

The Genomic Legacy of the Muhajirs: A Comprehensive Genetic Analysis of the Circassian Diaspora (1864–2025)

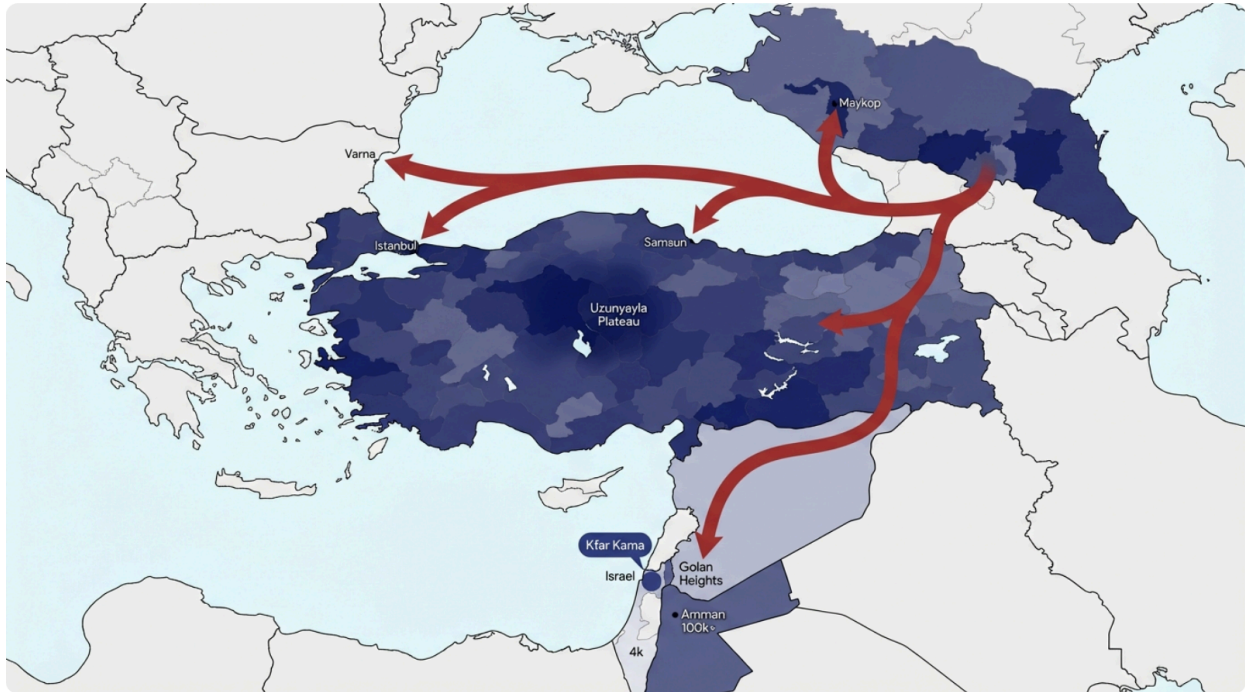
1. Introduction: The Demographics of Displacement and the Biological Archive

The mass expulsion of the Circassian (Adyghe) people from the Northwest Caucasus in 1864, following the conclusion of the Russo-Circassian War, stands as a defining demographic cataclysm of the 19th century. This event, known as the *Muhajirism*, resulted in the forced migration of approximately 90% of the indigenous population to the lands of the Ottoman Empire.¹ Today, the Circassian nation exists primarily as a diaspora, with populations fragmented across modern-day Turkey, Jordan, Syria, Israel, Iraq, and Europe. Of the estimated global population of 5.3 million, only a fraction—roughly 700,000 to 800,000—resides within the ancestral homeland in the Russian Federation (Republic of Adyghea, Kabardino-Balkaria, Karachay-Cherkessia, and Krasnodar Krai).¹

For geneticists and anthropologists, the Circassian diaspora presents a unique "natural experiment" in population genetics. Separated from the source population for 160 years—approximately six to seven generations—these communities have been subjected to distinct evolutionary pressures. In the ancestral homeland, the population faced Soviet-era demographic shifts and interaction with Slavic and other Caucasian groups. Conversely, diaspora communities faced assimilationist policies in Turkey, tribal isolation in Jordan, and distinct minority status in Israel. The central question of this report, based on literature from 2015 to 2025 and extensive DNA project data, is the extent to which the "Circassian genome" has been preserved, altered, or admixed in these disparate environments.

