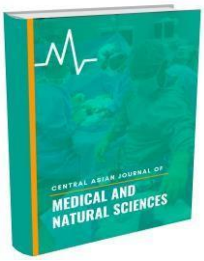

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Article

Y-Chromosome Variation in the Iraqi Population

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Abstract: Iraq is considered the cradle of civilizations and the oldest civilization in the world. Due to historical events over the ages, this has led to the gathering of many origins, nationalities, and religions within Iraq, resulting in genetic diversity within Iraq. Aim and methodology: Studying of genetic diversity among the origins and ethnicities of Iraq by collecting 1502 samples specifically from men from different parts of the country and from different ethnicities and religions, analyzing the Y chromosome, and comparing the results with Advanced Y-chromosome testing methods were employed, including Y-STR and Y-SNP markers, as well as the Big Y-700 and Family Finder tests based on next-generation sequencing (NGS) and SNP array technologies. In the present study, Y-chromosome analysis revealed that haplogroup J1 was the most prevalent (over 31%), followed by J2 (≈20%), E-M35 (12%), T1-M70 (6.6%), G-M201 (≈6.46%), R-M269 (6.4%), and R-M198 (6.2%).The genetic analysis, 1,093 Arab samples were examined, with 514 undergoing detailed SNP testing. The dominant paternal lineage was haplogroup J1 (36%), followed by J2 (17%), E-M35 (12%), T-M70 (7.7%), G-M201 (5.3%), R-M198 (5.22%), and R-M269 (4.3%), reflecting the major paternal components of the Arab population in Iraq. Genetic analyses in Iraq show that haplogroup J, particularly branches J1 and J2, comprise over half of male Y-chromosome lineages. Haplogroup J1-FGC1695 is predominant among Iraqi Arabs, representing 78% of J1 samples and indicating a population expansion about 3,000 years ago. Genetic diversity among Arabs is influenced by Iraq's lengthy history of migrations, although certain groups like the Romani and Kakais present approximate results due to smaller sample sizes. The Romani display 40% Indian ancestry and a paternal lineage suggesting recent migration, while the Yazidis lack distinct genetic clustering.

Keywords: Haplogroup, Genetic Analyses, Y-STR, Y-SNP, Big Y-700

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1. Introduction

Iraq is one of the earliest cradles of human civilization, located between the Tigris and Euphrates rivers, where fertile lands enabled the rise of advanced societies such as the Sumerian, Akkadian, Babylonian, and Assyrian civilizations. These cultures made pioneering contributions to writing, law, governance, and architecture, influencing the course of human history [1]. Due to its strategic position in the ancient Near East, Iraq has witnessed numerous invasions throughout history-from the Gutians, Elamites, and Kassites, to the Persians, Greeks, Parthians, Sasanians, and later the Mongols and Ottomans [2]. This long history of conquest and migration shaped Iraq into a highly diverse society in terms of ethnicity, language, religion, and culture [3]. In light of this diversity, the study focuses on exploring the genetic structure of Iraq's population. It analyzes Y-chromosome variation among 1,502 unrelated Iraqi males from eleven different ethno-religious groups, aiming to understand the paternal genetic diversity and the historical roots of Iraq's multiethnic composition (Table 1).

Table 1. Sample numbers according to groups.

Arab	Mandaean	Christ	Jew	Yazidi	Kurd	Turkmen	Kakai	Feyli	Shabak	Roma	Total
1093	30	113	47	20	106	43	13	15	15	7	1502

Iraq, located in Western Asia and forming the northeastern part of the Arab world, shares borders with Kuwait and Saudi Arabia to the south, Turkey to the north, Syria and Jordan to the west, and Iran to the east, with a short coastline along the Arabian Gulf [4]. The country's population, estimated at around 46 million, is characterized by remarkable ethnic and religious diversity [5]. Arabs make up about 75–80% of the population, followed by Kurds (15–20%), Turkmen (3-5%), and several minority groups including Christians, Yazidis, Mandaeans, Shabaks, Kakais, and Feyli Kurds [6]. This demographic complexity makes Iraq a rich case for anthropological and genetic investigation. To explore the paternal genetic structure of its population, the study analyzed 1,502 male samples representing various ethno-religious groups. Advanced Y-chromosome testing methods were employed, including Y-STR and Y-SNP markers, as well as the Big Y-700 and Family Finder tests based on next-generation sequencing (NGS) and SNP array technologies. The integration of these methods allowed for a high-resolution mapping of paternal lineages and precise placement of Iraqi samples within the global Y-DNA phylogenetic tree, providing valuable insights into the genetic diversity, historical migrations, and ancestral relationships of Iraq's multifaceted population [7].

Male Lineages in Humans

The study focuses on human male lineages, identified through Y-chromosome haplogroups, which serve as a key framework in population genetics and molecular anthropology [8]. These haplogroups are determined by analyzing single nucleotide polymorphisms (SNPs) on the Y chromosome-passed exclusively through the paternal line and minimally affected by recombination-making them a reliable marker for tracing paternal ancestry and reconstructing human migratory history (Figure 1).

