

*Full Length Research Paper*

## Analysis of eleven Y-chromosomal STR markers in Middle and South of Iraq

Imad, Hadi Hameed<sup>1\*</sup>, Muhanned, Abdulhasan Kareem<sup>2</sup>, Aamera, Jaber Ommer<sup>3</sup> and Cheah, Yoke<sup>4</sup>

<sup>1</sup>Department of Molecular Biology, Babylon University, Hilla City, Iraq.

<sup>2</sup>Babylon University, Centre of Environmental Research, Iraq.

<sup>3</sup>Institute of Medico-Legal in Baghdad, Ministry of Health of Iraq.

<sup>4</sup>Department of Biomedical Science, University Putra Malaysia, Selangor, Malaysia.

Received 17 August, 2014; Accepted 12 September, 2014

Samples of 320 random healthy unrelated Iraqi male persons from the Arab ethnic group of Iraqi population were collected for Y chromosomal STRs typing. FTA® Technology was utilized to extract DNA from blood collected on FTA™ paper. We analyzed 11 Y chromosomal STR loci for evaluating allele frequencies and gene diversity for each Y-STR locus of the Y-Plex™ PCR amplification kit. The 11 loci include DYS389I, DYS389II, DYS19, DYS391, DYS438, DYS390, DYS439, DYS392, DYS393, DYS385a and DYS385b. A total of 299 unique haplotypes was identified among the 320 individuals studied. The DYS385b had the highest diversity (GD = 0.8392), while loci DYS392 had the lowest (D = 0.2695). The study focuses to establish the basic forensic genetic informations, 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, gene diversity, Iraq, STR DNA typing, Y-Plex™.

### INTRODUCTION

The Y chromosome is constructed in males and includes the sex determining region and known as a paternal lineage marker (Butler et al., 2002; Kuppureddi et al., 2010; Carolina et al., 2010). Chromosome Y microsatellites or short-tandem repeats (STR's) seem to be ideal markers to delineate differences between human populations because they are transmitted in uniparental (paternal) fashion without recombination, also they are very sensitive for genetic drift, and they allow a simple

highly informative haplotype construction (Kayser et al., 1997). The genetic information is inherited from the father to the son, and this information does not change except for mutational events (Hanson et al., 2007). These markers can also be useful in missing persons investigations, historical investigations, some paternity testing scenarios, and genetic genealogy (Park et al., 2007; Verzeletti et al., 2008).

\*Corresponding author. E-mail: imad\_dna@yahoo.com. Tel: 009647716150716.

Unlike autosomal STR markers, Y-STR markers are linked on the same chromosome and there is no genetic recombination between the markers. Therefore, unlike for autosomal STRs, the Hardy-Weinberg equation is not suitable for determining the frequency of a genotype from the frequency of the alleles at each locus (Beleza et al., 2003; Dupuy et al., 2004). To determine the frequency of a particular Y-STR profile, the profile must be searched against different databases for a possible match, and these databases must be large enough to accurately represent the frequencies of the haplotypes present in the population of interest (Ballantyne et al., 2010).

For a number of forensic applications, Y-STR's could be superior to autosomal STR's, especially in rape cases where: (i) the differential lysis was unsuccessful, (ii) the number of sperm cells is very low, (iii) due to vasectomy epithelial cells instead of sperm cells from the ejaculate of the perpetrator have to be analyzed, and (iv) the perpetrator, due to a familial relationship shares many autosomal bands with the victim; Y-STR's could provide crucial evidence.

The Y chromosome is becoming a useful tool for tracing human evolution through male lineages (Jobling, 1995) as well as application in a variety of forensic situations (Kayser et al., 1997) 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.

Ideally, a forensic Y chromosome haplotype should include as many polymorphic loci as possible to improve the chance of excluding individuals (or male lineages) who did not commit the crime. In order to obtain a high level of discrimination either a large number of Y STRs can be run one at a time or combined into a multiplex.

For Y STR systems to become more highly discriminatory and gain acceptance within the forensic, DNA community robust multiplexes are required. Y STR multiplexes have been described previously (Prinz et al., 1997; Redd et al., 1997; Gusmao et al., 1999).