Current genetic research indicates that despite the geographic fragmentation, the Circassian diaspora retains a robust "North Caucasian" genetic signal, characterized by high frequencies of Y-DNA Haplogroup G2a and distinct autosomal components that differentiate them from their host populations in the Middle East and Anatolia.¹ However, this preservation is not uniform. The interplay between the strict cultural code of *Adyghe Xabze*, which mandates endogamy, and the inevitable pressures of globalization and integration, has created a complex mosaic of genetic identities. This analysis explores these dynamics through the lenses of uniparental markers (Y-DNA and mtDNA), genome-wide admixture, and medical genetics.

The Circassian Archipelago: Exile Routes and Modern Diaspora Concentrations



Map illustrating the primary expulsion routes from the Northwest Caucasus to the Ottoman Empire (circa 1864) and the current estimated populations of Circassians in key diaspora nations. Darker shading indicates higher population density. Key genetic study locations (e.g., Kfar Kama, Uzunyayla, Maykop) are marked.

2. Paternal Lineages: The Y-Chromosome as a Historical Archive

The study of the non-recombining portion of the Y-chromosome (NRY) offers the clearest window into the deep ancestry of the Circassian people. Because the Y-chromosome is passed exclusively from father to son, it mirrors the strict patrilineal clan structures (*tlapq*) that define Circassian society. The data from both academic studies (e.g., Yunusbayev et al., Balanovsky et al.) and citizen science projects (Family Tree DNA) converge on a single, dominant narrative: the overwhelming prevalence and persistence of Haplogroup G.

2.1 The G2a Hegemony: A Neolithic Signature

The most defining characteristic of the Circassian gene pool is the extremely high frequency of Haplogroup G2a (G-P15), specifically its subclades G-P303 and G-M406. In the Northwest Caucasus, frequencies of Haplogroup G reach between 40% and 70% depending on the specific tribe (e.g., Shapsug, Kabardian).¹ This haplogroup is considered a primary marker of

the Early European Farmers who migrated from Anatolia and the Caucasus into Europe during the Neolithic period, carrying agricultural technology. While G2a has become rare in modern Europe (replaced largely by R1b and I lineages), it survived in high concentrations in the isolated valleys of the Caucasus.⁵

In the diaspora, this signal remains intact. Data from the "Adyghe" and "Circassian" projects at Family Tree DNA, which include samples from Turkey, Jordan, and the US, show that G2a lineages account for the majority of tested men.³ This indicates that despite the chaos of the exile and the settlement in diverse lands, the core paternal lineage has not been diluted. The preservation of G2a is a direct result of the strict prohibition against exogamy (marriage outside the group) that was enforced for generations in the diaspora communities.⁸

Subclade Analysis and Tribal differentiation

The resolution of Y-DNA testing has improved significantly in the 2015-2025 period, allowing researchers to distinguish between different branches of G2a that correlate with specific tribes or regions:

- **G-P303:** This is the most frequent and widespread subclade among the Adyghe. It is found in both Western Adyghe (e.g., Shapsug, Abzakh) and Eastern Adyghe (Kabardian) populations. In the diaspora, its ubiquity helps confirm the "Circassian" origin of individuals who may have lost their specific tribal knowledge.⁵
- **G-M406:** This lineage is also present but shows different distribution patterns. It is found in significant numbers in Anatolia and the Southern Caucasus, suggesting ancient gene flow events prior to the exile. In the context of the diaspora, distinguishing G-M406 derived from the Caucasus versus G-M406 indigenous to Anatolia (where the diaspora settled) is complex but possible through deep SNP testing.⁶
- **G-P16:** This marker is found in Armenians and some neighboring Caucasian groups. Its presence in Circassian populations, albeit at lower frequencies, points to the deep, shared genetic history of the Caucasus region before the ethnolinguistic divergence of the modern era.⁹

