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Allele frequency present within the DYS635, DYS437, DYS448, DYS456, DYS458, YGATA H4, DYS389I, DYS389II, DYS19, DYS391, DYS438, DYS390, DYS439, DYS392, DYS393, DYS385a and DYS385b of unrelated individuals in Iraq

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The Y chromosome is becoming a useful tool for tracing human evolution through male lineages marker. The aim of this study was to determine the genetic structure in Babylon province in Iraq and evaluate the importance of these STRs loci for forensic genetic applications. FTA® Technology was utilized to extract DNA from blood collected on FTA™ paper. We have analyzed 17 Y chromosomal STR loci (DYS635, DYS437, DYS448, DYS456, DYS458, YGATA H4, DYS389I, DYS389II, DYS19, DYS391, DYS438, DYS390, DYS439, DYS392, DYS393, DYS385a and DYS385b) for evaluating allele frequencies and genetic diversity. A total of 94 unique haplotypes was identified among the one hundred individuals studied. The DYS456 had the highest diversity (GD = 0.752), while DYS392 locus had the lowest one (GD = 0.185). The light has been focused and directed in this study to establish the basic forensic genetic information, knowledge, data and statistics which might be so ultimately helpful practically in forensic science and criminology and to let evaluate and present the DNA weight evidences in Iraq medico-legal institute and courts of law.

Key words: Allele frequency, FTA™ paper, Iraq, STR DNA typing, Y filer™.

INTRODUCTION

Microsatellites are a group of molecular markers chosen for a number of purposes which include forensics individual identification and relatedness testing polymorphic (Yamamoto et al., 1999; Nakamura, 2009). Low quantities of template DNA is required (10 to 100 ng) (Markoulatos et al., 2002), when using microsatellites. There is a high genomic abundance of random distribution throughout the genome. There is also an abundance of polymorphism. A nuclear DNA present in one copy per cell and only in males is called the Y chromosome. It includes the sex determining region and known as a paternal lineage marker (Butler et al., 2002;

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Carolina et al., 2010; Kuppareddi et al., 2010). The genetic information is inherited from the father to the son, and this information does not change except for mutational events (Hanson and Ballantyne, 2007). The individual STRs are inherited as a single unit because of the lack of recombination and this is called a haplotype and behaves as single allele per individual (Parson et al., 2003; Kwak et al., 2005).

The Y - chromosome is specific to the male portion of a male-female DNA mixed such as is common in sexual assault cases (Park et al., 2007). These STRs can also be useful in missing persons investigations, historical investigations, some paternity testing scenarios, and genetic genealogy (Park et al., 2007; Andrea et al., 2008). Although, they are often used to suggest which haplogroup an individual matches, STR analysis typically provides a person haplotype. Most tests on the Y chromosome examine between 12 and 67 STR markers (Jobling et al., 1997; Kayser et al., 1997). The Y chromosome is less variable than the other chromosomes. Many markers are thus needed to obtain a high degree of discrimination between unrelated males marker. The Y chromosome is becoming a useful tool for tracing human evolution through male lineages marker[13] as well as application in a variety of forensic situations[12] including those involving evidence from sexual assault cases containing a mixture of male and female DNA (Prinz et al., 1997; Prinz et al., 2001). Using Y-chromosome, specific methods can improve the chances of detecting low levels of male DNA in a high background of female DNA.

MATERIALS AND METHODS

Preparation of blood stain samples

Blood samples were randomly collected from healthy unrelated males living in middle and south of Iraq and sent to the genetic laboratories.

DNA extraction

DNA was extracted from all dried blood samples on FTA cards following the manufacture's procedure as described in Whatman FTA Protocol BD01 except that the Whatman FTA purification reagent was modified to half the volume. A 1.2 mm diameter disc was punched from each FTA card with a puncher. The discs were transferred to new Eppendorf tubes and washed 3 times in 100 µl Whatman FTA purification reagent. Each wash was incubated for 5 min at room temperature with moderate manual mixing and the reagent was discarded between washing steps. The discs were then washed twice in 200 µl TE buffer (10 mM Tris-HCl, 0.1 mM EDTA, pH 8.0), the buffer was discarded and the discs were left to dry at room temperature for 1 h.