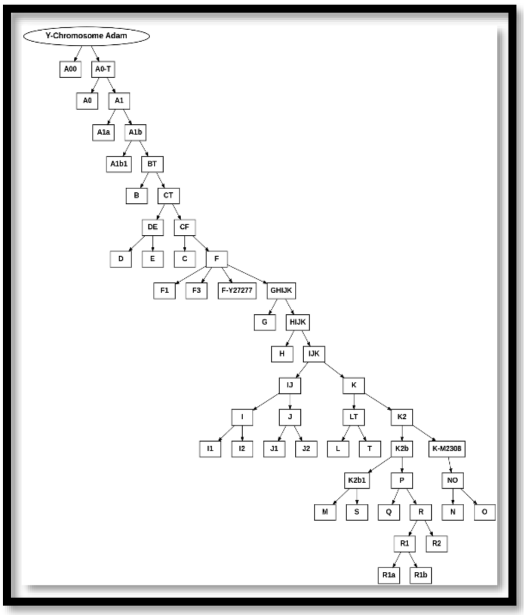

Figure 1. Comparative Table of Major Y-DNA Haplogroups (Ages from Karmin 2015, Poznik 2016, YFull 2024).

Y-chromosome analyses allow researchers to map the dispersal of Homo sapiens from Africa approximately 60–70 thousand years ago (Table 2) and to examine the demographic processes shaping modern human populations [9]. This genetic evidence also helps clarify the interplay between genetic variation and linguistic [10]; cultural, and historical factors, with further applications in archaeology, ancient history, and forensic science [11].

Table 2. Showed the Y- chromosome Haplogroups , Place of origin and Main spread.

Haplogroup	Poznik 2016	YFull 2024	Place of Origin	Main Spread
A00	~280–300k	249k	Africa (Cameroon)	Cameroon (localized)
A0–A1b	~200–230k	161k	Africa (East/West)	East, West, Southern Africa
BT	~190k	144k	Africa	Ancestor of all non-African
C	~45–50k	47k	South/Central Asia	East Asia, Oceania, Australia
D	~45–50k	45k	East Asia	Tibet, Japan, Andaman Islands
E	~45–50k	41k	East Africa	Africa (all regions), North Africa, Near East
G	~20–25k	26k	Anatolia / Caucasus	Caucasus, Anatolia, parts of Europe
H	~40–45k	40k	South Asia	India, Nepal, Roma (Gypsies)
I	~22–25k	27k	Balkans (Europe)	Central & Northern Europe, Balkans, Scandinavia
J1 (M267)	~20k	20.3k	Fertile Crescent / Near East	Arabian Peninsula, Fertile Crescent, Caucasus
J2 (M172)	~22k	24k	Fertile Crescent / Anatolia	Near East, Anatolia, Mediterranean, Iran, North India
L	~25–30k	25k	West Asia	West Asia, South Asia
N	~15–20k	19k	East Asia / Mongolia	Siberia, Baltic, Finland
O	~30–35k	31k	East Asia	China, Japan, Korea, Southeast Asia
Q	~15–20k	17k	Siberia	Americas, Siberia, Central Asia
R1a (M420)	~22–24k	24.5k	Caucasus, Southern Russia	Eastern Europe, Central Asia, India
R1a1a (M198)	~20–23k	8.7k	Central Asia	Eastern Europe, South Asia
R1a1a1 (M417/M512)	~6k	5.8k	Pontic–Caspian Steppe	Indo-European expansions (Europe, India)
R1b (M343)	~18–20k	18k	West Asia / Caucasus (debated)	Western Europe, West Asia, North Africa
T (M70)	~25–30k	28k	Near East / Fertile Crescent	Near East, North Africa, East Africa,

2. Results

According to Y chromosome analysis, Data: The results showed that 470 male samples had their Y chromosome results belong to J1-M267, while 306 samples were related to J2-M172 (Table 3). While the Y chromosome Subclade Haplogroup analysis, Data results showed that 227 male samples had their Y chromosome results belong to J1-M267, while 117 samples were related to J2-M172 (Table 4; Figure 2).

Table 3. Showed the Raw labels (Haplogroups) results according to samples.

Row Labels	Arab	Mandaean	Christ	Jew	Yazidi	Kurd	Turkmen	Kakai	Feyli	Shabak	Roma	Total
A-L419	2											2
B-M181	6											6
C-M130	7					1	1					9
D-M174	1					1						2
E-M2	8											8
E-M35	138	5	10	9		13	2	2	3			182
E-M96	2				1							3
G-M201	58		10	2		11	5		1	9	1	97
H-L901	5	2				2		1				10
I-M170	8					1						9
J1-M267	397	4	17	13	1	22	6	1	5	2	2	470
J2-M172	195	11	22	6	7	36	19	2	5	3		306
L-M20	30		1	2	2		1				4	40
N-M231	3		1									4
O-M175	3							2				5
Q-M242	29	1	1	1		3		1	1	1		38
R2-M479	9		1	5		2	1					18
R-M198	57	2	9	2	6	10	6	2				94
R-M269	47		39	2	2	2	2	2				96
T1-M70	84	5	2	5	1	2						99
T2-PH196	4											4
Total	1093	30	113	47	20	106	43	13	15	15	7	1502

Table 4. Subclade Haplogroups results according to samples.