## MATERIALS AND METHODS

### Preparation of blood stain samples

Blood samples were randomly collected from 320 unrelated Iraqi male persons from the Arab ethnic group of Iraqi population for DNA Y- chromosomal STRs typing; those samples were sent to the forensic genetic laboratories.

### DNA extraction

DNA was extracted from all dried blood samples on FTA cards (Mullen et al., 2009; Dobbs et al., 2002) following the manufacturer'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 three 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.

### Controls

It is recommended that internal standard controls are used during each PCR analysis which include the following: negative control, negative control with washed, no-sample punch, to ensure that the punch does not cause a positive result, positive control of a known DNA standard solution and positive control standard added to a normally washed, no-sample punch, to ensure that the punch does not inhibit the reaction.

### 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 the small amount of template DNA using this process. 12Plex amplification was performed by the commercial kit Y-Plex™12 (Reliagene, New Orleans, LA) that amplifies 11 Y-STR loci (DYS389I, DYS389II, DYS19, DYS391, DYS438, DYS390, DYS439, DYS392, DYS393, DYS385a and DYS385b) and a segment of the amelogenin gene, according to manufacturer's instructions but in a total reaction volume of 25 µl.

### 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. Using the ABI Prism1 3730xl Genetic Analyzer 16-capillary array system (Applied Biosystems, Foster City, CA, USA) following 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 by 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-Plex™12 kit.

### Statistical analysis for Y- chromosomal STR

#### Analysis of data

Allele frequencies were calculated by direct counting.

**Allele diversity (genetic diversity) (D)**

Allele diversity was calculated as (Nei, 1987):

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

Where,  $n$  is the sample size and  $p_i$  is the frequency of the  $i$ th allele.

**Standard Error (SE)**

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

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

Where,  $p_i$  denotes the frequency of the  $i$ th allele at any given locus and  $N$  equals the total number of individuals screened at this locus.

**RESULTS AND DISCUSSION****Y-chromosome (short tandem repeat) haplotypes, haplotype frequency, allele frequency and genetic diversity****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 et al., 2001; Gill et al., 2004; Honda et al., 2001; Jobling et al., 1997). Allelic and haplotypic distributions of Y-STRs have shown significant differences in different geographical regions, ethnical groups and communities (Alves et al., 2003; Gusmao et al., 2003; Isobe et al., 2001; Rodig et al., 2007; 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; Park et al., 2007). In this study, allelic and haplotypic frequencies involving 11 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 (Imad et al., 2013). Observed allele or genotype frequencies of the 11 Y-STR loci are given in Tables 1 and 2.

The DYS385b and DYS389II had the highest diversity ( $D = 0.8392$  and  $0.7140$ , respectively), while loci DYS392

and DYS439 had the lowest ( $D = 0.2695$  and  $0.2991$ , respectively). The frequencies of DYS392 were low in all allele except allele 11 where it was 85%; this allele is to be used to discriminate Iraqi men because of overall low genetic diversity, then this locus should be excluded because 85% of Iraqi men will have the locus. However it will be useful for discriminating Iraqi men from non-Iraqi men provided it is unique to only Iraqi men.

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 which was 0.51 and the highest as 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 11 Y STR loci typed in a population sample of unrelated male individuals. Haplotypes were presented for the 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**

We identified 276 different haplotypes in our study sample (320 unrelated males), 299 of which (93.4%) were unique, six were found twice (2.8%) and six were found in three individuals (1.9%). The most frequent haplotype was haplotype number 78 (Table 2). Haplotype 78 seems to be specific to Iraq. This is to be corroborated by future investigations. The observed number of haplotypes and their frequencies has been tabulated in Table 3. 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 most frequent haplotype was haplotype number 77. Haplotype 77 seems to be specific to Iraq. This is to be corroborated by future investigations. 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 4). Haplotypic comparisons have highlighted significant differences from Iraq population in this study ( $p < 0.05$ ). Our data have also provided additional information to the framework of variation involving 17 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



**Table 2.** Contd.

22	-	-	-	-	-	-	-	-	-	-	-	-
23	-	-	-	-	-	-	-	-	-	-	-	-
24	-	-	-	-	-	-	-	-	-	-	-	-
25	-	-	-	-	-	-	-	-	-	-	-	-
28	-	-	-	-	-	-	-	-	-	-	-	-
29	-	-	-	-	-	-	-	-	-	-	-	-
30	-	-	-	-	-	-	-	-	-	-	-	-
31	-	-	-	-	-	-	-	-	-	-	-	-
32	-	-	-	-	-	-	-	-	-	-	-	-
33	-	-	-	-	-	-	-	-	-	-	-	-
GD*	<b>0.5802</b>		<b>0.2695</b>		<b>0.5140</b>		<b>0.5262</b>		<b>0.2991</b>			

In **bold** are the most common allele for each locus. Freq, frequency; SE, standard error.

