International Journal of Medical Toxicology & Legal Medicine Volume 27, No. 4, 2024
e-ISSN: 0974-4614
p-ISSN: 0972-0448

Male genealogy study of the Iraqi Population

Halah Khalid Ibrahim Al-Sammarraie[1*], Mohammed M. Al-Zubaidi[2], Asia Abdul lateef Mahdi[3]

[1,2,3]Department of Forensic Biology, Higher Institute of Forensic Sciences, Al-Nahrain University, Baghdad, Iraq.
Email: hala_kh76@nahrainuniv.edu.iq, molecular_fdna@yahoo.com
*Corresponding Author

Received: 17.08.2024 Revised: 19.09.2024 Accepted: 21.10.2024

ABSTRACT
The Y-chromosome of Short Tandem Repeats (STRs) plays a vital role in the field of forensics, particularly in the identification of male DNA in instances of sexual assault. Moreover, it is important in facilitating the connection of families through the application of genetic genealogy.In this study, the genetic polymorphisms of 23 Y-STR loci were analysed by the Power Plex® Y23 system in 383 healthy, unrelated male individuals randomly chosen from Iraqi populations. The result revealed 356 different haplotypes, including 337 unique haplotypes and 19 duplicate haplotypes. Two hundred and twelvedifferent genetic variants (alleles), were detected at which are distributed across 23 specific locations on the Y chromosome.The study examined the highest and lowest frequencies at each genetic locus and found that at the DYS392 locus, the microvariant allele "11" was the most common and widespread allele within the Iraqi population. The highest frequency of haplotype was 0.0098, which was found in samples H44, H70, H140, H206, and H255, while 337 haplotypes had 0.0033 frequencies, and haplotype diversity was 0.997 with a discrimination capacity of 0.946, respectively.The gene diversity values ranged from 0.395062 at DYS392 to 0.93828 at DYS385a/b. The Y-haplogroups of male Iraqi Arabs were determined using the NevGen Y-DNA Haplogroup online Predictor program. The most common haplogroups in this study were J1 (38%), J2 (20%), R1 (11%), E1 (10%), and G2 (5%). Although less common, additional predicted haplogroups were also discovered.The present study indicated that the 23 Y-STR loci were highly polymorphic in the Bagdad population and played crucial roles in forensic applications as well as population genetics. The study revealed the genetic diversity of male lineages in the Bagdad population using a high-resolution 23 Y-STR collection, and as a result, it’s contributed to familial research.

Keywords: Arabs, haplogroups, haplogroups, chromosome

INTRODUCTION

The Y chromosome's non-recombining region contains repeating areas called "Y-STRs," or short tandem repeats. These regions are made up of 2–7 base pair-long repetitive units. Due to their ease of typing and high level of polymorphism, Y-STRs are frequently used as markers on the Y chromosome. They also show a male inheritance pattern. Y-STR analysis is possible even in situations where DNA quality is reduced because PCR is a dependable method that can tolerate deteriorated DNA samples. Because of this, Y-STRs have a variety of uses, such as forensic sexual assault investigations, paternity testing when the purported father is unavailable for testing, circumstances with numerous male DNA samples being used in gang rape, and genetic research [1, 2].
Iraq is a country located in western Asia. Due to its good climate, fertile soil, and the presence of the Tigris and Euphrates rivers, Iraq is known as the cradle of the ancient civilization of Mesopotamia, including the Sumerian and Babylonian cultures. It is distinguished by its geographical characteristics, which include a varied terrain made up of mountains, deserts, and a productive river valley. Iraq is bordered by a number of nations, including Iran to the east, Turkey to the north, Syria, Jordan, and Saudi Arabia to the west, and Kuwait and Saudi Arabia to the south. The estimated population of Iraq in July 2011 was 30,399,572. Participants for the aforementioned study were chosen from Baghdad, which serves as Iraq's capital and largest city [3]. As a key metropolitan hub and the site of the research study's sampling, Baghdad was chosen. Iraq wasexposed to the administration of many empires and civilizations over the span of its past history include the Mongols,Turkey,England and Iran. Arab Iraqi population made up of a wide of ethnic groups this highlights the significance conductinga study on history of society [4, 5].The short tandem repeat loci (STR loci) are repeating sequences inof the human genome. It’s highly polymorphic, different between people, have variable repeat counts which makes them very useful genetic markers. They can give information concern the bases behind the genetic origin of some diseases,

human migration anddemographical research [6].DNA typing used to determine individual's identification, paternity and maternity testes, investigated a criminal issue[7].Y-STRsmarkers demonstrate an inheritance patternof specific male- transmission. Y-STRs can be used by researchers inseveralgenetic applications [8, 9].PCR-dependent techniques help to have accurate findings, even when dealing with degraded DNA samples. This ability to adjust to damage DNA is helpful for the analysis of ancient DNA samples to confirm the presence of individuals who lack amelogenin (a particular genetic condition) and other forensic applications [10, 11]. This particular power-plex Y 23 genotyping kit made from Promega is used to improve the analysis, accuracy, and discrimination power of Y-STR [12, 13]. Previous studies focused on the inherited characteristics of individuals representing different ethnic backgrounds in Iraq and its bordering countries. [14, 15, 16].
This study's goal is to investigate the genetic makeup of the Iraqi Arab population, haplogroup distributions, identification of a novel haplotypes and the creation of a reference database.