Haplogroup	Arab	Christ	Feyli	Jew	Kakai	Kurd	Mandaean	Roma	Shabak	Turkmen	Yazidi	Total
A-L419	1											1
B-M181	1											1
C-M130	3											3
D-M174	1											1
E-M2	2											2
E-M35	56	1	3		2	3	1					66

E-M96	2										1	3
G-M201	13	1	1			2			6	3		26
H-L901	3											3
I-M170	4											4
J1-M267	209	1	4	2	1	2	2	2	2	2		227
J2-M172	87	2	2		2	9	4		3	5	3	117
L-M20	13			2				1		1		17
N-M231	1											1
O-M175	2				1							3
Q-M242	15		1									16
R2-M479	8			1								9
R-M198	21	2		1	1	1	1			3	1	31
R-M269	11	2			2					1		16
T1-M70	59	2					2					63
T2-PH196	2											
Total	514	11	11	6	9	17	10	3	11	15	5	612

In the present study, Y-chromosome analysis revealed that haplogroup J1 was the most prevalent (over 31%), followed by J2 (≈20%), E-M35 (12%), T1-M70 (6.6%), G-M201 (≈6.46%), R-M269 (6.4%), and R-M198 (6.2%). These findings reflect the predominant paternal lineages in the sampled population and contribute to understanding its genetic structure and ancestral composition (Table 5; Figure 3).

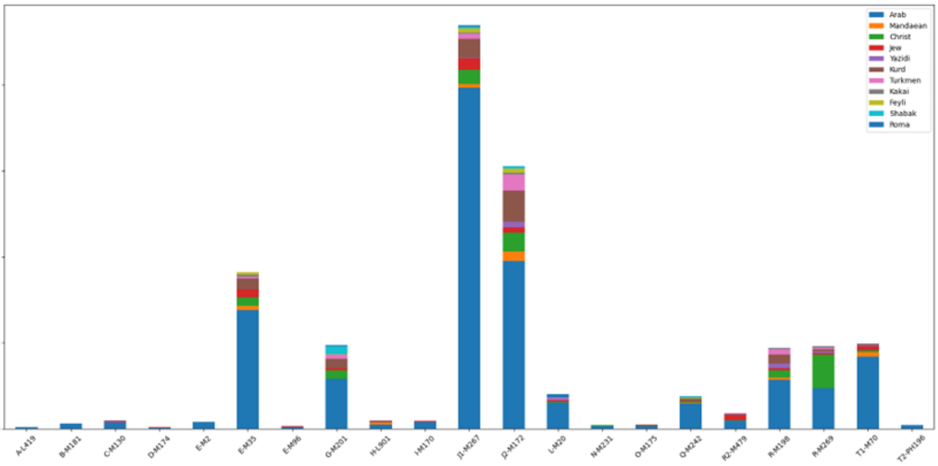

Figure 2. The analyzed samples, their detected mutations, and their distribution across paternal lineages by ethnic components.

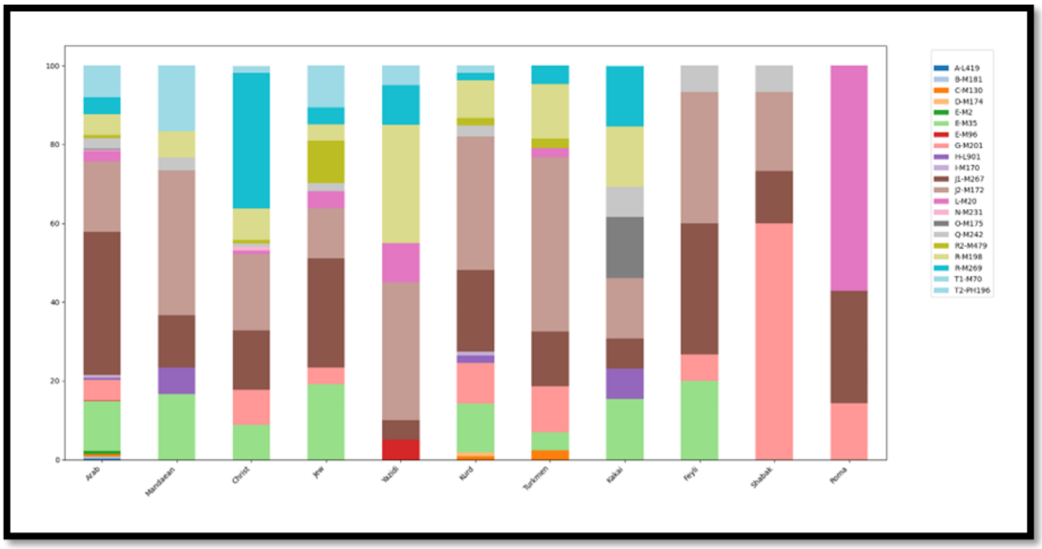

Figure 3. The analyzed samples percentage across paternal lineages by ethnic components.

Table 5. The percentage distribution of ethnic components and their allocation across paternal lineages.