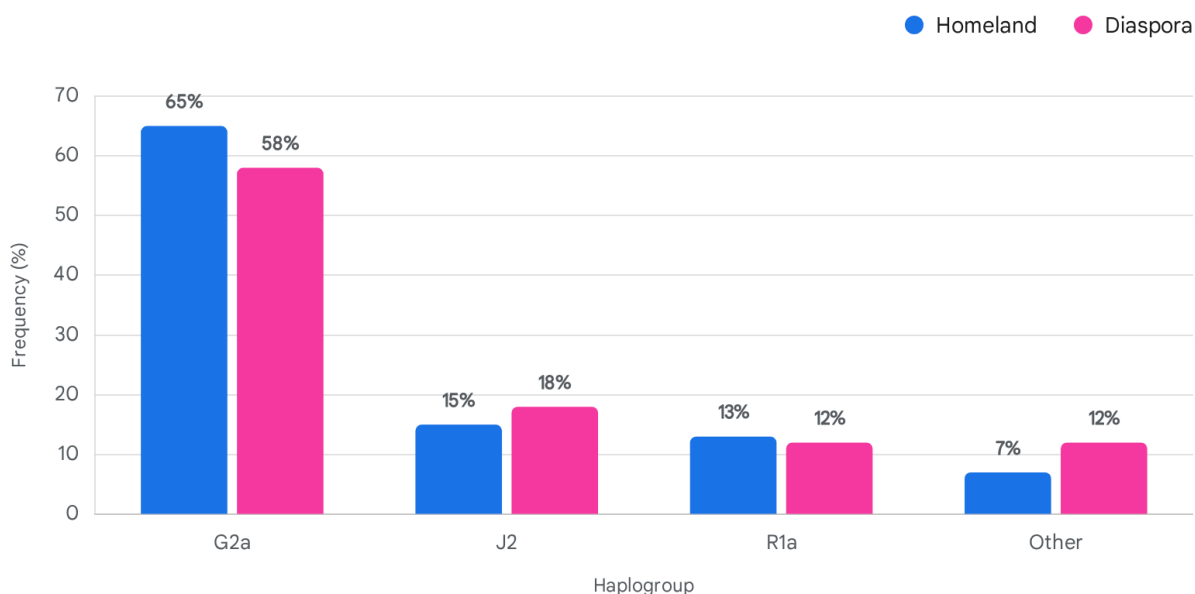
2.2 Secondary Lineages and Ancient Admixture

While G2a is the dominant signal, the Circassian Y-chromosomal pool is not monolithic. Approximately 30-40% of the paternal lineages belong to other haplogroups, which tell the story of the region's interactions with the Eurasian Steppe and the Near East over millennia.

- **Haplogroup J2 (J-M172):** This is the second most common lineage, comprising roughly 10-20% of the population.⁹ J2 is strongly associated with the spread of agriculture from the Fertile Crescent and the ancient civilizations of West Asia (e.g., Hattians, Hurrians). Its presence confirms the Circassians' status as a bridge population between the Caucasus and the Near East. In the diaspora, distinguishing "Circassian J2" from "Turkish J2" or "Arab J2" requires precise subclade analysis (e.g., looking for specific Caucasian clades like J2a* and J2a4b*-M67).⁴

- **Haplogroup R1a (R-M198):** Found at frequencies of approximately 13-20% in various Adyghe sub-groups¹, R1a represents the legacy of the "Steppe" populations to the north (e.g., Scythians, Sarmatians, Alans). The North Caucasus was a contact zone between the mountain peoples and the nomadic steppe confederations. The R1a lineages found in Circassians are distinct from the Eastern European Slavic branches, often belonging to the Z93 (Asian) or other specific subclades, confirming ancient assimilation of steppe elements rather than recent Slavic admixture.¹¹
- **Minor Lineages (I2, R1b, E1b1b, T):** These haplogroups appear at lower frequencies (1-5%). Haplogroup T, for instance, has been identified in samples from the Caucasus, linking to ancient expansions from the Near East.¹²

Preservation of Paternal Lineages: Y-DNA Haplogroup Frequencies (Homeland vs. Diaspora)



Comparison of major Y-DNA haplogroup frequencies between Circassians in the North Caucasus (Homeland) and aggregated Diaspora samples. Haplogroup G2a remains the dominant lineage in both groups, evidencing strong patrilineal preservation despite geographical displacement.