MATERIALS AND METHODS

Iraqi populations: The analysisof Y-STR included 383 healthy, unrelated men who were not related to each other and were not members of the same family. These people's blood was drawn at the Ministry of Health, more precisely at the Paternity and Kinship Section of the Medical Legal Directorate. The DNA for the analysis was derived from the acquired blood samples.

DNA extraction

In recent years**,**direct amplification has become more commonas a faster and simplersubstitute for conventional procedures. In comparison to earlier forensic science tests, more recent amplification kits seek to provide better and speedier results. However, some commercially available kits still call for pre-treating body fluids with washing chemicals or buffers in order to speed up the amplification procedure. The capacity to process more samples in less time and a significant reduction in analysis time are two key benefits of direct amplification without DNA purification. Blood samples spotted on FTA cards, air-driedthen carefully packaged in paper envelopes until DNA extraction carried out [17].

STR amplification

An approximately 1.2 mm punch of male blood FTA cards used for amplificationof23 Y STR loci by using a PowerPlexsystemfrom Promegaaccording to the manufacturer's instructions for ensuring accurate and reproducible results with 1 ± 2 ng of target DNA amplified using (verity)a thermo cycler from Applied Biosystems[18].

Genotyping

The products of PCR amplification diluted with formamide (Hi- Di™) about 1:15, then analyzed with 3130 XL genetic analyzer using 3.2 version of gene mapper software (Applied Biosystems, USA).

STATISTICAL ANALYSIS

In the present study, the estimation of allele frequencies of haplotypes was used by gene counting methods. With exception, the locus DYS385 a/b is found on the same chromosome examined by the formula $D = (n/n-1)(1-\Sigma pi2)$, where (n) refers to the total allele number and (pi) refers to the frequency of one allele for calculating the genetic diversity of each tested haplotype. Population diversity was performed to estimate the discrimination ability of haplogroups. The nevgen Y-DNA haplogroup predictor was used as a tool to identify ancestral genetic markers of the Y chromosome region. A molecular variance analysis (AMOVA) was conducted to estimate genetic diversity between the selected samples and compare it to the stored data from other populations using the Y-STR haplotype reference database 3.0 [19]. The multi-dimensional scaling (MDS) plot was performed using the results from the AMOVA analysis [20]. All the statistics used reveal information about ancestry, genetic origins, and the frequencies of Y haplotypes in a population [21, 22].

RESULTS

Statistical assessments were conducted to assess the appropriateness of the allele frequency databases derived from a sample of 383 Iraqi Arab individuals.The study performed an analysis to assess the frequency of particular haplotypes (combinations of genetic markers), in our sample population (Table1). The DYS385a/b locus, which has a total of 55 distinct alleles, was discovered to have the most genetic diversity of the loci under study.Also high level of genetic variety was seen at the DYS458 locus, where a total of 15 distinct alleles were found. The loci DYS570 and DYS481, each showed 10 distinct alleles, also showed high levels of variability in addition to DYS458. Contrarily the lowest levels of genetic variety polymorphic loci were DYS391 with 4 alleles then followed by DYS533, DYS438, DYS437 and DYS393 with 5 alleles each locus(Table1).

Table 1: Alleleand Genotype frequencies in23Y-STR haplotypeof Iraqi Arab males.

DYS576	
Allele	Ferq
14	0.003
15	0.047
16	0.123
17	0.274
18	**0.355**
19	0.162
20	0.026
21	0.010

DYS3891	
Allele	Ferq
9	0.003
10	0.005
11	0.003
12	0.131
13	**0.695**
14	0.157
15	0.005
17	0.003

DYS448	
Allele	Ferq
17	0.003
18	0.029
19	0.209
20	**0.634**
21	0.094
22	0.031

DYS389II	
Allele	Ferq
25	0.003
26	0.008
27	0.005
28	0.086
29	0.269
30	**0.460**
31	0.144
32	0.026

DYS19	
Allele	Ferq
10	0.005
12	0.008
13	0.094
14	**0.624**
15	0.191
15,16	0.003
16	0.057
17	0.018