Haplogroup	Arab	Mandaean	Christ	Jew	Yazidi	Kurd	Turkmen	Kakai	Feyli	Shabak	Roma	Total
A-L419	0.18%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.13%
B-M181	0.55%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.40%
C-M130	0.64%	0.00%	0.00%	0.00%	0.00%	0.94%	2.33%	0.00%	0.00%	0.00%	0.00%	0.60%
D-M174	0.09%	0.00%	0.00%	0.00%	0.00%	0.94%	0.00%	0.00%	0.00%	0.00%	0.00%	0.13%
E-M2	0.73%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.53%
E-M35	12.63%	16.67%	8.85%	19.15%	0.00%	12.26%	4.65%	15.38%	20.00%	0.00%	0.00%	12.12%
E-M96	0.18%	0.00%	0.00%	0.00%	5.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.20%
G-M201	5.31%	0.00%	8.85%	4.26%	0.00%	10.38%	11.63%	0.00%	6.67%	60.00%	14.29%	6.46%
H-L901	0.46%	6.67%	0.00%	0.00%	0.00%	1.89%	0.00%	7.69%	0.00%	0.00%	0.00%	0.67%
I-M170	0.73%	0.00%	0.00%	0.00%	0.00%	0.94%	0.00%	0.00%	0.00%	0.00%	0.00%	0.60%
J1-M267	36.32%	13.33%	15.04%	27.66%	5.00%	20.75%	13.95%	7.69%	33.33%	13.33%	28.57%	31.29%
J2-M172	17.84%	36.67%	19.47%	12.77%	35.00%	33.96%	44.19%	15.38%	33.33%	20.00%	0.00%	20.37%
L-M20	2.74%	0.00%	0.88%	4.26%	10.00%	0.00%	2.33%	0.00%	0.00%	0.00%	57.14%	2.66%
N-M231	0.27%	0.00%	0.88%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.27%
O-M175	0.27%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	15.38%	0.00%	0.00%	0.00%	0.33%
Q-M242	2.65%	3.33%	0.88%	2.13%	0.00%	2.83%	0.00%	7.69%	6.67%	6.67%	0.00%	2.53%
R2-M479	0.82%	0.00%	0.88%	10.64%	0.00%	1.89%	2.33%	0.00%	0.00%	0.00%	0.00%	1.20%
R-M198	5.22%	6.67%	7.96%	4.26%	30.00%	9.43%	13.95%	15.38%	0.00%	0.00%	0.00%	6.26%
R-M269	4.30%	0.00%	34.51%	4.26%	10.00%	1.89%	4.65%	15.38%	0.00%	0.00%	0.00%	6.39%
T1-M70	7.69%	16.67%	1.77%	10.64%	5.00%	1.89%	0.00%	0.00%	0.00%	0.00%	0.00%	6.59%
T2-PH196	0.37%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.27%
Total	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%

A. Haplogroup Results

1. Haplogroup J-M267 (J1)

Represents a major human paternal lineage believed to have originated approximately 20,000 years ago during the Last Glacial Maximum in the region encompassing the Caucasus, the Armenian Highlands, the Zagros Mountains, and northern Mesopotamia [12]. This haplogroup constitutes the predominant paternal lineage in Iraq, with a total of 470 identified samples. To achieve finer genetic resolution, 227 of these samples underwent single nucleotide polymorphism (SNP) genotyping, allowing for the identification of specific subclades and mutational variations within the J-M267 lineage. These results provide valuable insights into the genetic structure, evolutionary history, and demographic patterns of the Iraqi population (Table 6).

Table 6. Showed the Mutation Age of J1 haplogroup, Number of samples and their percentage.

Mutation	Mutation age/ years according to the YFull phylogenetic tree	No.	Percentage	Notes
FGC4415	2900	99	43%	The FGC4708 branch, estimated to be 1,650 years old, is considered the most widespread branch in Iraq
FGC1707	2600	72	31%	The FGC2 branch, estimated to be 1,400 years old, is considered the most widespread branch in Iraq
The rest		56	26%	
The total		227	100%	

2. **Haplogroup J2 (J-M172)**

is a significant paternal lineage thought to have originated in the Western Near East around 22,000 years ago, particularly within the Fertile Crescent and adjacent regions such as Anatolia, the Caucasus and the Iranian Plateau [13]. In this study, 306 samples were classified under haplogroup J2, and 117 samples underwent single nucleotide polymorphism (SNP) genotyping to identify detailed subclade mutations. The findings offer insights into the phylogenetic diversity of haplogroup J2 and contribute to understanding the historical and demographic processes shaping paternal genetic variation in the region (Table 7).

Table 7. Mutation Age of Haplogroup J2, Number of samples and their percentage.

Mutation	Mutation age/ years according to the YFull phylogenetic tree	No.	Percentage
M67	12000	21	18
L25	8800	17	14
M47	4900	15	13
M102	15600	9	8
The rest		55	47
The total		117	100

3. **Haplogroup E1b1b1 (E-M35)**

It is believed that E-M35originated in East Africa, the Horn of Africa, or adjacent regions in the Near East approximately 22,000–24,000 years ago [14]. A total of 182 samples were classified with in this haplogroup, of which 66 samples were analyzed using single nucleotide polymorphism (SNP) testing to identify their specific mutations (Table 8).

Table 8. Showed the Mutation Age of Haplogroup E-M35, Number of samples, and their percentage.