DNA amplification for Y- Chromosomal STR

PCR is the process used to amplify a specific region of DNA. It is possible to create multiple copies from small amount of template DNA. A commercial kit Y filer™ PCR amplification kit (Applied Biosystems, Foster City, CA) that amplifies 17 Y-STR loci: DYS635, DYS437, DYS448, DYS456, DYS458, YGATA H4, DYS389I, DYS389II, DYS19, DYS391, DYS438, DYS390, DYS439, DYS392, DYS393, DYS385a and DYS385b and a segment of the amelogenin gene was used, according to manufacturer's instructions but in a total reaction volume of 25 µl. The master mix was homogenized by vortex for 3 s, then centrifuged briefly, then 25 µl of PCR amplification mix was pipetted into each reaction well. 1.2 mm punch from a card containing whole blood was loaded into the appropriate wells of the reaction plate. The positive amplification control, 1 µl of 2800 M Control DNA (10 ng/µl) was added to a reaction well containing 25 µl of PCR amplification mix. The preferred protocol used with the GeneAmp® PCR System 9700 thermal cycler is provided below. The estimated total cycle time was 1.5 h. PCR program is as follows: 96°C for 1 min, then 94°C for 10 s , 59°C for 1 min, 72°C for 30 s, for 25 cycles, then: 60°C for 20 min 4°C soak. After completion of the thermal cycling protocol, the amplified samples were kept or stored at –20°C in a light-protected box.

PCR amplicon analysis (capillary electrophoresis)

The major application of CE in forensic biology is in the detection and analysis of short tandem repeats (STRs). STR markers are preferred because of the powerful statistical analysis that is possible with these markers and the large databases that exist for convicted offenders' profiles. The ABI Prism1 3130xl Genetic Analyzer 16-capillary array system (Applied Biosystems, Foster City, CA, USA) was used following the manufacturer's protocols, with POP-7™ Polymer and Data Collection Software, Genemapper version 3.5 software (Applied Biosystems). The allele designations were determined by comparison of the PCR products with those of allelic ladders provided with the kit. Nomenclature of loci and alleles is according to the International Society of Forensic Genetics (ISFG) guidelines reported in Gill et al. (2001). By comparison of the size of a sample's alleles to size of alleles in allelic ladders for the same loci being tested in the sample, the STR genotyping was conducted.

Quality control

Allelic ladders, male DNA (positive internal control), female DNA (negative control) and the amelogenin (internal control), provided by Reliagene (Reliagene Tech.), were used in each reaction with the Y filer™ kit.

Statistical analysis for Y- Chromosomal STR

Analysis of data

Allele frequencies were calculated by direct counting.

Allele diversity (genetic diversity)

Allele diversity was calculated as described by Nei (1987).

$$D = \frac{n}{n-1}\left(1 - \sum_{i=1}^{n} p_i^2\right)$$

Where, *n* is the sample size and *pi* is the frequency of the *i*th allele.

Table 1. Allele frequencies and genetic diversity of (DYS635, DYS437, DYS448, DYS456, DYS458 and YGATA H4) Y-STR loci.

Allele	DYS635		DYS437		DYS448		DYS456		DYS458		YGATA H4	
	Freq.	SE	Freq.	SE	Freq.	SE	Freq.	SE	Freq.	SE	Freq.	SE
9	-	-	-	-	-	-	-	-	-	-	-	-
10	-	-	-	-	-	-	-	-	-	-	0.050	0.020
11	-	-	-	-	-	-	-	-	-	-	0.260	0.043
12	-	-	-	-	-	-	-	-	-	-	0.550	0.049
13	-	-	-	-	-	-	0.010	0.009	-	-	0.110	0.031
14	-	-	0.540	0.049	-	-	0.070	0.025	0.020	0.014	0.020	0.014
15	-	-	0.300	0.047	-	-	0.630	0.051	0.430	0.049	-	-
16	-	-	0.150	0.036	-	-	0.230	0.041	0.190	0.038	-	-
17	-	-	-	-	-	-	0.050	0.020	0.100	0.030	-	-
18	-	-	-	-	0.160	0.037	-	-	0.070	0.025	-	-
19	-	-	-	-	0.550	0.049	-	-	0.010	0.030	-	-
20	0.010	0.030	-	-	0.230	0.042	-	-	0.050	0.020	-	-
21	0.080	0.027	-	-	0.040	0.019	-	-	-	-	-	-
22	0.070	0.025	-	-	0.010	0.009	-	-	-	-	-	-
23	0.360	0.048	-	-	-		-	-	-	-	-	-
24	0.330	0.047	-	-	-		-	-	-	-	-	-
25	0.020	0.014	-	-	-		-	-	-	-	-	-
GD*	0.729		0.595		0.617		0.752		0.751		0.615	

Freq, Frequency; SE, standard error; GD, genetic diversity.