DYS385/a, b	
Allele	Freq
9,13	0.003
10,13	0.003
10,14	0.005
11,11	0.003
11,13	0.003
11,14	0.065
11,15	0.013
11,16	0.005
11,17	0.005
12,12	0.003
12,14	0.021
12,14.2	0.003
12,15	0.029
12,16	0.026
12,17	0.005
12,18	0.018
12,19	0.003
12,20	0.003
12,22	0.005
13,13	0.021
13,14	0.018
13,14.2	0.003
13,15	0.047
13,16	0.042
13,17	0.037
13.,17.2	0.003
13,18	**0.178**
13,19	0.112
13,20	0.021
13,21	0.003
14,14	0.013
14,15	0.016
14,15.2	0.005
14,16	0.050

DYS391	
Allele	Ferq
9	0.044
10	**0.603**
11	0.308
12	0.044

DYS481	
Allele	Ferq
20	0.016
21	0.052
22	0.196
23	**0.209**
24	0.154
25	0.149
26	0.178
27	0.039
28	0.005
29	0.003

DYS549	
Allele	Ferq
10	0.005
11	0.099
12	**0.499**
13	0.332
14	0.055
15	0.010

DYS533	
Allele	Ferq
9	0.029
10	0.097
11	**0.535**
12	0.300
13	0.039

DYS438	
Allele	Ferq
7	0.003
9	0.245
10	**0.593**
11	0.115
12	0.044

DYS437	
Allele	Ferq
11	0.003
13	0.029
14	**0.692**
15	0.196
16	0.081

DYS570	
Allele	Ferq
13	0.013
14	0.013
15	0.050
16	0.110
17	0.235
18	**0.326**
19	0.167
20	0.063
21	0.016
22	0.008

DYS635	
Allele	Ferq
16	0.003
19	0.003
20	0.081
21	**0.514**
22	0.178
23	0.162
24	0.039
25	0.013
26	0.005
28	0.003

DYS390	
Allele	Ferq
18	0.003
21	0.016
22	0.086
23	**0.572**
24	0.235
25	0.073
26	0.016

DYS439	
Allele	freq
9	0.003
10	0.055
11	**0.564**
11,13	0.003
12	0.319
13	0.052
14	0.005

DYS392	
Allele	Ferq
9	0.008
10	0.070
11	**0.770**
12	0.026
13	0.073
14	0.039
15	0.010
16	0.003

DYS635	
Allele	Ferq
8	0.023
9	**0.423**
10	0.274
11	0.104
12	0.115
13	0.052
14	0.008

DYS393	
Allele	Ferq
11	0.018
12	**0.569**
13	0.316
14	0.078
15	0.018

DYS456	
Allele	Ferq
12	0.003
13	0.044
14	0.321
15	**0.418**
16	0.146
17	0.063
18	0.003
22	0.003

YGATAH4	
Allele	Ferq
9	0.003
10	0.065
11	**0.627**
12	0.238
13	0.063
14	0.005

DYS458	
Allele	Ferq
12	0.005
13	0.003
14	0.005
15	0.138
16	**0.222**
16.2	0.005
17	0.128
17.2	0.031
18	0.094
18.2	0.183
19	0.052
19.2	0.102
20	0.021
20.2	0.008
21.2	0.003

14,17	0.018
14,18	0.031
14,19	0.010
14,21	0.003
14,22	0.003
15,15	0.005
15,16	0.029
15,17	0.010
15,21	0.003
15.2,17	0.003
16,16	0.008
16,17	0.016
16,18	0.018
16,19	0.005
16,20	0.005
17,17	0.003
17,18	0.010
17,19	0.005
18,18	0.003
18,19	0.021
19,19	0.005

Frequency (Ferq): The bold refers to the most common allele's frequencies in each locus in the sample population.Except for DYS385a/b, the study calculated the genotype frequencies based on the combination of two alleles.

The study, as shown in Table 2, presents information about the occurrence of the highest and lowest allele frequencies at each genetic locus. Specifically, it points out that at the DYS392 locus, the microvariant allele "11" was the most common and prevalent one in the Iraqi population.This information is important in genetic research as it helps understand the genetic makeup and diversity of a population.