Mutation	Mutation age/ years According to the YFull phylogenetic tree	No.	Percentage
V22	8100	22	33
M34	14900	20	30
V13	4800	14	21

The rest		10	16
The total		66	100

4. Haplogroup T1 (T-M70)

Research indicates that T-M70 originated in the Near East, including the Levant, Anatolia, the Jazira region, and Iraq, approximately 20,000 years ago [15]. A total of 99 samples were classified within this haplogroup, of which 63 samples were analyzed using single nucleotide polymorphism (SNP) testing to identify their specific subclade mutations (Table 9).

Table 9. Showed the Mutation Age of Haplogroup T-M70, Number of samples and their percentage.

Mutation	Mutation age/ years according to the YFull phylogenetic tree	No.	Percentage
CTS6507	4300	26	41
The rest		37	59
The total		63	100

5. Haplogroup G (G-M201)

Haplogroup G-M201 is believed to have originated within the eastern Anatolia– Armenia– western Iran region (South Caucasus/Zagros Mountains) approximately 48,000 years ago [16]. A total of 97 samples were classified within this haplogroup, of which 26 samples were analyzed using single nucleotide polymorphism (SNP) testing to identify their specific mutations (Table 10).

Table 10. Showed the Mutation Age of Haplogroup G-M201, Number of samples, and their percentage.

Mutation	Mutation age/ years according to the YFull phylogenetic tree	No.	Percentage
L30	14400	18	69
The rest		8	31
The total		26	100

6. Haplogroup R1b (R-M269)

It is a paternal lineage associated with the Pontic Steppe region—including the Caucasus [17], Armenia, and northwestern Iran—and linked to the Yamnaya culture, later spreading to Western and Northwestern Europe through the Beaker culture around 5,000–7,000 years ago [18]. In this study, 96 samples were identified as belonging to R-M269, with 16 samples analyzed through SNP testing to determine their specific subclade mutations, providing insights into the lineage's genetic composition and historical dispersion (Table 11).

Table 11. Showed the Mutation Age of Haplogroup R-M269, Number of samples, and their percentage.

Mutation	Mutation age/ years according to the YFull phylogenetic tree	No.	Percentage
Z2103	5900	12	75
The rest		4	25
The total		16	100

7. Haplogroup R1a1a (R-M198)

Likely originated near present-day Iran or eastern Anatolia, where rare basal branches have been detected, indicating an early diversification in this region about 6,000–7,000 years ago [19]. In this study, 94 samples were assigned to this haplogroup, and 31 samples underwent SNP analysis to identify specific subclade mutations, offering insight into its regional genetic diversity and ancestral development (Table 12)

Table 12. Showed the Mutation Age of Haplogroup R-M198, Number of samples and their percentage.

Mutation	Mutation age/ years according to the YFull phylogenetic tree	No.	Percentage
Z94	4500	23	74
The rest		8	26
The total		31	100

B. Component Results

Iraq exhibits exceptional ethnic, religious, and cultural diversity, shaped by its historical role as a crossroads of civilizations in the Mesopotamian Valley [20]. The population is primarily composed of Arabs and Kurds, with significant Turkmen and Christian minorities including Chaldeans, Assyrians, Syriacs, and Armenians [21]. Religiously, Islam is dominant, divided into Sunni and Shia branches, alongside ancient communities such as Christians, Yazidis, Mandaeans, and Kakais, all of which have preserved their distinct identities through centuries of coexistence and cultural exchange.

1. The Arabs

They are an ethno-linguistic group of Semitic origin, historically rooted in the Arabian Peninsula and documented in Assyrian sources from the 9th–8th centuries BCE [22]. Their early settlements extended across the Levant, Mesopotamia, and the Arabian deserts, with significant historical developments such as the Kingdom of Al-Hirah in southern Iraq and later expansions during the Islamic conquests of the 7th century CE [23]. In the genetic analysis, 1,093 Arab samples were examined, with 514 undergoing detailed SNP testing. The dominant paternal lineage was haplogroup J1 (36%), followed by J2 (17%), E-M35 (12%), T-M70 (7.7%), G-M201 (5.3%), R-M198 (5.22%), and R-M269 (4.3%), reflecting the major paternal components of the Arab population in Iraq. At the level of internal branches and the most common subclades within each haplogroup (Table 13).

Table 13. Showed the Haplogroups, Number of samples, Subclade and percentage of Arab samples.

Haplogroups	The number of analyzed samples	Subclades	Percentage	Notes
J1-M267	209	FGC4415	47	
		FGC1707	33	
		Others	20	
J2-M172	87	M67	18	
		L25	14	
		M47	13	
		Others	55	
E-M35	56	M34	32	
		V22	29	
		V13	21	
		Others	18	
T-M70	59	CTS6507	40	
		Others	60	

G-M201	13	L30	69
		Others	31
R-M198	21	Z94	71
		Others	29
R-M269	11	Z2103	73
		Others	27

2. Kurds

They are a major ethnic group predominantly Muslim, inhabiting the transnational region of Kurdistan, which covers areas of Iraq, Iran, Turkey, and Syria [24], [25]. They speak Kurdish, an Indo-European language of the Iranian branch. Historical and genetic studies suggest that the Kurds emerged from a blend of ancient Zagros Mountain populations [26] including the Medes, Carduchians, Sassanids, and other local groups over centuries. In this study, 106 Kurdish samples were analyzed, with 17 undergoing SNP testing for detailed mutation profiling. The dominant paternal lineage was haplogroup J2 (34%) followed by J1 (21%), E-M35 (12%), G-M201 (10%), and R-M198 (9.4%), reflecting the genetic composition and historical ancestry of the Kurdish population in Iraq (Table 14).