Data sources: [Wikipedia \(Circassians\)](#), [Khazaria.com](#), [Wikipedia \(Caucasus\)](#), [Wikipedia \(Haplogroup G\)](#), [FamilyTreeDNA](#)

2.3 Comparative Table: Y-DNA Frequencies Across Populations

The table below synthesizes data from multiple studies to compare the Circassian Y-DNA

profile with neighboring populations, highlighting the distinctiveness of the Circassian genetic signature.

Populati on	Languag e Group	G2a (%)	J2 (%)	R1a (%)	R1b (%)	Source
Adyghe (Circassi an)	NW Caucasia n	50-70	10-20	13	<5	¹
Abkhaz	NW Caucasia n	40-50	25	<5	<5	⁹
Ossetian (Digor)	Indo-Irani an	56-73	5-10	<5	<5	¹⁴
Turkish (Anatolia)	Turkic	11	24	7.5	16	¹⁵
Armenia n	Indo-Eur opean	10-12	20-30	5-10	25-30	⁹

Table 1: Comparison of major Y-DNA haplogroup frequencies. Note the significantly higher frequency of G2a in Circassians compared to the Turkish host population, and the similarity with neighboring Ossetians and Abkhazians.

3. Maternal Lineages: Diversity and Social Structure

While paternal lineages in Circassian society show a marked homogeneity (the "G2a dominance"), maternal lineages (mtDNA) display a strikingly different pattern: high diversity. This contrast is a classic signature of a **patriloc** society, where men remain in their birth communities while women move in from other groups for marriage.

3.1 The Matrilineal Mosaic

Genetic studies of mtDNA in the North Caucasus reveal a rich tapestry of haplogroups, primarily of West Eurasian origin. The most common haplogroups include **H, U, T, and I**.

- **Haplogroup U:** This is the most frequent maternal lineage among the Adyghe, accounting for approximately 32% of the population. Within this group, **U3** (14%) and **U5**

(8%) are particularly significant.⁴ U5 is an ancient European hunter-gatherer lineage, while U3 is more closely associated with the Near East and the Caucasus, often linked to the spread of agriculture.

- **Haplogroup H:** Found in roughly 22% of Circassian samples, Haplogroup H is the most common maternal lineage in Europe. Its presence in the Caucasus connects the Circassians to the broader European genetic landscape.⁴
- **Haplogroup T and I:** Haplogroup T (14%) and I (6%) are also well-represented.

3.2 Implications for Diaspora Admixture

In the diaspora, this high maternal diversity complicates the detection of admixture. Since Circassian mtDNA haplogroups (H, U, T, J) overlap significantly with those of the host populations in Turkey and the Levant (who also carry high frequencies of H, U, and J), distinguishing an "indigenous" Circassian maternal line from a line acquired through intermarriage in the diaspora can be difficult without full-sequence testing.

- **Turkey:** In Central Anatolia, studies have shown that while Circassian villages (like those in Uzunyayla) maintain their distinct paternal profiles, their maternal diversity is high and geographically homogeneous with the surrounding region.¹⁶ This supports the hypothesis that while the *patriline* was strictly guarded (endogamy), the *matriline* may have historically been more permeable, or simply that the starting diversity was high enough to mirror the host population.
- **Levant:** In Jordan, the bottleneck effect of the migration (where many perished) reduced the overall genetic diversity. However, studies show that the Circassian sub-populations still maintain distinct mtDNA frequencies compared to the local Arab populations, clustering with other Caucasian and West Eurasian groups rather than the Bedouin or Peninsular Arab clusters.¹⁷

4. Genome-Wide Structure and Admixture Analysis

Moving beyond single-lineage markers, genome-wide association studies (GWAS) and autosomal DNA analysis provide a holistic view of the Circassian genetic identity. These studies look at thousands of markers across the entire genome to determine "genetic distance" and ancestry components.