Standard error (SE)

The standard error (SE) of allele frequencies was calculated as:

$$SE\,(p_i) = \sqrt{[(1 - p_i)\,p_i]/N},$$

Where, pi denotes the frequency of the *ith* allele at any given locus and N equals the total number of individuals screened at this locus.

RESULTS AND DISCUSSION

Y-STR-Allele frequency and genetic diversity

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) (Betz et al., 2001; Corach et al., 2001; Dekairelle and Hoste, 2001; Honda et al., 2001; Gill et al., 2004). Allelic and haplotypic distributions of Y-STRs have shown significant differences in different geographical regions, ethnical groups and communities (Alaves et al., 2003; Gusmao et al., 2003; Rustamov et al., 2004; Yan et al., 2007). 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 (Budowle et al., 2003). In this study, allelic and haplotypic frequencies involving 17 Y-STR loci have been determined with such a necessity in a representative group of Iraq population in order to make comparisons with other populations. Seventeen Y-STRs have been analyzed for diversity in 100 healthy and unrelated male individuals. Observed allele or genotype frequencies of the 17 Y-STR loci have been given in Tables 1, 2 and 3.

Gene diversity values for each Y-STR loci have been given (Table 1, 2 and 3). The lowest gene diversity (0.185) has been found in DYS392 locus, wherein the most frequent allele has been allele 11 with a frequency of 0.90. The highest gene diversity (0.752) has been found in DYS385 locus, wherein the most frequent allele has been allele 15 with a frequency of 0.630. Data comparison between our samples and a previously published sample from the Iraq population was performed for markers which are common to both studies using the exact test for population differentiation implemented in GENEPOP (Raymond, 1995). In another study on 17 Y-STR Y-chromosomal short tandem repeat loci from the Cukurova region of Turkey, the DYS391 recorded lowest gene diversity in this region was 0.51 and the highest was 0.95 for DYS385a/b and no significant differences were found when this data was compared with haplotype data of other Turkish populations (Ayse et al., 2011). In Northern Greece the haplotype diversity was 0.9992 in 17 Y STR loci typed in a population sample of unrelated male individuals. Haplotypes are presented for the

Table 2. Allele frequencies and genetic diversity of (DYS19, DYS385a, DYS385b, DYS389I, DYS389II and DYS390) Y-STR loci.

Allele	DYS19		DYS385a		DYS385b		DYS389I		DYS389II		DYS390	
	Freq.	SE	Freq.	SE	Freq.	SE	Freq.	SE	Freq.	SE	Freq.	SE
11	-	-	0.100	0.030	-	-	-	-	-	-	-	-
12	-	-	0.040	0.019	-	-	0.180	0.038	-	-	-	-
13	0.390	0.046	0.540	0.049	0.030	0.017	0.500	0.020	-	-	-	-
14	0.400	0.094	0.120	0.031	0.270	0.043	0.320	0.038	-	-	-	-
15	0.140	0.036	0.010	0.009	0.150	0.036	-	-	-	-	-	-
16	0.020	0.014	0.060	0.024	0.150	0.036	-	-	-	-	-	-
17	0.010	0.009	0.070	0.025	0.020	0.014	-	-	-	-	-	-
18	-	-	-	-	0.190	0.039	-	-	-	-	-	-
19	-	-	0.020	0.014	0.150	0.036	-	-	-	-	-	-
20	-	-	-	-	0.030	0.017	-	-	-	-	-	-
21	-	-	-	-	-	-	-	-	-	-	0.030	0.017
22	-	-	-	-	-	-	-	-	-	-	0.040	0.019
23	-	-	-	-	-	-	-	-	-	-	0.450	0.049
24	-	-	-	-	-	-	-	-	-	-	0.280	0.043
25	-	-	-	-	-	-	-	-	-	-	0.150	0.036
28	-	-	-	-	-	-	-	-	0.090	0.028	-	-
29	-	-	-	-	-	-	-	-	0.200	0.040	-	-
30	-	-	-	-	-	-	-	-	0.510	0.020	-	-
31	-	-	-	-	-	-	-	-	0.100	0.030	-	-
32	-	-	-	-	-	-	-	-	0.070	0.025	-	-
GD*	0.668		0.670		0.819		0.608		0.727		0.693	

Table 3. Allele frequencies and genetic diversity of (DYS391, DYS392, DYS393, DYS438, and DYS439) Y-STR loci.