Table 14. Haplogroups, Number of samples, Subclade and percentage of Kurds samples.

No	Haplogroups	The number of analyzed samples	Subclades	Percentage
1.	J2-M172	9	M67	22
			M47	22
			L25	11
			Others	45
2.	J1- M267	2	Booth negative L858	
3.	E-M35	3	M34	67
			V13	33

3. Christians

The Christians of Iraq represent one of the oldest continuous religious communities in the Middle East, with origins tracing back to the Aramean peoples who settled in Mesopotamia during the 11th–10th centuries BCE [27]. Their historical language, Aramaic, later evolved into Syriac, which remains in liturgical use [28]. Iraqi Christians today belong to several major denominations, chiefly Chaldeans (about 67%), followed by Assyrians (20%), Syriacs (10%), and Armenians (3%), with smaller groups comprising the remainder [29]. These communities are concentrated mainly in the Nineveh Plains, Dohuk, and Erbil regions. Genetic analysis of 113 samples, including 11 SNP-tested samples, revealed that haplogroup R-M269 was the most prevalent (35%), followed by J2 (19%), J1 (15%), G-M201 (8.8%), E-M35 (8.8%), and R-M198 (8%). These results reflect a diverse paternal genetic structure, consistent with the long historical presence and mixed regional ancestry of Christian populations in Iraq (Table 15).

Table 15. Haplogroups, Number of samples, Subclade and percentage of Christians samples.

No	Haplogroups	The number of analyzed	Subclades
1.	R-M269	2	All samples fall under haplogroup mutation Z2103
2.	J2-M172	2	Scattered samples
3.	J1-M267	1	Negative L858

4. Jews

The Jews constitute a religious–ethnic group that has historically preserved a distinct identity through social, cultural, and linguistic continuity [30]. Their ancestral language is Hebrew, and in the modern era, Jewish populations are categorized into three major groups [31]: Sephardic Jews (originating from the Iberian Peninsula), Ashkenazi Jews (from Central and Eastern Europe), and Mizrahi Jews (native to the Middle East and North Africa) [32]. In Mesopotamia, Jewish settlement dates back to the Assyrian exile (722 BCE) and the Babylonian exile (586 BCE), during which Babylon became a major center of Jewish life and scholarship [33]. Historical accounts also suggest that some Arab tribes later adopted Judaism in the Arabian Peninsula. In this study, 47 Jewish samples were analyzed, with 6 subjected to SNP testing for fine-scale genetic analysis. The predominant paternal lineage was haplogroup J1 (28%), followed by E-M35 (19%), J2 (13%), T1 (11%), and R2 (11%), reflecting the genetic diversity and historical depth of Jewish populations in Iraq and the surrounding regions (Table 16).

Table 16. Haplogroups, Number of samples, Subclade and percentage of Jew samples.

Haplogroups	The number of analyzed	Subclades
J1-M267	2	All samples fall under haplogroup mutation ZS227 and ages 5000 years

5. Turkmen

The Turkmen are an ethnic group of Turkish origin, historically descended from the Oghuz Turks of Central Asia [34]. Their language belongs to the Turkic language family. Iraq witnessed several waves of Turkmen migration: the first in the mid-7th century CE with the recruitment of Oghuz fighters into Islamic armies [35]; the second during the Seljuk period (from 1055 CE); and the third during the Ottoman era in the 16th–17th centuries CE, notably under Sultans Suleiman the Magnificent and Murad IV [36], which led to widespread Turkmen settlement in northern Iraq. Over time, the Turkmen became an integral part of Iraq's ethnic mosaic. Genetic analysis of 43 samples, including 15 SNP-tested, showed that haplogroup J2 was dominant (44%), followed by J1 and R-M198 (each 14%), and G-M201 (12%), reflecting the Turkmen's mixed genetic heritage shaped by historical migrations and regional integration (Table 17).

Table 17. Haplogroups, Number of samples, Subclade and percentage of Turkmen samples.

No	Haplogroups	The number of analyzed	Subclades	Percentage
1.	J2-M172	5	L25	40
			Others	60
2.	J1- M267	2	Negative L858	
3.	R-M198	3	Z94	100
4.	G-M201	3	L30	67
			Others	33

6. Mandaeans (Sabians)

The Mandaean Sabians are an ancient monotheistic–Gnostic religious community distinct from the pagan Sabians of Harran [37]. Most evidence points to their origin in southern Mesopotamia (modern Iraq), where they have resided since the 2nd–3rd centuries CE, particularly in the marshlands and along the Tigris and Euphrates rivers [38]. The Mandaic language, a branch of Eastern Aramaic, reflects their deep historical and cultural continuity. Central to their faith is the ritual of baptism, a defining feature of Mandaean religious practice [39]. In this study, 30 samples were analyzed, with 10 subjected to SNP testing for detailed genetic analysis. The results showed that haplogroup J2 was predominant (37%), followed by E-M35 and T-M70 (each 17%), and J1 (13%), illustrating the Mandaean community's distinct yet regionally connected paternal genetic profile (Table 18)

Table 18. Showed the Haplogroups, Number of samples, Subclade and percentage of Mandaeans samples.