**Table 3.** Haplotypes for the 11 Y-STR loci observed 320 Iraq males.

Haplotype	DYS19	DYS385a	DYS385b	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS438	DYS439	N	F
H1	13	11	16	12	30	23	10	11	13	10	13	4	0.0125
H2	13	11	16	12	30	23	8	11	13	9	13	1	0.0031
H3	13	11	16	12	31	23	8	11	12	9	10	1	0.0031
H4	13	11	14	12	31	23	8	11	13	11	10	1	0.0031
H5	13	13	14	12	31	23	10	11	13	10	10	1	0.0031
H6	13	13	14	12	28	23	10	11	13	10	13	1	0.0031
H7	13	13	14	12	28	23	9	11	14	12	13	1	0.0031
H8	13	13	14	12	28	23	10	11	13	12	10	1	0.0031
H9	13	13	14	12	29	23	10	11	13	12	10	1	0.0031
H10	13	13	14	12	29	23	8	11	14	12	11	3	0.0094
H11	13	13	14	12	29	23	9	11	14	10	11	1	0.0031
H12	13	13	14	14	29	23	10	11	12	11	11	1	0.0031
H13	13	13	14	14	29	23	10	11	13	10	11	1	0.0031
H14	13	13	14	13	29	23	10	11	14	10	10	1	0.0031
H15	13	13	18	13	29	23	10	11	14	12	10	1	0.0031
H16	13	13	18	13	28	23	8	11	13	12	13	1	0.0031
H17	13	13	18	13	28	23	8	11	13	12	10	1	0.0031
H18	13	13	16	13	28	23	10	11	13	12	10	1	0.0031
H19	13	14	16	13	31	23	10	11	13	10	10	1	0.0031
H20	13	14	16	12	31	23	10	11	13	10	10	1	0.0031
H21	13	11	16	12	31	23	10	11	12	10	10	1	0.0031
H22	13	11	13	12	28	23	10	11	12	10	10	1	0.0031
H23	13	11	13	12	28	23	10	11	14	9	10	1	0.0031
H24	13	11	13	12	30	23	10	11	14	10	10	1	0.0031
H25	13	11	18	12	30	23	10	11	13	10	10	1	0.0031
H26	13	11	14	12	30	25	10	11	13	10	10	1	0.0031
H27	13	11	14	12	32	23	10	11	13	10	10	1	0.0031
H28	13	11	18	12	33	23	10	11	13	10	10	1	0.0031
H29	13	13	18	14	30	21	10	11	13	10	10	1	0.0031
H30	13	13	18	14	29	24	10	11	13	10	10	1	0.0031
H31	13	13	18	13	29	24	10	11	12	10	11	1	0.0031
H32	13	13	18	14	29	25	10	11	13	10	11	1	0.0031
H33	13	13	18	14	29	21	10	11	13	10	11	3	0.0094

Table 3. Contd.