Allele	DYS391		DYS392		DYS393		DYS438		DYS439	
	Freq.	SE	Freq.	SE	Freq.	SE	Freq.	SE	Freq.	SE
8	0.040	0.019	-	-	-	-	-	-	-	-
9	0.170	0.038	-	-	-	-	0.130	0.034	-	-
10	0.570	0.045	-	-	-	-	0.650	0.048	0.420	0.049
11	0.110	0.030	0.900	0.030	-	-	0.130	0.034	0.320	0.038
12	0.060	0.024	0.010	0.009	0.240	0.043	0.070	0.025	0.130	0.034
13	-	-	0.060	0.024	0.650	0.048	-	-	0.100	0.030
14	-	-	0.030	0.017	0.090	0.028	-	-	-	-
GD*	0.624		0.185		0.504		0.531		0.694	

Freq, Frequency; SE, standard error; GD, genetic diversity.

following loci: DYS456, DYS389I, DYS390, DYS389II, DYS458, DYS19, DYS385a/b, DYS393, DYS391, DYS439, DYS635, DYS392, Y GATA H4, DYS437, DYS438 and DYS448. This database study provides additional information for the application of Y chromosomal STRs to forensic identification efforts in Greece (Leda et al., 2008).

Y-STR- Haplotypes and Haplotype frequency

The observed numbers of haplotypes and their frequencies have been shown (Tables 4, 5 and 6). We identified 96 different haplotypes in our study sample. 89 of which (93%) were unique, one was found twice and one was found in three individuals. The most frequent haplotype was haplotype number 77. Haplotype 77 seems to be specific to Iraq. Haplotypes detected in this study group have been compared with seven other populations: German (n = 88), Indian (n = 25), Chinese (n = 36), Italians(n = 100) (Manfred et al., 2001), Tunis (n = 105) (Imen et al., 2005) and India (n = 154) (Kuppareddi et al., 2010) (Table 7). Haplotypic comparisons have high-lighted that significant differences from Iraq population

Table 4. Haplotypes and haplotypes frequency for the 17 Y-STR loci (haplotype 1- haplotype 32).

Haplotype	DYS635	DYS437	DYS448	DYS456	DYS458	YGATA H4	DYS19	DYS385a	DYS385b	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS438	DYS439	N	F
H1	24	15	20	15	14	12	13	11	16	12	30	23	10	11	13	10	13	1	0.0025
H2	24	15	18	15	14	13	13	11	16	12	30	23	8	11	13	9	13	1	0.0025
H3	24	15	20	15	15	12	13	11	16	12	31	23	8	11	12	9	10	1	0.0025
H4	24	15	19	15	15	11	13	11	14	12	31	23	8	11	13	11	10	1	0.0025
H5	24	15	19	16	15	10	13	13	14	12	31	23	10	11	13	10	10	1	0.0025
H6	24	15	19	16	17	12	13	13	14	12	28	23	10	11	13	10	13	1	0.0025
H7	24	15	19	14	17	12	13	13	14	12	28	23	9	11	14	12	13	1	0.0025
H8	24	15	19	16	17	11	13	13	14	12	28	23	10	11	13	12	10	1	0.0025
H9	24	15	20	16	17	14	13	13	14	12	29	23	10	11	13	9	10	1	0.0025
H10	24	15	19	16	15	14	13	13	14	12	29	23	9	11	14	12	11	1	0.0025
H11	24	15	19	13	15	11	13	13	14	12	29	23	9	11	14	10	11	1	0.0025
H12	24	15	21	15	15	10	13	13	14	14	29	23	10	11	12	11	11	1	0.0025
H13	25	15	21	15	15	13	13	13	14	14	29	23	10	11	13	10	11	1	0.0025
H14	21	15	22	15	15	12	13	13	14	13	29	23	10	11	14	10	10	1	0.0025
H15	21	15	19	15	20	12	13	13	18	13	29	23	10	11	12	9	10	1	0.0025
H16	21	15	19	15	16	12	13	13	18	13	28	23	9	11	13	9	13	1	0.0025
H17	21	15	19	15	18	12	13	13	18	13	28	23	8	11	13	12	10	1	0.0025
H18	21	15	19	14	18	13	13	13	16	13	28	23	10	11	13	12	10	1	0.0025
H19	21	15	19	16	18	12	13	14	16	13	31	23	10	11	13	10	10	1	0.0025
H20	24	15	21	16	15	12	13	14	16	12	31	23	10	11	13	10	10	1	0.0025
H21	24	14	21	16	16	12	13	14	16	12	31	23	10	11	12	10	10	1	0.0025
H22	24	14	19	15	15	12	13	13	13	12	28	23	10	11	12	10	10	1	0.0025
H23	24	14	19	15	20	12	16	13	13	13	28	23	10	11	14	9	10	1	0.0025
H24	24	14	19	15	15	12	16	13	13	13	30	23	10	11	14	10	10	1	0.0025
H25	24	14	20	15	15	12	15	13	18	13	30	23	10	11	13	10	10	1	0.0025
H26	24	16	18	15	19	12	15	13	14	13	30	25	10	11	13	10	10	1	0.0025
H27	24	16	18	16	15	12	15	13	14	13	32	23	10	11	13	10	10	1	0.0025
H28	21	14	19	15	15	12	15	13	18	13	33	23	11	11	13	10	10	1	0.0025
H29	24	14	19	15	20	12	15	13	18	14	30	21	10	11	13	10	10	1	0.0025
H30	24	14	20	15	19	12	15	13	18	14	29	24	10	11	13	10	10	1	0.0025
H31	21	14	20	16	15	12	15	13	18	13	29	24	11	11	12	10	11	1	0.0025
H32	24	14	20	15	15	11	15	13	18	14	29	25	10	11	13	10	11	1	0.0025