Table 2: The occurrence of the highest and lowest allele frequencies at each genetic locus

	Freq		Freq		Freq		Freq
DYS576 High allele 18 Low allele 14	 0.355 0.003	DYS391 High allele 13 Low allele 9,17	0.695 0.003 	DYS448 High allele 17 Low allele 20	 0.634 0.003	DYS389II High allele 25 Low allele 30	 0.460 0.003
DYS391 High allele 14 Low allele 15,16	 0.624 0.003	DYS385/a,b High allele 13,18 Low allele 9,13, 10,13, 11,11, 11,13 , 12,12, 12,14.2, 12,19, 12,20, 13,14.2,13.,17.2, 13,21	**0.178** 0.003	DYS481 High allele 23 Low allele 29	 0.209 0.003	DYS549 High allele 12 Low allele 10	 0.499 0.005
DYS391 High allele 10 Low allele 9,12	 0.603 0.044 	DYS533 High allele 11 Low allele 9	 0.535 0.029	DYS438 High allele 10 Low allele 7	 0.593 0.003	DYS437 High allele 14 Low allele 11	0.692 0.003
DYS570 High allele 18 Low allele 13,14	0.326 0.013	DYS635 High allele 21 Low allele 16,19	 0.514 0.003	DYS390 High allele 23 Low allele 18	 0.572 0.003	DYS439 High allele 11 Low allele 9,11,13	 0.564 0.003
DYS392 **High allele** **11** Low allele 16	 **0.770** 0.003	DYS635 High allele 9 Low allele 14	 0.423 0,008	DYS393 High allele 12 Low allele 11,15	 0.569 0.018	DYS456 High allele 15 Low allele 12,18,22	0.418 0.003
DYS458 High allele 16 Low allele 21.2	0.222 0.003	YGATAH4 High allele 11 Low allele 9	 0.627 0.003				

There were a total of 383 different Y-STR haplotypes studied, out of these, 356 were unique, meaning they were not repeated in the dataset. This is seen as being quite very satisfying and demonstrates the potency of the PowerPlex Y 23 kit, a tool for examining genetic information. Several distinct haplotypes were discovered in the dataset more than once. For instance, there were three instances of each haplotype in samples H44, H70, H140, H206, and H255. These haplotypes were included in the sample populationmore frequently than others, compared to the other haplotypes, occurring at a frequency of 0.0098. In contrast, there were 337 different haplotypes that occurred with a lower frequency of 0.0033.Table (3)provides a genetic profile for each individual, showing the alleles they possess at various genetic markers.

Table 3: Y-STR haplotypes and haplotype frequencies in Iraq Arab populations

ID	DYS576	DYS3891	DYS448	DYS389II	DYS19	DYS391	DYS481	DYS549	DYS533	DYS438	DYS437	DYS570	DYS635	DYS390	DYS439	DYS392	DYS643	DYS393	DYS458	DYS385	DYS456	YGATAH4	FERQ
H1	18	13	20	30	17	10	25	12	12	11	14	20	23	25	10	11	10	13	16	10,13	16	12	0.0033
H2	17	13	20	31	15	10	24	13	12	11	14	19	23	26	11	12	10	13	15	10,14	15	12	0.0033
H3	19	13	20	30	16	11	23	11	12	11	14	20	23	25	10	11	10	13	15	10,14	16	12	0.0033
H4	17	13	20	30	15	11	23	12	12	10	14	19	23	25	11	11	10	13	15	11,11	15	11	0.0033
H5	16	14	19	30	14	10	20	11	11	10	14	20	22	23	11	12	11	14	16	11,13	14	12	0.0033
H6	17	13	19	30	14	10	22	12	12	12	15	17	21	24	12	12	10	12	16	11,14	15	12	0.0033
H7	17	13	19	30	14	10	22	13	12	12	15	17	23	24	12	13	9	12	16	11,14	15	12	0.0033
H8	17	13	19	30	14	10	22	13	12	12	15	17	23	24	12	13	10	12	16	11,14	15	12	0.0065
H9	17	13	19	30	14	10	22	13	12	12	15	17	23	25	12	13	10	12	16	11,14	16	12	0.0033
H10	17	13	19	29	14	10	22	14	12	12	15	17	23	24	13	13	10	12	16	11,14	15	13	0.0033
H25	18	13	20	30	17	10	23	12	12	11	14	18	23	23	11	11	10	13	15	11,16	15	13	0.0065
H37	18	13	20	30	14	10	23	12	11	9	14	16	21	23	11	11	10	12	17	12,15	16	11	0.0065
H44	**19**	**12**	**21**	**28**	**15**	**10**	**22**	**12**	**9**	**10**	**16**	**19**	**21**	**23**	**12**	**11**	**11**	**15**	**16**	**12,16**	**15**	**12**	**0.0098**
H58	18	14	19	30	14	10	24	11	10	11	15	17	24	23	11	11	10	15	15	12,22	15	12	0.0065
H70	**16**	**13**	**20**	**29**	**14**	**10**	**24**	**13**	**11**	**10**	**15**	**18**	**24**	**23**	**10**	**11**	**11**	**12**	**16**	**13,16**	**15**	**11**	**0.0098**
H93	18	13	20	30	14	10	25	12	11	10	14	18	20	23	11	10	9	13	17.2	13,16	15	11	0.0065
H140	**18**	**13**	**20**	**30**	**14**	**11**	**26**	**13**	**11**	**10**	**14**	**18**	**21**	**23**	**11**	**11**	**9**	**12**	**18.2**	**13,18**	**14**	**11**	**0.0098**
H150	19	13	20	30	14	11	26	12	10	9	14	18	21	23	11	11	9	12	19.2	13,18	13	11	0.0065
H175	18	13	20	30	14	11	25	12	11	10	14	18	21	23	11	11	9	12	18.2	13,19	14	11	0.0065
H185	18	13	20	31	17	10	25	13	11	10	14	18	21	23	11	11	9	13	19.2	13,19	16	11	0.0065
H195	17	13	20	30	14	11	26	13	11	10	14	18	21	23	11	11	9	12	18.2	13,20	14	11	0.0065
H204	16	13	20	29	14	10	22	13	11	9	14	16	21	22	12	11	8	12	15	14,15	16	11	0.0065
H206	**17**	**13**	**21**	**30**	**15**	**10**	**20**	**12**	**12**	**9**	**16**	**18**	**21**	**26**	**11**	**11**	**9**	**13**	**16**	**14,16**	**15**	**11**	**0.0098**
H217	19	13	20	30	15	10	22	11	11	9	15	16	22	23	11	11	12	12	18	14,16	15	12	0.0065
H228	17	13	20	31	14	10	24	14	12	10	14	18	20	23	11	11	9	12	18.2	14,18	15	11	0.0065
H255	**16**	**13**	**19**	**30**	**13**	**10**	**25**	**12**	**12**	**10**	**14**	**20**	**23**	**24**	**12**	**11**	**13**	**13**	**16**	**15,16**	**17**	**11**	**0.0098**
H248	17	12	20	29	13	9	26	13	11	10	14	18	20	23	12	11	11	14	17	15,17	15	12	0.0065