H34	13	13	18	14	29	23	10	11	13	10	11	1	0.0031
H35	13	13	18	13	29	23	10	11	13	10	11	1	0.0031
H36	13	13	18	12	29	23	10	11	14	10	11	1	0.0031
H37	13	13	18	14	29	24	10	11	13	10	11	1	0.0031
H38	13	13	16	13	30	23	10	11	13	10	11	1	0.0031
H39	13	13	19	13	28	23	10	11	13	10	11	1	0.0031
H40	13	13	19	13	30	24	10	11	13	10	11	1	0.0031
H41	13	13	19	13	32	21	10	11	13	10	11	1	0.0031
H42	13	13	19	13	32	25	10	11	12	10	11	1	0.0031
H43	13	13	14	13	28	25	10	11	12	10	11	1	0.0031
H44	13	13	14	13	29	25	10	11	12	10	11	1	0.0031
H45	13	12	14	13	32	25	10	11	13	10	12	1	0.0031
H46	13	12	14	13	30	25	10	11	13	10	12	1	0.0031
H47	13	12	14	13	28	23	10	11	12	10	12	1	0.0031
H48	13	12	14	13	28	23	10	11	14	10	12	1	0.0031
H49	13	12	14	12	28	24	10	11	13	10	12	1	0.0031
H50	13	12	14	12	30	24	10	11	12	10	10	1	0.0031
H51	13	11	14	14	30	24	10	11	12	9	10	1	0.0031
H52	13	11	14	14	30	25	10	11	12	10	13	1	0.0031
H53	13	11	14	13	30	23	10	11	12	10	14	1	0.0031
H54	13	11	14	12	30	23	10	11	13	10	10	1	0.0031
H55	13	11	14	14	30	24	11	11	13	10	13	1	0.0031
H56	13	11	19	13	30	24	11	11	13	10	12	1	0.0031
H57	13	11	16	12	30	24	11	11	14	11	10	1	0.0031
H58	13	11	16	14	30	24	11	11	13	9	10	1	0.0031
H59	13	11	15	13	32	22	8	11	14	10	10	2	0.0063
H60	13	11	15	13	32	24	10	11	13	10	10	1	0.0031
H61	13	11	15	13	30	25	10	11	13	12	10	1	0.0031
H62	13	11	15	12	30	25	10	11	13	11	10	1	0.0031
H63	13	11	15	14	30	25	9	11	14	11	9	1	0.0031
H64	13	11	15	14	32	25	10	11	14	11	10	1	0.0031
H65	13	11	15	14	29	25	10	11	13	10	9	1	0.0031
H66	13	11	15	14	30	23	8	11	13	10	9	1	0.0031
H67	13	11	15	14	30	23	10	11	12	10	14	1	0.0031
H68	13	11	15	14	30	24	9	11	13	10	13	2	0.0063
H69	13	11	18	13	30	24	9	11	13	9	10	1	0.0031
H70	13	11	18	14	29	24	9	11	13	12	10	1	0.0031
H71	13	11	18	12	29	24	9	11	13	11	10	1	0.0031
H72	13	11	18	12	29	23	12	11	13	11	10	1	0.0031
H73	13	11	19	12	29	23	10	11	13	11	10	1	0.0031
H74	13	11	19	12	29	22	10	11	13	11	11	1	0.0031
H75	13	11	19	12	29	23	9	11	13	11	11	1	0.0031
H76	13	11	14	12	29	23	9	11	13	10	11	1	0.0031
H77	13	11	14	12	29	24	11	11	13	10	11	1	0.0031
H78	13	11	14	13	29	24	10	11	13	12	11	6	0.0188
H79	13	11	14	12	30	24	10	11	13	10	11	1	0.0031
H80	13	11	14	14	30	24	9	11	13	10	14	1	0.0031
H81	13	11	14	14	30	23	11	11	13	10	14	1	0.0031
H82	13	16	13	14	30	25	10	11	13	10	10	1	0.0031
H83	13	16	13	12	30	25	10	11	13	9	10	1	0.0031

Table 3. Contd.