in this study ($p < 0.05$). Our data have also provided additional information to the framework of variation involving seventeen Y-STR loci as well as a further contribution to the Y-STR database for Iraq population. This supports the observations, by others (Jorde et al., 2000), that, especially among European populations, Y STRs are very powerful in the detection of genetic differences between populations, compared with autosomal STRs. This can be attributed to the greater sensitivity of nonrecombining Y-chromosomal markers to founder effects and genetic drift. A similar conclusion was reached recently by Forster et al. (2000), on the basis of a phylogenetic approach only. The use of Y STRs allows the simple construction of highly variable haplotypes. With these haplotypes, it is possible to analyze differences in population structure by a comparison of haplotype diversity and of the number of population-specific haplotypes.

Conclusion

We identified 96 different haplotypes in our study sample. 94 of which (97.9%) were unique, one was found twice and one was found in three individuals. The DYS385b and DYS458 had the highest diversity (GD = 0.8392 and 0.806, respectively), while loci DYS392 and DYS439 had the lowest (D = 0.2695 and 0.2991, respectively).

Table 5. Haplotypes and haplotypes frequency for the 17 Y-STR loci (haplotype 33- haplotype 64).

Haplotype	DYS635	DYS437	DYS448	DYS456	DYS458	YGATA H4	DYS19	DYS385a	DYS385b	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS438	DYS439	N	F
H33	22	16	20	15	15	11	16	13	18	14	29	21	10	11	13	10	11	1	0.0025
H34	24	15	20	15	16	12	14	13	18	14	29	23	10	11	13	10	11	1	0.0025
H35	24	15	18	15	16	10	14	13	18	13	29	23	10	11	13	10	11	1	0.0025
H36	22	15	18	14	16	13	14	13	18	12	29	23	10	12	12	10	11	1	0.0025
H37	22	15	19	15	16	11	14	13	18	14	29	24	10	11	13	10	11	1	0.0025
H38	22	14	20	15	15	12	14	13	16	13	30	23	10	11	13	10	11	1	0.0025
H39	24	14	19	15	15	10	14	13	19	13	28	23	10	11	13	10	11	1	0.0025
H40	24	14	19	14	15	12	14	13	19	13	30	24	10	11	13	10	11	1	0.0025
H41	24	14	19	15	15	12	14	13	19	13	32	21	9	11	13	10	11	1	0.0025
H42	24	14	19	16	15	12	14	13	19	13	32	25	9	11	12	10	11	1	0.0025
H43	22	14	19	15	16	12	14	13	15	13	31	25	10	11	12	10	11	1	0.0025
H44	24	14	19	15	20	12	14	13	15	13	29	25	10	11	12	10	11	1	0.0025
H45	24	14	19	15	19	12	14	12	15	13	32	25	10	11	13	10	12	1	0.0025
H46	24	14	18	15	16	12	13	12	15	13	30	25	10	11	13	10	12	1	0.0025
H47	24	14	18	15	16	11	13	12	15	13	31	23	10	11	12	10	12	1	0.0025
H48	23	14	19	15	16	13	13	12	14	13	31	23	11	11	14	10	12	1	0.0025
H49	23	14	19	15	15	12	13	13	14	12	31	24	10	11	13	10	12	1	0.0025
H50	23	14	19	16	15	12	13	13	14	13	30	24	10	11	12	10	10	1	0.0025
H51	23	14	18	16	15	11	13	11	14	14	30	24	10	11	12	9	10	1	0.0025
H52	23	14	20	15	15	11	15	11	14	14	30	25	11	11	12	10	13	2	0.0050
H53	22	14	20	15	16	11	15	11	14	13	30	23	10	14	12	10	14	1	0.0025
H54	22	14	18	15	20	11	14	11	14	12	30	23	10	14	13	10	10	1	0.0025
H55	23	14	20	15	19	11	13	13	19	14	30	24	11	14	13	10	13	1	0.0025
H56	23	14	20	15	18	12	13	13	19	13	30	24	11	11	13	10	12	1	0.0025
H57	23	14	20	14	18	11	14	15	16	12	30	24	11	11	14	11	10	1	0.0025
H58	23	14	20	15	17	12	13	17	16	14	30	24	11	11	13	9	10	1	0.0025
H59	23	14	19	17	17	11	13	17	15	13	32	22	12	11	14	10	10	2	0.0050
H60	23	16	19	15	17	11	14	17	15	13	32	24	10	11	13	10	10	1	0.0025
H61	23	14	19	16	17	13	13	17	15	13	30	25	10	11	13	9	10	1	0.0025
H62	23	14	18	16	17	11	13	17	15	13	30	25	10	11	13	11	10	1	0.0025
H63	23	15	19	15	17	11	13	16	15	14	30	25	9	11	12	11	12	1	0.0025
H64	23	15	19	14	15	12	17	16	15	14	32	25	10	11	12	11	10	1	0.0025