No	Haplogroups	Number of analyzed	Subclades	%
1.	J2-M172	4	M67	50
			Others	50
2.	E-M35	1	V22	100
3.	T-M70	2	CTS6507	100

7. Yazidis

The Yazidis are a distinct religious–ethnic group primarily residing in northern Iraq, particularly in the Sinjar region and parts of Nineveh Governorate [40]. They speak a Kurdish dialect and belong to the Kurdish ethno-linguistic sphere, while maintaining a unique cultural and religious identity. Yazidism integrates elements from ancient faiths such as Mithraism and Zoroastrianism [41], alongside influences from Christianity and Sufi Islam. The formation of Yazidi religious identity in its current form is traced to the 11th–12th centuries CE, under Sheikh Adi ibn Musafir, whose shrine at Lalish remains the spiritual center of Yazidism [42]. Genetic analysis of 20 samples, including 5 SNP-tested, revealed that haplogroup J2 was predominant (35%), followed by R-M198 (30%), and R-M269 and L-M20 at equal frequencies (10% each). These findings reflect a close genetic affinity with Kurdish populations, while preserving distinct paternal lineage patterns characteristic of the Yazidi community (Table 19).

Table 19. Haplogroups, Number of samples, Subclade and percentage of Mandaeans samples.

No	Haplogroups	The number of analyzed	Subclades	%
1.	J2-M172	3	scattered	
2.	R-M198	1	Z94	

8. Romani (Gypsies)

They are a distinct ethnic group whose origins trace back to the northwestern Indian subcontinent, particularly Rajasthan and Punjab [43]. Linguistic and genetic evidence confirms this ancestry, as modern DNA analyses reveal a significant Indian genetic component. Historical research suggests that Romani migrations began during the 7th–8th centuries CE [44], linked to sociopolitical changes following the Islamic conquests, and that their arrival in Iraq likely occurred in the 9th century CE during the Abbasid era, before their gradual dispersion across West Asia and Europe [45]. In this study, 7 Romani samples were analyzed, with 3 undergoing SNP testing. The results showed that 57% (4 of 7) belonged to haplogroup L-M20 (L1), a finding that differs from previous studies on European Romani populations, where haplogroup H1a1a (M82) predominates and L-M20 (M22) is comparatively rare. These results may reflect regional genetic differentiation among Romani groups in Iraq (Table 20).

Table 20. Haplogroups, Number of samples, Subclade and percentage of Romani samples.

No	Haplogroups	The number of analyzed	Subclades	%
1	L-M20	1	BY79946 age 2600 years according to Yfull	
2	J1- M267	2	Scattered	

9. Shabak

The Shabak are an ethnic group primarily inhabiting Nineveh Governorate in northern Iraq, with uncertain origins that remain debated. Linguistic and cultural evidence links them closely to the Kurds [46], given that the Shabaki language resembles Kurmanji Kurdish and contains Persian and Arabic influences, while other perspectives emphasize affinities with the Turkmen or view the Shabak as a distinct ethnic community [47]. Religiously, the Shabak identity emerged in the 16th century CE as a Sufi–Shia movement, influenced by Bektashi and Safavid traditions, and has since evolved into a Twelver Shia community [48]. Historical sources associate their settlement in northern Iraq with the Ottoman era (16th–17th centuries CE), possibly linked to migrations from northwestern Iran during Safavid–Ottoman conflicts. Genetic analysis based on Y-37 testing estimates their most recent common ancestor at approximately 275–375 years ago [49]. From the 15 samples analyzed (including 11 SNP-tested), the results revealed a dominant paternal lineage of haplogroup G-M201 (60%), followed by J2 (20%) and J1 (13%), indicating a relatively homogeneous genetic profile with regional Near Eastern affinities (Table 21).

Table 21. Haplogroups, Number of samples, Subclade and percentage of Shabak samples.

No	Haplogroups	The number of analyzed	Subclades	%
1	G-M201	6	Z6414	100

10. Kakais (Yarsanis)

The Kakais, also known as Yarsanis, are a distinct religious–ethnic community residing mainly in northern Iraq, particularly in Kirkuk, Khanaqin, Sulaymaniyah, and Erbil. Their belief system blends elements of Sufism [50], Twelver Shi'ism, and ancient Persian religious traditions. Most Kakais speak Kurdish, reflecting their integration within the Kurdish cultural sphere, and many identify ethnically as Kurds [51]. Historically, Yarsanism originated in western Iran—notably in Kermanshah, Hamadan, and Lorestan—in the late 14th century CE under Sultan Ishaq Barzanjî, its spiritual founder. The religion spread into northern Iraq during the 15th–16th centuries CE, forming distinct local communities. Genetic analyses reveal high diversity among Kakai individuals, indicating that the community arose from the admixture of multiple ethnic groups rather than a single paternal origin. In this study, 13 samples were analyzed, including 9 SNP-tested, with no clear genetic clustering detected-consistent with the group's heterogeneous ancestry and complex historical development.