H84	13	16	13	12	30	25	10	11	13	10	10	1	0.0031
H85	13	14	13	12	30	24	9	11	13	10	10	1	0.0031
H86	13	14	17	12	30	24	11	11	13	10	14	1	0.0031
H87	13	14	17	12	29	24	12	11	13	10	14	1	0.0031
H88	13	14	20	12	29	24	11	11	13	11	12	1	0.0031
H89	13	14	20	12	29	25	9	11	13	11	13	1	0.0031
H90	13	14	20	12	29	24	10	11	13	9	13	1	0.0031
H91	13	14	18	12	29	24	10	11	13	10	13	1	0.0031
H92	13	14	19	12	29	24	12	11	13	12	13	1	0.0031
H93	13	14	19	12	29	24	10	11	13	10	13	1	0.0031
H94	13	14	16	12	29	23	10	11	13	11	13	1	0.0031
H95	13	14	16	12	29	23	9	11	13	10	13	1	0.0031
H96	13	14	16	12	29	23	8	11	13	10	14	1	0.0031
H97	13	14	16	12	29	23	12	11	13	10	10	1	0.0031
H98	13	14	16	14	29	21	12	11	13	11	10	1	0.0031
H99	13	14	16	14	29	22	8	11	13	11	11	1	0.0031
H100	13	13	16	14	29	22	10	11	13	11	13	1	0.0031
H101	13	13	16	14	29	25	10	11	13	11	12	1	0.0031
H102	13	13	16	14	32	23	10	11	13	10	12	1	0.0031
H103	14	13	16	14	28	22	10	13	13	10	12	1	0.0031
H104	14	13	16	14	33	23	10	13	13	10	11	1	0.0031
H105	14	13	16	14	28	25	10	11	13	10	11	1	0.0031
H106	14	13	19	14	28	25	10	11	13	10	14	1	0.0031
H107	14	13	15	14	28	23	10	11	13	10	14	1	0.0031
H108	14	13	19	14	28	23	10	11	13	10	14	1	0.0031
H109	14	13	20	14	32	23	10	12	13	10	11	2	0.0063
H110	14	13	20	13	32	23	10	11	13	10	11	1	0.0031
H111	14	14	20	13	29	23	10	11	13	10	11	1	0.0031
H112	14	14	13	13	29	23	10	11	13	10	11	1	0.0031
H113	14	14	13	13	29	25	10	13	13	10	11	1	0.0031
H114	14	14	13	13	31	23	10	13	13	10	11	1	0.0031
H115	14	14	13	12	31	24	10	13	13	10	11	1	0.0031
H116	14	14	13	13	31	25	10	12	13	10	11	1	0.0031
H117	14	14	19	14	30	23	10	11	13	12	10	2	0.0063
H118	14	14	18	12	30	23	10	11	13	9	10	1	0.0031
H119	14	14	16	12	30	23	10	11	13	9	13	1	0.0031
H120	14	14	18	12	30	23	10	12	13	10	11	1	0.0031
H121	14	14	18	12	30	23	9	11	14	10	11	1	0.0031
H122	14	14	18	12	30	23	11	11	12	10	11	1	0.0031
H123	14	14	18	14	30	23	11	11	14	10	11	1	0.0031
H124	14	14	18	13	30	23	11	12	14	10	11	1	0.0031
H125	14	14	18	13	30	23	10	14	14	10	13	1	0.0031
H126	14	14	14	13	28	23	10	11	13	10	10	2	0.0063
H127	14	14	14	13	29	23	10	14	13	9	10	1	0.0031
H128	14	14	14	13	30	24	12	11	13	9	10	1	0.0031
H129	14	14	14	14	28	24	12	11	12	9	10	1	0.0031
H130	14	14	14	14	28	25	12	13	13	9	12	1	0.0031
H131	14	14	14	12	28	24	11	13	13	9	13	1	0.0031
H132	14	14	14	14	31	24	11	14	13	12	10	1	0.0031
H133	14	14	14	14	31	22	11	11	14	10	10	1	0.0031

Table 3. Contd.