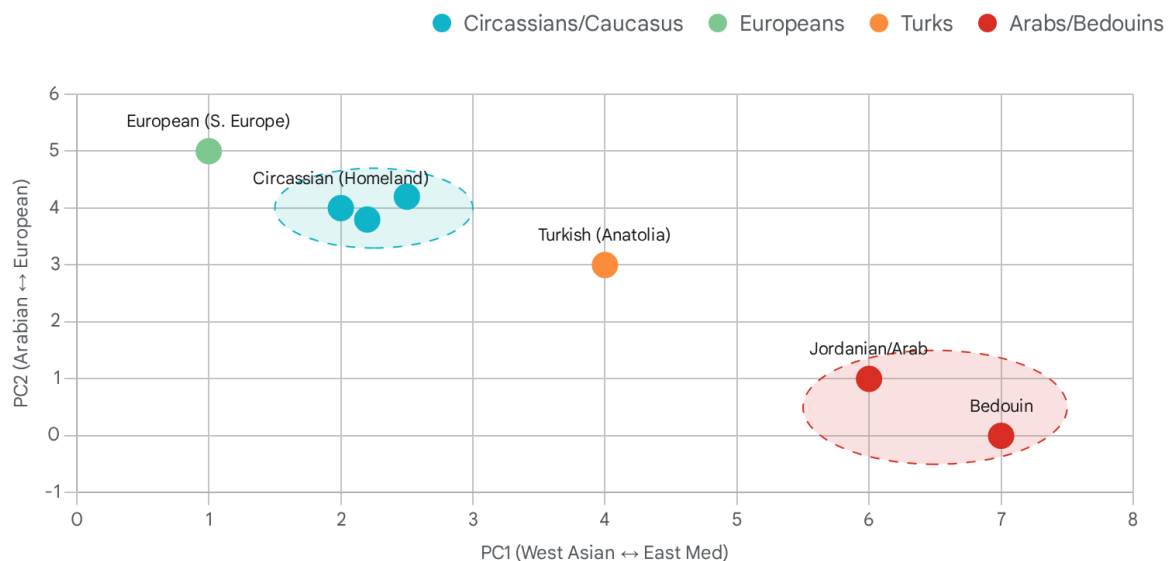
4.1 The "North Caucasian" Autosomal Cluster

Principal Component Analysis (PCA) consistently identifies a distinct "North Caucasian" cluster. This cluster acts as a bridge between Europe and the Near East but is distinct from both.

- **Genetic Position:** Circassians (Adyghe) cluster closely with other Northwest Caucasian speakers (Abkhazians) and Northeast Caucasian speakers (Chechens, Ingush). They occupy a position on the PCA plot that is shifted towards Europe compared to populations from the Southern Caucasus (Armenians, Azeris) and the Middle East.¹

- **Separation from Host Populations:** In the diaspora, this distinction remains visible.
 - **vs. Arabs:** In Jordan and Israel, Circassians are genetically distinct from the local Arab populations. The Arab populations typically show higher "Red Sea" or "Southwest Asian" ancestry components, which are minimal or absent in unmixed Circassians.⁸
 - **vs. Turks:** The relationship with the Turkish population is more complex. The modern "Turkish" gene pool itself is a hybrid, containing significant native Anatolian, Caucasian, Balkan, and Central Asian (Turkic) ancestry.¹⁸ However, PCA plots show that Circassians cluster separately from the main Anatolian Turkish cluster, lacking the Central Asian (Siberian/East Eurasian) admixture that characterizes Turkic heritage (roughly 9-22% in ethnic Turks).¹⁸

Genetic Distance and Clustering: A Schematic PCA of West Eurasian Populations



Schematic Principal Component Analysis (PCA) based on aggregated autosomal data. The Circassian diaspora (Adyghe) forms a distinct cluster closely related to other North Caucasian groups (Abkhaz, Chechen) and Southern Europeans, while showing clear separation from Middle Eastern populations (Jordanian, Bedouin), illustrating the retention of ancestral genetic structure.