The haplotype diversity was calculated to be 0.997. This score shows that the Y-STR haplotypes under study have a very high level of variety. In other words, the population contains a large number of distinct haplotypes.Discrimination Capacity" (DC) now mean the degree to which a set of genetic markers can discriminate between individuals is measured by the DC. The ability to recognize unique haplotypes—those haplotypes that are encountered just once in the population is specifically at issue in this instance. The DC is determined by dividing the total number of haplotypes in the dataset by the number of unique haplotypes (Table 4).

Table 4: Genetic information of Y-STR haplotypes.

23Y-STR haplotype	
Sample size	383
Number of haplotypes	356
Unique haplotype	337
Repeating haplotype	19
Haplotype Diversity	0.997
Discrimination capacity	0.946

Average gene diversity (GD) is a measure used in genetic studies to assess the level of genetic variation within a population. In this context, the study population has an average gene diversity of 0.63981 (Table 5). This value indicates how genetically diverse or similar the individuals within this population are. The range of GD values within this population spans from 0.395062 to 0.93828. This range suggests that there is some variability in the genetic makeup of the individuals in the population, with some loci showing higher diversity and others showing lower diversity.The highest gene diversity was observed at the DYS385a/b loci, with a GD value of 0.93828. This means that these particular genetic markers (DYS385a/b) have a high degree of variation within the population;andthe lowest gene diversity was found at the DYS392 locus, with a GD value of 0.395062. The NevGen Y-DNA Haplogroup online Predictor tool was used to identify the Y-haplogroups of male Iraqi Arabs. In this study, the most prevalent haplogroups were J1 (38%), J2 (20%), R1 (11%), E1 (10%), and G2 (5%). Additional expected haplogroups were also found, even though they were less common, as shown in Table 6.

Table 5: Gene Diversity in 23Y-STR haplotype of Iraqi Arab males

Locus	GD	Locus	GD
DYS576	0.756456	DYS570	0.793351
DYS3891	0.477233	DYS635	0.671155
DYS448	0.544598	DYS390	0.606141
DYS389II	0.689486	DYS439	0.576203
DYS19	0.563176	**DYS392**	**0.395062**
DYS391	0.538775	DYS635	0.720367
DYS481	0.83827	DYS393	0.570899
DYS549	0.630008	DYS458	0.860566
DYS533	0.613263	DYS456	0.696868
DYS438	0.574809	R-Y-GATA-H4	0.544079
DYS437	0.476782	**DYS385a/b**	**0.93828**

GD: Gene Diversity.The highest and lowestGene Diversity in bold

Table 6: Haplogroups prediction for Iraqi Population.