Table 6. Haplotypes and haplotypes frequency for the 17 Y-STR loci (haplotype 65- haplotype 96).

Haplotype	DYS635	DYS437	DYS448	DYS456	DYS458	YGATA H4	DYS19	DYS385a	DYS385b	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS438	DYS439	N	F
H65	23	15	19	17	16	12	14	16	15	14	29	25	10	13	13	10	9	1	0.0025
H66	23	14	20	17	19	12	14	13	15	14	30	23	12	13	13	10	9	1	0.0025
H67	23	14	20	15	19	11	13	13	15	14	30	23	10	13	12	10	14	1	0.0025
H68	23	14	19	16	19	13	13	13	15	14	30	24	9	11	13	10	13	1	0.0025
H69	23	14	19	16	15	12	13	11	18	13	30	24	9	11	13	9	10	1	0.0025
H70	23	14	19	16	18	12	13	13	18	14	29	24	9	11	13	12	10	1	0.0025
H71	20	14	19	15	15	12	13	13	18	13	29	24	9	11	13	11	10	1	0.0025

Table 6. Contd.

H72	20	14	20	16	16	12	14	13	18	13	29	23	12	11	13	11	10	1	0.0025
H73	20	14	19	16	15	10	14	13	19	13	30	23	10	11	13	11	10	1	0.0025
H74	23	14	19	16	15	11	14	13	19	13	30	22	10	11	13	11	11	1	0.0025
H75	23	14	19	14	15	11	14	13	19	13	30	23	9	13	13	11	11	1	0.0025
H76	23	14	19	15	15	12	14	13	14	13	30	23	9	11	13	10	11	1	0.0025
H77	23	14	18	15	15	13	14	13	14	13	30	24	11	11	13	10	11	3	0.0075
H78	23	16	18	15	15	12	14	13	14	13	30	24	10	13	13	9	11	1	0.0025
H79	23	15	18	15	16	12	14	19	14	13	30	24	10	13	13	10	11	1	0.0025
H80	23	16	18	15	16	11	14	19	16	14	30	24	9	11	13	10	14	1	0.0025
H81	23	16	19	15	19	11	14	13	16	14	30	23	11	11	13	10	14	1	0.0025
H82	23	16	19	15	19	12	15	16	19	14	30	25	10	11	13	10	10	1	0.0025
H83	23	16	19	15	16	12	14	16	19	14	30	25	10	11	13	9	10	1	0.0025
H84	23	14	19	15	15	12	14	16	19	14	30	25	10	11	13	10	10	1	0.0025
H85	23	16	20	15	15	11	14	14	19	14	30	24	9	11	13	10	10	1	0.0025
H86	23	16	20	16	16	13	14	14	17	14	30	24	11	11	13	10	14	1	0.0025
H87	23	14	19	15	16	11	14	14	17	14	30	24	12	11	13	10	14	1	0.0025
H88	23	15	19	15	19	12	14	14	20	14	30	24	11	11	12	11	12	1	0.0025
H89	23	14	19	15	15	12	14	14	20	14	30	25	9	11	12	10	11	1	0.0025
H90	20	16	20	15	18	12	15	14	20	14	30	24	10	11	12	9	11	1	0.0025
H91	20	16	19	15	16	12	15	14	18	14	30	24	10	11	13	10	11	1	0.0025
H92	20	16	19	15	15	11	14	14	19	13	30	24	12	11	13	12	10	1	0.0025
H93	20	16	19	16	16	12	14	14	19	13	30	24	10	11	12	10	11	1	0.0025
H94	20	15	19	15	15	12	14	14	16	13	30	23	10	11	12	11	12	1	0.0025
H95	20	14	19	15	16	12	14	17	16	13	30	23	9	11	13	10	12	1	0.0025
H96	20	14	19	17	15	12	15	17	16	13	30	22	12	11	12	10	12	1	0.0025