Data sources: [PGG Database / PMC](#), [Nasidze et al. \(ResearchGate\)](#), [Gedmatch User Data](#), [Gökçümen \(2008\)](#)

4.2 The "Turkish Variome" and Admixture

The "Turkish Variome" project (2021) provided deep insights into the genetic structure of Turkey. It revealed that the country is a genetic crossroads. For the Circassian diaspora, this presents a dual reality:

1. **Enclaves:** In isolated rural areas like **Uzunyayla**, Circassians have maintained a genetic profile that is distinct from their neighbors, with "paternal genetic diversity structured among settlements".¹⁶ This means a Circassian village and a neighboring Turkman/Afshar village can remain genetically distinct for a century despite geographic proximity.
2. **Urban Admixture:** In urban centers (Istanbul, Ankara), the boundaries blur. Self-identified Circassians in these areas show higher rates of admixture with the general Turkish population. Additionally, the "Turkish" population itself has absorbed significant Caucasian DNA, meaning that "Turkish" ancestry often includes hidden Circassian components from assimilated ancestors.²⁰

5. Regional Case Studies in the Diaspora

The Circassian diaspora is not a monolith; it is a collection of communities shaped by the specific histories of their host nations.

5.1 The Levant (Jordan & Israel): Isolation and Founder Effects

The Circassian communities in Jordan (approx. 100,000) and Israel (approx. 4,000-5,000) represent the most genetically isolated segments of the diaspora.

- **Kfar Kama and Rehaniya (Israel):** The village of Kfar Kama, founded by Shapsug exiles in 1878, is a textbook example of a genetic isolate. The community descends from a small number of founding families, leading to a **founder effect**. This has reduced overall genetic diversity compared to the homeland and has increased the frequency of certain alleles due to genetic drift.²²
- **Jordan:** Similarly, the Circassian community in Jordan has practiced strict endogamy for generations to preserve their identity in an Arab-majority environment. Genetic studies confirm that they remain distinct from the Jordanian Arab population, clustering with Caucasian and European populations.⁸ However, this isolation has also led to the concentration of specific genetic traits and susceptibilities.

5.2 Turkey (Anatolia): The Demographic Center

Turkey holds the largest Circassian population (2-3 million).

- **Uzunyayla:** This plateau in Kayseri province is the cultural and genetic heart of the diaspora in Turkey. Studies by Gökçümen et al. have shown that despite living alongside Turkish and Avshar (Turkmen) neighbors, the Circassian villages here have preserved their ancestral Y-DNA profiles. The "social boundaries" of the community have acted as effective genetic barriers.¹⁵
- **Integration:** Unlike in the Levant, where religious or ethnic differences created sharp

divides, the shared Sunni Muslim faith facilitated greater integration in Turkey. Consequently, while the core identity remains strong, the genetic boundaries in urban areas are more permeable than in Israel or Jordan.

5.3 The Balkans and Repatriation: The Kosovo Case

In 1998-1999, during the Kosovo War, a unique event occurred: the repatriation of a community of Circassians from Kosovo back to the Republic of Adygea. This community, which had lived in the Balkans since the 1860s, represents a "double diaspora"—exiled first to the Balkans, then returning to the Caucasus. Their genetic profile is of intense interest as it represents a branch of the family tree separated for 135 years. Their successful reintegration highlights the biological and cultural continuity that persists despite distinct historical trajectories.²⁴

6. Medical Genetics and Epidemiology

The genetic history of the Circassian diaspora—marked by bottlenecks, founder effects, and endogamy—has direct implications for medical genetics.

6.1 Hereditary Disorders and Founder Mutations

In the isolated communities of the Levant, particularly Kfar Kama and the Jordanian community, endogamy has increased the risk of autosomal recessive disorders.