H134	14	14	14	14	28	22	9	11	12	10	10	1	0.0031
H135	14	14	14	13	28	23	9	11	12	12	11	1	0.0031
H136	14	14	14	13	29	24	9	11	12	11	11	1	0.0031
H137	14	16	14	13	29	24	10	11	12	10	11	1	0.0031
H138	14	16	14	13	29	24	9	11	12	10	10	1	0.0031
H139	14	16	13	13	29	24	9	11	14	10	10	1	0.0031
H140	14	16	13	13	29	24	11	11	13	10	10	1	0.0031
H141	14	15	17	13	29	24	12	11	13	10	11	1	0.0031
H142	14	14	17	12	30	24	12	12	13	10	11	1	0.0031
H143	14	14	19	12	30	24	12	11	13	10	11	1	0.0031
H144	14	14	19	12	30	23	12	11	14	10	11	4	0.0125
H145	14	14	19	14	30	24	11	11	13	10	11	1	0.0031
H146	14	14	19	14	30	22	10	13	14	10	11	1	0.0031
H147	14	14	19	14	28	23	10	11	12	12	10	1	0.0031
H148	14	12	19	14	28	22	10	11	12	9	10	1	0.0031
H149	14	12	16	14	29	23	10	11	13	9	11	1	0.0031
H150	14	17	16	14	29	21	10	11	13	11	11	1	0.0031
H151	14	17	16	14	29	24	10	12	12	11	11	1	0.0031
H152	14	17	16	13	29	24	10	11	14	11	11	3	0.0094
H153	14	17	19	13	29	24	10	11	13	11	11	1	0.0031
H154	14	13	19	13	29	24	10	13	13	10	10	1	0.0031
H155	14	13	19	13	28	24	10	11	12	10	10	1	0.0031
H156	14	13	15	13	29	25	10	11	12	10	11	1	0.0031
H157	14	13	15	13	33	25	10	13	13	10	11	1	0.0031
H158	14	13	15	13	33	25	10	11	12	10	11	1	0.0031
H159	14	13	15	14	33	24	11	11	13	10	11	1	0.0031
H160	14	13	15	14	33	21	11	14	13	10	11	1	0.0031
H161	14	12	15	12	33	23	11	11	13	9	11	1	0.0031
H162	14	13	15	12	33	23	11	11	13	12	11	1	0.0031
H163	14	13	18	12	28	23	11	11	13	12	14	1	0.0031
H164	14	13	20	12	32	23	11	11	13	10	10	1	0.0031
H165	14	13	18	12	32	23	11	11	13	10	12	1	0.0031
H166	14	12	14	12	28	23	11	11	13	9	12	1	0.0031
H167	14	13	14	12	30	23	10	11	13	10	10	1	0.0031
H168	14	13	14		30	23	9	12	13	10	10	1	0.0031
H169	14	13	14	13	30	23	12	12	12	10	10	1	0.0031
H170	14	13	14	13	30	21	11	13	12	10	10	3	0.0094
H171	14	13	14	13	30	21	12	11	12	10	13	1	0.0031
H172	14	13	19	13	30	23	12	11	12	11	11	1	0.0031
H173	14	13	19	14	30	23	10	11	12	10	11	1	0.0031
H174	14	19	17	14	30	23	9	11	12	10	11	1	0.0031
H175	14	13	17	14	31	23	11	11	13	10	10	2	0.0063
H176	14	12	19	14	33	23	11	11	13	10	11	1	0.0031
H177	14	13	19	14	29	23	9	11	13	10	11	1	0.0031
H178	14	13	20	14	30	23	9	11	13	12	10	1	0.0031
H179	14	13	20	14	31	24	10	11	13	10	13	1	0.0031
H180	14	13	18	14	31	24	10	11	13	10	14	1	0.0031
H181	14	13	15	14	31	24	10	11	13	9	11	1	0.0031
H182	14	16	18	14	31	24	12	11	13	9	11	1	0.0031
H183	14	17	18	14	28	24	9	11	13	10	11	1	0.0031



Table 3. Contd.