Table 7. Comparison of the haplotypes and haplotype diversity in different human population groups.

Parameter	Iraq[1]	Tunis[2]	German[3]	Italy[4]	China[5]	India[6]	India[7]
Individuals number	100	105	88	100	36	25	154
Haplotypes number	96	81	77	82	34	16	152
Unique haplotypes	89	67	39	53	28	13	150
Proportion of unique haplotypes	0.93	0.83	0.51	0.65	0.82	0.81	0.98
Non-unique haplotypes	7	14	38	29	6	3	2
Proportion of non-unique haplotypes	0.07	0.17	0.49	0.35	0.18	0.19	0.01
Ratio (unique : non-unique)	12.71	4.88	1.03	1.83	4.67	4.33	98
Haplotypes diversity	0.892	0.9932	0.9963	0.9941	0.9968	0.950	0.9935

[1]This study.[2]Reference: Imen et al. (2005); [3]Reference: Manfred et al. (2001); [4]Reference: Manfred et al. (2001); [5]Reference: Manfred et al. (2001); [6]Reference: Manfred et al. (2001); [7]Reference: Kuppareddi et al. (2010).

Conflict of interests

The authors did not declare any conflict of interest.

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REFERENCES

Alaves C, Gusmao L, Barbosa J, Amorim A (2003). Evaluating the informative power of Y-STRs: A comparative study using European and new African haplotype data. Forensic Sci. Int. 134: 126- 133.

Andrea V, Nicoletta C, Fausta G, Anna P (2008). Population Data for 15 Autosomal STRs Loci and 12 Y Chromosome STRs Loci in a