- **Familial Mediterranean Fever (FMF):** This inflammatory disorder is prevalent in the region. However, genetic studies suggest that the specific mutations found in Circassians may differ in frequency or type from those found in Armenians, Turks, or Arabs, pointing to distinct ancestral mutational events or founder effects within the Circassian gene pool.²⁶
- **Rare Diseases:** Studies in Jordan have identified unique genetic predispositions to conditions such as diabetes and hypertension within the Circassian and Chechen communities. These communities often possess distinct biomarkers that differ from the general Arab population, necessitating community-specific medical screening.⁸
- **Pharmacogenetics:** Recent research (2015-2025) has highlighted significant differences in pharmacogenetic markers (genes that affect how the body processes drugs) between Circassians and their Arab neighbors. For example, allele frequencies for genes affecting the metabolism of certain medications were found to be distinct, suggesting that "one-size-fits-all" medical guidelines in Jordan might not be optimal for the Circassian minority.⁸

6.2 The "Healthy Migrant" and Selection

Conversely, some researchers have posited that the arduous conditions of the exile itself—which killed a significant portion of the population—may have acted as a fierce selective pressure. The survivors of the Black Sea crossing and the subsequent settlement in

malaria-ridden regions (like the Golan and parts of Turkey) may have possessed robust immune systems. While speculative, the resilience of these communities in the face of new pathogens in the Middle East is a topic of ongoing anthropological and genetic interest.²⁵

7. The Role of Citizen Science and Future Directions

The landscape of Circassian genetic research has been transformed by "citizen science."

7.1 Family Tree DNA (FTDNA) Projects

The **Adyghe-Abkhaz DNA Project** and the **Circassian DNA Project** at Family Tree DNA have become central repositories for diaspora genetics. With hundreds of members, these projects allow for a granularity of analysis that academic studies often miss.

- **Validation of Oral History:** Participants use Y-DNA results to confirm their *tlapq* (clan) affiliations. For example, a man in New Jersey can confirm his "Shapsug" lineage by matching markers with a distant cousin in Maykop or Kfar Kama.³
- **Identifying Subclades:** These projects have been instrumental in defining the specific "Circassian" branches of Haplogroup G2a (e.g., G-L1264), distinguishing them from other Caucasian or Middle Eastern branches.²⁷

7.2 Genetic Citizenship and Repatriation

In the 21st century, genetics has entered the political arena. For the Circassian repatriation movement, DNA serves as a "biological passport." In a context where historical records were often lost during the exile, genetic data provides irrefutable proof of ancestry. The distinctiveness of the Circassian genome is used to argue against narratives of assimilation and to support the claim for a right of return to the North Caucasus.²⁸

8. Conclusion

The genetic analysis of the Circassian diaspora from 2015 to 2025 reveals a story of remarkable biological resilience. Despite 160 years of displacement, the fragmentation of the nation into disparate host countries, and the pressures of assimilation, the Circassian people have retained a distinct genetic identity.

This identity is anchored by the stability of paternal lineages (Haplogroup G2a), which link the diaspora unequivocally to the Northwest Caucasus and the ancient agriculturalists of the Neolithic. It is reinforced by genome-wide patterns that distinguish Circassians from the Turkic and Arab populations among whom they live. Yet, the data also reveals the scars of history: the founder effects in Israel and Jordan, the complex admixture in Turkey, and the unique medical profiles born of isolation.

As the diaspora engages more deeply with the homeland through digital networks and repatriation, this "genetic memory" serves as more than just biological data; it is a tangible

connection to a lost past and a foundation for a future where the "spirit" and the "body" of the nation might one day be reunited.

Citations

- ¹: General demographics and history of the exile.
- ¹: Y-DNA Haplogroup G2a frequencies and subclades.
- ⁴: mtDNA haplogroup frequencies (U3, U5, H).
- ⁸: PCA analysis and genetic distance in the Levant.
- ¹⁶: Genetic structure of Uzunyayla and Central Anatolia.
- ²²: Founder effects and genetics of Kfar Kama.
- ⁸: Medical genetics and pharmacogenetics.
- ³: FTDNA project data and citizen science.
- ¹⁸: Turkish Variome and general Turkish admixture.
- ³¹: Yunusbayev et al. studies on the Caucasus.

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