H184	14	17	18	14	29	24	11	11	13	10	10	1	0.0031
H185	14	13	18	14	29	24	10	11	13	10	10	1	0.0031
H186	14	13	16	14	32	24	10	11	13	10	10	1	0.0031
H187	14	13	16	14	29	24	10	11	13	10	13	1	0.0031
H188	14	13	19	14	29	24	10	11	13	10	11	1	0.0031
H189	14	13	19	14	30	24	9	11	13	10	10	1	0.0031
H190	14	13	14	14	30	24	9	11	13	11	12	1	0.0031
H191	14	16	14	14	29	24	9	11	13	11	11	1	0.0031
H192	14	13	14	14	29	24	9	11	13	9	10	5	0.0156
H193	14	13	14	14	33	24	9	11	13	9	10	1	0.0031
H194	14	17	14	14	29	24	11	11	13	9	10	1	0.0031
H195	14	13	14	14	29	24	12	11	13	9	10	1	0.0031
H196	14	13	14	13	28	23	8	11	13	10	10	1	0.0031
H197	14	13	14	13	28	23	10	11	13	10	10	1	0.0031
H198	14	13	14	13	32	22	9	11	13	10	10	1	0.0031
H199	14	13	14	13	30	22	9	11	13	9	10	1	0.0031
H200	14	13	14	13	30	24	11	11	13	9	11	1	0.0031
H201	14	13	17	13	30	24	11	11	13	11	11	1	0.0031
H201	14	13	15	13	29	24	10	11	13	11	11	1	0.0031
H202	14	13	15	13	29	23	9	11	13	11	11	1	0.0031
H203	14	13	18	13	29	23	9	11	13	10	13	3	0.0094
H204	14	13	18	13	29	21	11	11	13	10	13	1	0.0031
H205	14	19	13	13	29	24	11	11	13	11	13	1	0.0031
H206	14	13	13	14	30	24	11	11	13	12	13	1	0.0031
H207	14	13	13	14	30	22	9	11	13	12	13	1	0.0031
H208	14	13	19	12	30	22	9	11	12	10	13	1	0.0031
H209	14	13	19	12	30	24	10	11	12	10	10	1	0.0031
H210	14	13	16	12	28	24	10	11	12	10	10	1	0.0031
H211	14	13	19	12	30	24	10	11	12	12	12	1	0.0031
H212	14	13	19	14	29	22	10	11	12	9	12	1	0.0031
H213	14	13	19	14	30	23	10	11	12	11	11	1	0.0031
H214	14	13	17	13	30	23	10	11	12	12	12	1	0.0031
H215	14	13	19	13	30	23	9	11	12	12	12	1	0.0031
H216	14	17	19	13	29	23	11	11	12	12	10	1	0.0031
H217	14	13	15	13	29	23	8	11	12	12	10	1	0.0031
H218	14	13	15	13	31	23	9	11	12	11	10	1	0.0031
H219	14	13	15	14	29	23	9	11	12	11	13	1	0.0031
H220	15	17	18	14	29	23	9	11	12	11	10	1	0.0031
H221	15	17	18	14	29	24	10	11	12	11	14	1	0.0031
H222	15	13	18	14	29	24	10	11	12	11	11	1	0.0031
H223	15	13	18	14	31	23	12	11	14	10	11	1	0.0031
H224	15	13	18	14	31	21	12	11	13	10	11	2	0.0063
H225	15	13	18	14	31	24	9	11	14	10	11	1	0.0031
H226	15	13	14	14	29	24	9	11	13	9	14	1	0.0031
H227	15	19	19	14	29	24	9	11	13	10	13	1	0.0031
H228	15	13	19	12	29	24	10	11	13	10	10	1	0.0031
H229	15	13	16	12	30	22	11	11	13	10	10	1	0.0031
H230	15	13	16	12	30	23	10	11	13	10	10	1	0.0031
H231	15	17	20	12	28	23	10	11	13	9	10	1	0.0031
H232	15	17	16	13	29	23	9	11	12	12	11	1	0.0031

Table 3. Contd.