11. Feyli (Feyli Kurds)

The Feyli are an ethnic group residing along the Iraq–Iran border, mainly in the Iraqi governorates of Wasit, Diyala, and Baghdad, and extending into Ilam and Kermanshah provinces in Iran [52]. Their presence in this region likely dates back to the medieval period. The linguistic and ethnic classification of the Feyli remains debated: some scholars identify them as Kurds, given their southern Kurdish dialect [53] while others view them as closer to the Lur, noting linguistic similarities and their proximity to traditional Luri regions. Some consider the Feyli language a transitional form between Kurdish and Luri [54]. Genetic analyses reveal a close relationship between the Feyli and neighboring

Kurdish populations, though with distinct characteristics within the broader Kurdish genetic continuum. In this study, 15 samples were analyzed, including 11 SNP-tested, showing that haplogroups J1 and J2 were most common (33% each), followed by E-M35 (20%), reflecting a Near Eastern paternal lineage composition consistent with their regional and linguistic affiliations (Table 22).

Table 22. Haplogroups, Number of samples, Subclade and percentage of Feyli samples.

No	Haplogroups	The number of analyzed	Subclades	%
1	J1- M267	3	Z2217	75
			Others	25
2	J2-M172	2	scattered	

3. Discussion

Genetic research shows that modern Iraqis share paternal haplogroups with ancient human remains from Iraq, the Levant, Iran, and Anatolia, indicating both ancient migrations into Mesopotamia and long-term genetic continuity in the region [55]. Shared lineages include J1-FGC4745 (Alalakh, ~4,400 years ago), J1-YSC0000076 (Assyrian period, ~4,200 years ago), J1-FGC11 (Phoenician Lebanon, ~3,900 years ago), J1-FGC4453 (Islamic-period Syria, ~2,000 years ago), J2b-FTA1458 (Ain Ghazal, Jordan, ~5,000 years ago), J2-M67/Z1847 (Alalakh, ~4,800 years ago), and H2-BY4105 (Ubaid-period Anatolia, ~7,400 years ago). These correspondences demonstrate that Iraq's current population retains deep genetic links to ancient Near Eastern peoples, reflecting millennia of population continuity and admixture across Mesopotamia and neighboring regions [56], [57]. Y-chromosome analyses reveal that Iraq's genetic landscape has been shaped by multiple migration waves from the Levant, Arabian Peninsula, Anatolia, and Iran, with limited input from Central Asia [58], Africa, and Europe. There is no major genetic evidence of migrations from the Americas, Oceania, East Asia, or Siberia. The dominant haplogroups across Iraqi populations are J, E, R, G, and T, reflecting deep regional roots. Ancient DNA from Ain Ghazal (Jordan) and Alalakh/Ebla (Syria–Turkey) confirms that haplogroups such as E1b1b1, J1, J2, G2a, H2, T1a, L2, R1a, and R1b have been present in the Near East since the Neolithic and Bronze Ages, underscoring the ancient continuity of these lineages in Mesopotamia and surrounding regions [59], [60], [61]. Rare haplogroups such as A, B, C, D, E1a, E1b1a, G1, H, I, N, and O are present in less than 1% of the Iraqi population. Meanwhile, E2, L2, M, and S have not been detected in any Iraqi genetic samples to date, indicating that these lineages are absent or extremely rare within the country's gene pool.

Genetic analyses indicate that haplogroup J, with its main branches J1 andJ2, accounts for more than half of the male Y-chromosome lineages in Iraq. Genetic analyses reveal that haplogroup J1-FGC1695 dominates among Iraqi Arabs, dating to around 3,000 years ago and comprising 78% of Iraqi J1 samples, indicating a relatively recent population expansion. The diversity of Arab haplogroups reflects both the large sample size and Iraq's long history of integration with multiple migration waves [62]. However, results for groups such as the Romani, Kakais, Feyli, and Shabak remain approximate due to small sample sizes. The Romani exhibit about 40% Indian ancestry, with additional Middle Eastern and European admixture [63], and a paternal lineage dating back ~650 years indicate a recent migration into Iraq. The Yazidis show no clear genetic clustering, consistent with their formation through diverse ancestral origins.

4. Conclusion

Genetic analyses in Iraq show that haplogroup J, particularly branches J1 and J2, comprise over half of male Y-chromosome lineages. Haplogroup J1-FGC1695 is predominant among Iraqi Arabs, representing 78% of J1 samples and indicating a population expansion about 3,000 years ago. Genetic diversity among Arabs is influenced by Iraq's lengthy history of migrations, although certain groups like the Romani and Kakais present approximate results due to smaller sample sizes. The Romani display 40% Indian ancestry and a paternal lineage suggesting recent migration, while the Yazidis lack distinct genetic clustering. A strong genetic cluster within haplogroup G-Z6414 was detected among the Shabak, representing 60% of samples and suggesting a distinct ethnic and genetic identity with limited overlap with neighboring groups. In contrast, the Kakais show no clear clustering, consistent with the community's historical diversity and mixed origins.

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