Haplogroup	Number	Freq
J1	137	0.385
J2	72	0.202
R1	40	0.112
E1	37	0.104
G2	19	0.053
T	17	0.048
L1	6	0.017
Q	5	0.014
I2	4	0.011
R2	4	0.011
G1	4	0.011
Unsupported sub-clade	3	0.008
H1	2	0.006
N1	1	0.003
O2	1	0.003
I1	1	0.003
C2	1	0.003
O1	1	0.003
E2	1	0.003
	356	**1.000**

DISCUSSION

The Y-STR haplotypes, which are distinctive sets of genetic markers found on the Y chromosome, were examined in the context of this study. The analysis of these Y-STR haplotypes' diversity in the Iraqi Arab population was the main goal of the study. Y-STR haplotype databases are helpful for examining differences within a given population as well as between other demographic groupings and establishing databases, which is

essential for the forensic importance and reliability of Y-STR evidence [21].The PowerPlex Y-23 kit contains more Y-STR loci than other Y-STR kits, which was done to improve the capacity to identify between individuals. It is a common option for use in forensic investigations and demographic research due to its strengthened discriminative power[22].The result reveled 212 genetic variations (alleles) spread across 23 distinct locations on the Y chromosome known as Y-STR loci[Table 1].A Significant genetic variation within the population is indicated by polymorphism in these loci, which is important for different forensic and genetic research. The DYS385a/b locus had the most genetic diversity, with a total of 55 different alleles andhighest gene diversity for this locus was 0.93828, indicating that different individuals within the population have distinct genetic profiles at these loci. These results are consistent with previous study published on the Arab and Kurdish populations in Iraq [23].Conversely, the lowest gene diversity was found at the DYS392 locus, with a GD value of 0.395062. This suggests that the genetic variation at the DYS392 locus is relatively low within the populationwith 4 alleles, meaning that most individuals in the population have very similar genetic profiles at this specific genetic marker [24].The observation that the GD values align with the polymorphism findings in the study indicates consistency in the genetic diversity patterns. In this study, it appears that the GD values correspond to the polymorphism levels observed at these genetic markers in the population. The fact that the GD values align with the study's polymorphism findings suggests that the genetic diversity patterns are consistent. In this situation, it appears that the GD values match the polymorphism levels seen at these genetic markers in the population. Polymorphism is the existence of several genetic variations (alleles) at a single genetic locus[25].
The micro-variant alleles "11" found in the DYS392 locus exhibited the highest frequency (0.770) and were widely prevalent throughout the Iraqi population. The aforementioned data holds significant relevance within the field of genetic research as it facilitates comprehension of the genetic composition and variability exhibited by a given population; this information plays a crucial role in population genetics and forensic investigations. They enable researchers to gain insights into genetic variety and facilitate the identification of individuals through the analysis of their DNA profiles [26].A total of 356 haplotypes were identified as unique within the dataset, indicating their absence of repetition. This observation is regarded as highly satisfying and serves as evidence of the efficacy of the PowerPlex Y 23 kit, a genetic analysis tool. Additionally, multiple distinct haplotypes were found to occur more than once in the dataset. The correlation between a decrease in genetic diversity at specific genetic loci and an increased incidence of inbreeding has been established. Inbreeding observed in numerous regions of Iraq results in a gradual reduction in genetic variety over an extended period [27, 26,29,30].The study revealed that the prevailing genetic groups, referred to as haplogroups, were J1 and J2, constituting 38% and 20% of the sample, respectively. Whit Athey'sHaplogroup Predictor was used to identify Y-haplogroups in this research. According to the results, J1 was shown to be the most common haplogroup among Iraqi Arabs (38%). This fits in with what has been seen before. Many people from different parts of West Asia, North Africa, the Horn of Africa, Southern Europe, Central Asia, and South Asia share DNA with the haplogroup J1. People who speak other Semitic languages, most notably Arabic, are more likely to be familiar with it [27,28,31].

CONCLUSION

The current study successfully constructed a comprehensive database consisting of 23 Y-STR loci that were specifically designed and optimized for the Iraqi Arab community. The utilization of haplotype patterns and haplogroup predictions has demonstrated significant efficacy in understanding the geographic origins of individuals. the DYS385a/b loci showed the highest level of genetic diversity,Followed by DYS458. In contrast, DYS391 exhibited the most limited extent of genetic diversity. The microvariant allele "11" has been observed to be the predominant allele at the DYS392 locus throughout the Iraqi population. The prevalence of the J1 haplogroup was noted to be highest among Iraqi Arabs. The result has significance for the development of a comprehensive population database, providing crucial insights for the fields of population genetics and forensic research. In addition, these tools enhance comprehension of genetic variability and allow for the differentiation of individuals through analysis of their DNA profiles.

Funding
There was no outside funding used to carry out the investigation.

