12	28	23	9	15	11	*1*	20/19	13	*1*
HPT179	16	15, 13	14	28	25	12	13	13	*1*	23/22	14	*1*
HPT180	14	20, 14	14	31	23	12	16	14	*1*	22/19	13	*1*
HPT181	16	19, 14	12	29	23	11	15	11	*1*	21/17	13	*1*
HPT182	15	12, 9	13	27	26	11	15	13	*1*	18/18	13	*1*
HPT183	16	14, 13	12	27	23	11	14	14	*1*	19/19	13	*1*
HPT184	15	15, 10	14	30	24	11	13	14	*1*	23/21	13	*1*
HPT185	16	10, 10	13	31	24	11	13	14	*1*	24/23	12	*1*
HPT186	16	14, 10	13	27	23	12	13	14	*1*	24/21	13	*1*
HPT187	15	12, 10	12	26	26	11	11	13	*1*			
HPT188	16	12, 9	15	33	26	12	11	14	*1*			
HPT189	14	12, 9	14	29	25	11	13	12	*1*			
HPT190	15	15, 12	15	30	24	11	15	14	*1*			
HPT191	16	13, 11	14	30	24	11	11	12	*1*			
HPT192	14	12, 11	13	29	23	12	14	13	*1*			
HPT193	16	12, 10	12	30	23	13	13	12	*1*			
HPT194	15	13, 11	14	32	24	10	13	12	*1*			
HPT195	14	14, 10	13	33	25	11	15	12	*1*			
HPT196	15	17, 13	13	30	23	13	13	12	*1*			
HPT197	14	15, 11	13	32	24	11	13	13	*1*			
HPT198	15	16, 9	14	31	24	11	14	12	*1*			
HPT199	15	14, 8	13	30	21	12	12	13	*1*			
HPT200	16	16, 8	13	30	25	10	12	13	*1*			
HPT201	16	16, 13	12	31	23	11	12	14	*1*			
HPT202	15	14, 10	12	29	22	12	14	12	*1*			
HPT203	16	14, 8	13	32	23	11	12	14	*1*			
HPT204	16	14, 11	14	32	20	11	12	15	*1*			
HPT205	17	11, 8	13	30	25	12	12	13	*1*			
HPT206	14	19, 16	14	31	24	11	12	13	*1*			
HPT207	15	14, 11	13	30	25	11	12	12	*1*			
HPT208	14	17, 10	12	30	24	11	12	12	*1*			

***Haplotype containing 10 Y-STR loci; **Haplotype containing 8 Y-STR loci; ***Number of individuals bearing each haplotype.**

Table 3. Comparative presentation of haplotype numbers, gene diversities, average gene diversities and $P_{d\ combined}$ values belonging to three haplotypes surveyed in this study.

Haplotypes	**n**	**Gene diversity**	**Average gene diversity per locus**	***PDc****
*Ht*10	186	1.0000 ± 0.0006	0.7476	0.9999989
MinHt	208	1.0000 ± 0.0005	0.7518	0.9999869
aHt	186	1.0000 ± 0.0006	0.7834	0.9999936

***Combined Power of Discrimination.**

(n = 166) [26], Czech (n = 50) [27], German (n = 166), Indian (n = 108), Mozambican (n = 112) [12], Japanese (n = 161) [28], Turkish (Antalya) (n = 210) [29], and Turkish (n = 280) [30]. Haplotypic comparisons have highlighted that no significant difference has been observed with Czech population ($p > 0.05$) while comparisons with all other populations have produced statistically significant differences from Turkish population in this study ($p < 0.01$), as shown in **Table 4**.

Our results suggest that an alternative haplotype (*aHt*), which differs slightly from *minHt* in respect of its Y-STR loci contents, maybe alternative for *minHt* in Turkish population. *aHt* has included the selected 8 Y-STR loci: DYS19, DYS385a/b, DYS389I, DYS389II, DYS390, DYS392, DYS393, and YCAIIa/b. The only difference between the *minHt* and the proposed *aHt* is the inclusion of YCAIIa/b locus in place of DYS391 locus in *aHt* due to its higher gene diversity value of 0.8087 as compared with 0.6101 of DYS391 locus (**Table 1**). We have found 186 unique haplotype in *aHt* (data not shown). The *aHt* has reflected a better $P_{d\ combined}$ value when compared with *minHt* (0.9999936 vs 0.9999869) and, has higher average gene diversity per locus (0.7834 vs 0.7518) (**Table 3**). The data has exhibited that *aHt* has a higher discriminatory potential than that of *minHt*.

Table 4. Exact test P values of populational genetic differentiation measures based on *minHt* haplotype frequencies between all pairs involving samples of eight populations and Turkish population in this study.

Population	Turkish (This study)	Croatian	Czech	German	Indian	Mozambican	Japanese	Turkish	Turkish (Antalya)
Turkish (This study)	-								
Czech[27]	0.32474 ±0.0283	-							
Mozambican[12]	0.0000	0.00103 ±0.0010	-						
Croatian[26]	0.0000	0.0000	0.0000	-					
Indian[12]	0.0000	0.0000	0.0000	0.0000	-				
Japanese[28]	0.00205 ±0.0017	0.01176 ±0.0026	0.0000	0.0000	0.0000	-			
German[12]	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	-		
Turkish[30]	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	-	
Turkish (Antalya)[29]	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	-

In conclusion this study results have yielded sufficient evidence that *aHt* can reliably be proposed as an alternative to *minHt* in paternity testing and forensic medicine applications for Turkish population. Our data have also provided additional information to the framework of variation involving 10 Y-STR loci as well as a further contribution to the Y-STR database for Turkish population.

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