population sample from the Sardinia Island (Italy). Leg Med. 11(1):37-40.
Ayse S, Husniye C, Yasar S (2011). Haplotype frequencies of 17 Y-chromosomal short tandem repeat loci from the Cukurova region of Turkey. Croat Med. J. 52(6):703-708.
Betz A, Bäbler G, Dietl G, Syeil X (2001). DYS STR analysis with epithelial cells in a rape case. Forensic Sci. Int. 118:126-130.
Budowle SSK, Lee HS, Chakraborty R (2003). Utility of Y chromosome STR haplotypes in forensic applications, Forensic Sci. Rev. 15:153-164.
Butler JM, Schoske R, Vallone PM, Kline MC (2002). A Novel Multiplex for Simultaneous Amplification of 20 Y-Chromosome STR Markers. Forensic Sci. Int. 129(1):10-24.
Carolina N, Miriam B, Cecilia S, Yolanda C (2010). Reconstructing the population history of Nicaragua by means of mtDNA, Y-chromosome STRs, and autosomal STR markers. Am. J. Phy. Anthropol. 143(4):591-600.
Corach D, Figueira RL, Marino M, Penacino G (2001). Routine Y-STR typing in forensic casework. Forensic Sci. Int. 118: 131-135.
Dekairelle AF, Hoste B (2001). Application of a Y-STR-pentaplex PCR (DYS19, DYS389I and II, DYS390 and DYS393) to sexual assault cases. Forensic Sci. Int. 118:122-125.
Forster P, Roh A, Lu¨nnemann P, Brinkmann C, Zerjal T, Tyler- Smith C,Brinkmann B (2000). A short tandem repeat-based phylogeny for the human Y chromosome. Am. J. Hum. Genet. 67:182-196.
Gill P, Brenner C, Brinkmann B, Budowle B (2001). DNA Commission of the International Society of Forensic Genetics: recommendations for forensic analysis using Y-chromosome STRs. Forensic Sci. Int. 124:5-10.
Gill P, Werrett DJ, Budowle B, Guerrieri R (2004). An assessment of whether SNPs will replace STRs in national DNA databases—joint considerations of the DNA working group of the European Network of Forensic Science Institutes (ENFSI) and the Scientific Working Group on DNA Analysis Methods (SWGDAM). Science Justice 44:51-3.
Gusmao L, Sanchez-Diz P, Alves C, Beleza S (2003). Grouping of Y-STR haplotypes discloses European geographic clines. Forensic Sci. Int. 134:172-179.
Hanson EK, Ballantyne J (2007). An ultra-high discrimination Y chromosome short tandem repeat multiplex DNA typing system. PLoS ONE 2(8): e688.
Honda K, Tun Z, Matoba R (2001). DNA testing of Klinefelter's syndrome in a criminal case using XY-chromosomal STR multiplex-PCR. J. Forensic Sci. 46(5): 1235-8.
Imen A, Leila A, Ahmed R (2005). Haplotypes of 13 Y-chromosomal STR loci in south Tunisia population (Sfax region). Legal Medicine 4627: 1-5.
Jobling MA, Pandya A, Tyler-Smith C (1997). The Y chromosome in forensic analysis and paternity testing. Int. J. Leg. Med. 110:118-124.
Jorde LB, Watkins WS, Bamshad MJ, Dixon ME, Ricker CE, Seielstad MT, Batzer MA (2000). The distribution of human genetic diversity: a comparison of mitochondrial, autosomal, and Y-chromosome data. Am. J. Hum Genet. 66:979-988.
Kayser M, Caglia A, Corach D, Fretwell N (1997). Evaluation of Y-chromosomal STRs: a multicenter study. Int. J. Legal Med. 110:125-133.
Kuppareddi BG, Suhasini M, Vijaya S (2010). Kanthimathi. Chromosome STR Allelic and Haplotype Diversity in Five Ethic Tamil Populations from Tamil Nadu, India. Leg. Med. 12:265-269.
Kwak KD, Jin HJ, Shin DJ, Kim JM, Roewer L, Krawczak M (2005). Y-Chromosomal STR Haplotypes and Their Applications in Forensic and Population Studies in East Asia. Int. J. Leg. Med. 119(4):195-201.
Leda K, Jessica L, Jodi A (2008). Population genetics of Y-chromosome STRs in a population of Northern Greeks. Forensic Sci. Int. 175 (2-3): 250-5.
Manfred K, Michael K, Laurent E, Patrick D (2001). An extensive analysis of Y-Chromosomal microsatellite haplotypes in globally dispersed human populations. Am. J. Hum. Genet. 68:990-1018.
Markoulatos P, Siafakas N, Moncany M (2002). Multiplex polymerase chain reaction: a practical approach. J. Clin. Lab Anal. 16:47-51.
Nakamura Y (2009). DNA variations in human and medical genetics: 25years of my experience. J. Hum. Genet. 54 (1):1-8.
Nei M (1987). Molecular Evolutionary Genetics, Columbia University Press, New York.
Park MJ, HY Lee, Chang U, Kang SC (2007). Y-STR analysis of degraded DNA Using reduced-size amplicons. Int. J. Leg Med. 121(2):152-157.
Parson WH, Niederstätter A, Berger B (2003). Improved specificity of Y-STR typing in DNA mixture samples. Int. J. Leg Med. 117 (2):109-114.
Prinz A, Ishii A, Coleman HJ (2001). Validation and casework application of a Y chromosome specific STR multiplex. Forensic Sci. Int. 120: 177-188.
Prinz M, Boll K, Baum H, Shaler B (1997). Multiplexing of Y chromosome specific STRs and performance for mixed samples. Forensic Sci. Int. 85:209-218.
Raymond FR (1995). GENEPOP (version 1.2). Population genetics software for exact tests and ecumenicism. J. Heredity. 86:248-249.
Rustamov A, Gümüş G, Karabulut HG, Elhan AH (2004). Y-STR polymorphism in Central Anatolian region of Turkey. Forensic Sci. Int. 139:227-230.
Yamamoto T, Uchihi R, Nozawa H, Huang XL, Leong YK, Tanaka M (1999). Allele distribution at nine STR loci-D3S1358, vWA, FGA, TH01, TPOX, CSF1PO, D5S818,D13S317 and D7S820-in the Japanese population by multiplex PCR and capillary electrophoresis. J. Forensic Sci. 44 (1):167-170.
Yan J, Tang H, Liu Y, Jing Y (2007). Genetic polymorphisms of 17 Y-STRs haplotypes in Chinese Han population residing in Shandong province of China. Legal Med. 9:196-202.