Ethical approval
The study obtained ethical clearance by the institutional Ethics Committee of the Forensic DNA Centre for Research and Training at Al-Nahrain University, situated in Jadriya, Baghdad, Iraq. The approval was officially obtained on the:10/ 9 /2022, and is linked to a distinct reference number (43).

Consent for publication
The consent to publish had been taken from each participant in this work.

Abbreviations

Y-STR: Y-chromosome of Short Tandem Repeats, PCR: polymerase chain reaction, AMOVA; Analysis of Molecular Variance, YHRD: STR Haplotype Reference Database,MDS: multidimensional scaling, DC: Discrimination Capacity, GD: Gene Diversity.

REFERENCES

1. Kovačević L, Fatur-Cerić V, Hadžić N, Čakar J, Primorac D, Marjanović D. "Haplotype Data for 23 Y-chromosome markers in a reference sample from Bosnia and Herzegovina"Croat Med J. 2013 ;54:286-90. Medline:23771760 doi:10.3325/cmj.2013.54.286
2. DhuhaSalimNamaa, ThooalnoonYounes Al-Janabi, Halah Khalid Ibrahim AlSammarraie.(2024). "A Comparison Study of Cryopreservation of Seminal Fluid between Flinders Technology Associates (FTA-card) and Swab for Multiplex Short Tandem Repeats (STR) Analysis". Iraqi Journal of Science, Vol. 65, No. 7, pp: 3680-3691.DOI: 10.24996/ijs.2024.65.7.10
3. K. Haider, M. Mohammed, I. Kh. Halah, M. Ali, R. Sahar, H. Reem , N. Sura, A. Asia, A. Ali " Revealed of A novel Allele in Wasit – Iraqi Population" Iraqi Journal of Science, vol. 56, no. 4A, pp. 2798-2806, 2015.
4. Central_Intelligence_Agency. The World Factbook (2016): Central Intelligence Agency; 2016.
5. Kirmanj S. Identity and Nation in Iraq: Lynne Rienner Publishers; 2013.
6. Kh. Halah, A. S. Majeed, and M. Mohammed.(2020) " Allele Frequencies of 15 Autosomal STR Loci in Hilla City population / Iraq" Journal of Biotechnology Research Center, vol. 40, no. 1, pp. 86- 91.
7. Al-Zubaidi, M. M., Ibrahem, H. K., Ameen, R. S., &Ameen, B. (2022). Allele frequencies of 15 Autosomal STR loci in Some of Iraqi population.Iraqi Journal of Science, 63(6), 2434–2443.https://doi.org/10.24996/ijs.2022.63.6.10
8. Ban Ameen , Mohammed Mahdi Al-Zubaidi , MajeedArsheedSabbah , Mohammed I. Nader , DhuhaSalimNamaa , Hala K. Ibrahem , ThooalnoonYounes Al-Janabi , Asia Abdul Lateef Mahdi , ReemHusam Al-Tabra, Miriam Jasim. (2022)."Genetic polymorphism of 17Y-STR loci in central of Iraq Population".International Journal for Research in Applied Sciences and Biotechnology, Vol.9, No. 2, P: 348-356
9. cenanović M, Pojskić n, Kovacević l, Dzehverović M, cakar J, MusemićDz, et al. (2010)"Diversity of Y-short tandem repeats in the representative sample of the population of canton Sarajevo residents, bosnia and herzegovina". coll antropol.;34:545-50. Medline:20698129
10. grsković b, Mršić g, Vrdoljak a, Merkas S, andelinović S. (2010)"Population genetic analysis of haplotypes based on 17 short tandem repeat loci on Y-chromosome in population sample from eastern croatia". croat Med J.;51:202-8. Medline:20564762 doi:10.3325/ cmj.2010.51.202
11. RashaSadeqAmeen , MajeedArsheedSabbah , Asia abdullateef , SuraNabeel , Hala Khalid Ibrahem , Mohammed Mahdi Al-Zubaidi1 , Ban Ameen (2022)."Evaluation The Quality Of Dna Extracted From Teeth". nternational Journal of Medical Toxicology & Legal Medicine Vol. 25 Nos. 3-4, pp(97-101). DOI No: 10.5958/0974-4614.2022.00058.4
12. Dogan, S., Primorac, D., &Marjanović, D. (2014). "Genetic analysis of haplotype data for 23 Y-chromosome short tandem repeat loci in the Turkish population recently settled in Sarajevo, Bosnia and Herzegovina."Croatian medical journal, 55(5), 530.
13. Roewer, L.; Kayser, M.; de Knijff P, Anslinger, K.; Betz, A.; Caglià ,A. et al.(2000)."A new method for the evaluation of matches in non-recombining genomes: application to Y-chromosomal short tandem repeat (STR) haplotypes in European males". Forensic Sci Int.114: 31–43.
14. Imad ,H.;Cheah, Q.; Mohammad, J. and Aamera, J. (2013). "Genetic variation of 17 Y-chromosomal short tandem repeats (STRs) loci from unrelated individuals in Iraq."Int. J. Biotechnol. Mol. Biol. Res. 120-130.
15. Al-Zahery, N.; Pala, M.; Battaglia, V. et al.(2011). "In search of the genetic footprints of Sumerians: a survey of Y-chromosome and mtDNAvariation in the Marsh Arabs of Iraq". BMC EvolBiol **11,** 288 .
16. Dogan, S.; Gurkan ,C,; Dogan, M.; Balkaya, H.E.; Tunc, R.; Demirdov, D.K. et al. (2017). "A glimpse at the intricate mosaic of ethni-governorates from Mesopotamia: Paternal lineages of the Northern Iraqi Arabs, Kurds, Syriacs, Turkmens and Yazidis". PLoS ONE 12(11).
17. Hall, D. E., & Roy, R. (2014). "An evaluation of direct PCR amplification". Croatian Medical Journal, Vol. 55, pp. 655–661. https://doi.org/10.3325/cmj.2014.55.655
18. PromegaPowerPlex® Y23 system – technical manual (tMD035). Madison, Wi: Promega corporation; 2012.
19. Roewer ,L.Kayser, M,; Dieltjes, P.; Nagy, M.; Bakker, E. and Krawczak,M., et al. (1996). "Analysis of molecular variance (AMOVA) of Y-chromosome-specific microsatellites in two closely related human populations". Hum Mol Genet. 5(7): 1029–33.