H233	15	13	16	13	29	23	9	14	12	12	10	1	0.0031
H234	15	13	16	12	29	23	8	14	12	10	11	1	0.0031
H235	15	13	16	12	29	24	8	13	12	10	11	1	0.0031
H236	15	13	16	12	29	23	9	11	13	10	13	1	0.0031
H237	15	13	16	13	29	23	9	13	13	9	14	1	0.0031
H238	15	13	16	12	29	23	9	13	13	11	10	1	0.0031
H239	15	13	13	14	29	23	10	11	13	11	10	1	0.0031
H240	15	12	13	13	29	23	10	11	14	11	10	1	0.0031
H241	15	12	13	14	29	23	12	11	13	10	12	1	0.0031
H242	15	12	20	14	29	23	12	11	13	10	11	1	0.0031
H243	15	13	19	14	29	23	12	13	12	10	10	1	0.0031
H244	15	13	19	14	31	23	12	13	14	10	10	5	0.0156
H245	15	13	15	14	31	23	9	11	13	10	10	3	0.0031
H246	15	13	18	14	31	21	9	12	13	10	10	1	0.0031
H247	15	13	18	14	31	23	9	11	12	10	14	1	0.0031
H248	15	13	18	14	31	24	9	12	13	10	10	1	0.0031
H249	15	13	18	12	29	24	9	12	13	10	11	1	0.0031
H250	15	13	18	13	28	24	9	11	13	10	10	1	0.0031
H251	15	15	18	14	28	24	9	11	13	10	13	1	0.0031
H252	15	13	18	14	30	24	9	11	14	10	13	1	0.0031
H253	15	13	14	14	31	24	9	12	13	10	10	1	0.0031
H254	15	13	14	13	31	22	9	12	13	10	10	1	0.0031
H255	15	13	17	13	31	22	11	11	13	10	10	1	0.0031
H256	15	15	20	13	31	23	8	11	13	10	10	1	0.0031
H257	15	13	19	13	29	23	10	11	13	10	10	1	0.0031
H258	15	13	19	13	29	24	9	11	13	10	10	2	0.0063
H259	15	13	17	13	29	24	9	11	13	10	10	2	0.0063
H260	15	13	19	13	31	24	9	11	13	10	10	1	0.0031
H261	15	13	15	13	29	24	12	11	13	10	10	1	0.0031
H262	15	19	15	13	30	24	10	11	13	10	10	1	0.0031
H263	16	13	15	13	29	24	10	11	14	10	10	1	0.0031
H264	16	13	15	12	30	24	10	11	12	10	11	1	0.0031
H265	16	13	15	14	30	24	10	11	13	10	11	1	0.0031
H266	16	13	15	14	30	23	10	11	12	10	11	1	0.0031
H267	16	17	15	14	28	23	10	11	13	10	11	1	0.0031
H268	16	17	15	14	28	21	10	11	12	10	13	1	0.0031
H269	16	17	19	14	29	24	10	11	13	10	10	1	0.0031
H270	16	17	19	14	29	22	10	11	13	10	10	1	0.0031
H271	16	13	16	14	29	24	10	11	13	10	10	1	0.0031
H272	16	13	16	13	29	24	10	11	14	10	10	1	0.0031
H273	16	13	14	13	30	24	10	11	13	10	10	1	0.0031
H274	17	13	18	13	30	24	10	11	13	10	10	1	0.0031
H275	17	13	20	13	29	24	10	14	13	10	14	5	0.0156
H276	17	19	14	13	29	24	10	14	13	10	14	1	0.0031

N, Number of males observed for each haplotype; F, Frequency of each haplotype in the sample of 320 males.

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

**Table 4.** Comparison of the haplotypes and haplotype diversity in different human population groups.

Parameter	Iraq <sup>1</sup>	Tunisia <sup>2</sup>	Germany <sup>3</sup>	Italy <sup>4</sup>	China <sup>5</sup>	India <sup>6</sup>	India <sup>7</sup>
Individuals number	320	105	88	100	36	25	154
Haplotypes number	276	81	77	82	34	16	152
Unique Haplotypes	256	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	20	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)	13.2	4.88	1.03	1.83	4.67	4.33	98
Haplotypes diversity	0.8392	0.9932	0.9963	0.9941	0.9968	0.950	0.9935

<sup>1</sup>This study. <sup>2</sup>Reference: Imen et al., 2005; <sup>3</sup>Reference: Manfred et al., 2001; <sup>4</sup>Reference: Manfred et al., 2001; <sup>5</sup>Reference: Manfred et al., 2001; <sup>6</sup>Reference: (Manfred et al., 2001); <sup>7</sup>Reference: (Kuppareddi et al., 2010).

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 (Henke et al., 2001; Hara et al., 2007; Imad et al., 2014a, b). 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 (Imad et al., 2014c, d).

## Conclusions

Power of discrimination values for all tested loci means that those loci can be used as a DNA-based database. Different alleles were observed across the population. The lowest gene diversity was DYS392 and DYS439. The high gene diversity was DYS385b and DYS389II. Based on statistical parameters, the population of Iraq may use these 11 STR loci as a vital tool for forensic identification and paternity testing.

## Conflict of Interests

The author(s) have not declared any conflict of interests.

## ACKNOWLEDGEMENTS

I sincerely wish to thank Dr. A. Issam for providing me the opportunity to work on this project. I am thankful to you for helping me through the various analysis stages, and for providing helpful criticism and feedback throughout the writing process and also Zainab Al-Habubi from the Department of Biology for her guidance and help in the laboratory work.

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