20. Willuweit, S. and Roewer, L. (2007). "Y chromosome haplotype reference database YHRD: Update".Forensic Science International: Genetics, 1: 83-87.
21. Dogan, S., Primorac, D., &Marjanovic, D. (2014). "Genetic analysis of haplotype data for 23 Y-chromosome short tandem repeat loci in the Turkish population recently settled in Sarajevo, Bosnia and Herzegovina". Croatian Medical Journal, 55, 530–536. https://doi.org/10.3325/cmj.2014.55.530
22. Balnd M. Albarzinji ,Farhad M. Abdulkarim , Shaho A. Hussein , Dlshad Rashid and HayderLazim. (2022).” Population genetic study of 17 Y-STR Loci of the Sorani Kurds in the Province of Sulaymaniyah, Iraq”.BMC Genomics.23:763.
23. Marino, M., Sala, A., &Corach, D. (2007). "Genetic attributes of the YHRD minimal haplotype in 10 provinces of Argentina". Forensic Science International:Genetics, 1(2), 129–133. https://doi.org/10.1016/j.fsigen.2007.01.013
24. Marchi N, Hegay T, Mennecier P, Georges M, Laurent R, Whitten M et al (2017) "Sex-specific genetic diversity is shaped by cultural factors in Inner Asian human populations". Am J PhysAnthropol 162(4):627–640
25. Mahmood, H. K., Salman, N. F., Salih, K. M., Hasan, D. H., & Al-Zubaidi, M. M. (2020). "Frequency of Y-chromosome STRs using PowerPlex® Y23 System in Iraqi population".Egyptian Journal of Forensic Sciences, Vol. 10.https://doi.org/10.1186/s41935-020-00186-3
26. Charlesworth, D. (2003)"Efects of inbreeding on the genetic diversity of populations Philosophical Transactions of the Royal Society of London B: Biological Sciences 358, 1051–1070.
27. Lazim, H., Almohammed, E. K., Hadi, S., & Smith, J. (2020). ".Population genetic diversity in an Iraqi population and gene flow across the Arabian Peninsula".Scientific Reports, Vol. 10.https://doi.org/10.1038/s41598-020-72283-1.
28. Al-Zubaidi, Mohammed .M. ,Majeed ,Arsheed .,Sabbah, Hanan, Khaleel. Mahmood., Molecular diversity of 23-YSTR markers in Iraqi populations, Gene, 2023 vol . 872 , no .147440 . https://doi.org/10.1016/j.gene.2023.147440.
29. Sabbah, M.A., Al-Zubaidi, M.M., Al-janabi, T.Y. et al, Short tandem repeat (STR) variation from 6 cities in Iraq based on 15 loci,J Genet EngBiotechnol , 2023 , vol .21,no. 160. https://doi.org/10.1186/s43141-023-00570-1.
30. ShehabM. J., NamaaDH. S. and AL-Zubaidi M. M. (2022). Assessment of Short tandem Repeat profiling that obtained from Some Biological Sources as Forensic Tool. International Journal of Medical Toxicology & Legal Medicine, 25 (3 and4): 90-96. DOI: 10.5958/0974-4614.2022.00057.2.