

Genomic Stratigraphy of the North Caucasus: A Comprehensive Phylogenetic Analysis of Haplogroup Q (2018–2025)

1. Introduction

The North Caucasus, a rugged isthmus connecting the Pontic-Caspian steppe to the Near East, represents one of the most genetically complex regions in Eurasia. For millennia, this mountainous corridor has functioned simultaneously as a barrier, a refuge, and a conduit for human migration. The population history of the region is characterized by a deep, autochthonous genetic substrate—represented predominantly by Y-chromosome haplogroups G2a and J2—overlaid by successive strata of exogenous gene flow originating from the Eurasian steppes. Among these intrusive lineages, Haplogroup Q (Q-M242) occupies a position of singular bio-historical importance. While it is not the most frequent haplogroup in the region, its presence serves as a critical diagnostic marker for East-West trans-Eurasian exchange, offering a molecular record of the nomadic confederations that have punctuated the region's history from the Iron Age to the medieval period.

This report presents an exhaustive analysis of Haplogroup Q within the North Caucasus, synthesizing high-throughput sequencing data, ancient DNA (aDNA) findings, and population genetic studies published between 2018 and 2025. This period has witnessed a paradigm shift in anthropological genetics, driven by the "ancient DNA revolution," which has allowed researchers to move beyond inferential models based on modern populations to direct observation of ancestral genomes. The publication of landmark datasets—specifically those concerning Scythian, Alanic, and Khazar burials—has necessitated a fundamental re-evaluation of the timing and nature of Steppe introgression into the Caucasian gene pool.

Unlike the pervasive Haplogroups G and J, which signal continuity with the Neolithic agriculturalists and local Bronze Age cultures (such as the Koban and Maykop), Haplogroup Q represents a vector of discontinuity and admixture. It is the genetic signature of the "Horse Lords"—the Scythians, Sarmatians, Huns, and Turkic peoples—who dominated the distinct ecological niche of the pre-Caucasian steppe. This analysis argues that the distribution of Haplogroup Q in the modern North Caucasus is not the result of a singular migration event, nor a simple diffusion from a uniform source. Rather, it is a stratified accumulation of distinct phylogenetic lineages—specifically Q-L940, Q-M25, and Q-L712—each linked to specific historical entities and demographic processes ranging from the Scythian expansion to the formation of the Karachay-Balkar ethnogenesis.

1.1. Geographic and Ethnographic Scope

The geographical scope of this analysis encompasses the North Caucasian Federal District of the Russian Federation, extending from the Black Sea coast in the west to the Caspian Sea in the east. This region includes the republics of Adygea, Karachay-Cherkessia, Kabardino-Balkaria, North Ossetia-Alania, Ingushetia, Chechnya, and Dagestan, as well as the Stavropol Krai.

Ethnographically, the report focuses on three primary linguistic clusters:

1. **The Turkic-speaking populations:** Specifically the Karachays and Balkars of the central high Caucasus, and the Nogays and Kumyks of the steppe and piedmont zones. These groups exhibit the highest frequencies of Haplogroup Q and are central to understanding its dissemination.¹
2. **The Northwest Caucasian (Abkhazo-Adyghe) speakers:** Including the Adyghe, Cherkess, Kabardians, and Abaza. These populations are genetically predominantly West Asian but harbor significant traces of Steppe admixture.³
3. **The Northeast Caucasian (Nakh-Dagestanian) speakers:** Including the Chechens, Ingush, and the diverse peoples of Dagestan. While dominated by locally rooted lineages, recent aDNA evidence has revealed crucial links between these groups and ancient Q-bearing populations.⁴

1.2. The Phylogenetic Marker: Haplogroup Q-M242

Haplogroup Q is defined by the M242 single nucleotide polymorphism (SNP). It is one of two major branches of the macro-haplogroup P1, the other being Haplogroup R (R-M207). While Haplogroup R became the dominant lineage of Western Eurasia (R1b) and Eastern Europe/Central Asia (R1a), Haplogroup Q is most famously associated with the peopling of the Americas, where it reaches near-fixation in Indigenous populations.⁵

However, the Eurasian diversity of Haplogroup Q is profound and ancient. Originating in South Central Siberia or Central Asia approximately 17,000 to 31,700 years ago ⁵, it diversified into several major clades that spread westward across the steppe belt. In the context of the North Caucasus, we are concerned primarily with two phylogenetic branches:

- **Q1b (Q-L275):** A Western Eurasian branch that includes the "Scythian" marker Q-L940.⁷
- **Q1a (Q-F1096):** Specifically the Q-M25 subclade and its downstream lineage Q-L712, which appear to be linked to later Hunnic and Turkic expansions.⁹

The distinction between these branches is not merely academic; it is historical. As this report will demonstrate, discriminating between Q-L940 and Q-L712 allows us to disentangle the genetic legacy of the Iron Age Indo-Iranian nomads from that of the medieval Turkic confederations.

2. Methodology and the Ancient DNA Revolution (2018–2025)

The period from 2018 to 2025 represents a "Golden Age" for Caucasian population genetics, defined by the transition from low-resolution Short Tandem Repeat (STR) typing to high-coverage Whole Genome Sequencing (WGS) and the industrial-scale analysis of ancient DNA. This technological leap has been instrumental in resolving the origins of Haplogroup Q in the region.

2.1. The Shift to High-Throughput Sequencing

Prior to 2018, studies on North Caucasian genetics relied heavily on Y-STR haplotypes and a limited set of SNPs. While useful for estimating coalescence times, these markers often failed to provide the phylogenetic resolution necessary to distinguish between closely related migratory waves. For instance, a Q-M242 sample could theoretically be Native American, Siberian, or Central Asian.

The adoption of Next-Generation Sequencing (NGS) and the definition of stable SNP hierarchies (ISOGG, YFull) have allowed researchers to drill down to terminal SNPs. The identification of **Q-L712** as a specific sub-branch of Q-M25, for example, was only possible through deep sequencing efforts such as the "Karachay-Balkar DNA" project and academic collaborations.¹⁰ This resolution permits the construction of precise phylogenetic trees that map directly onto historical timelines.

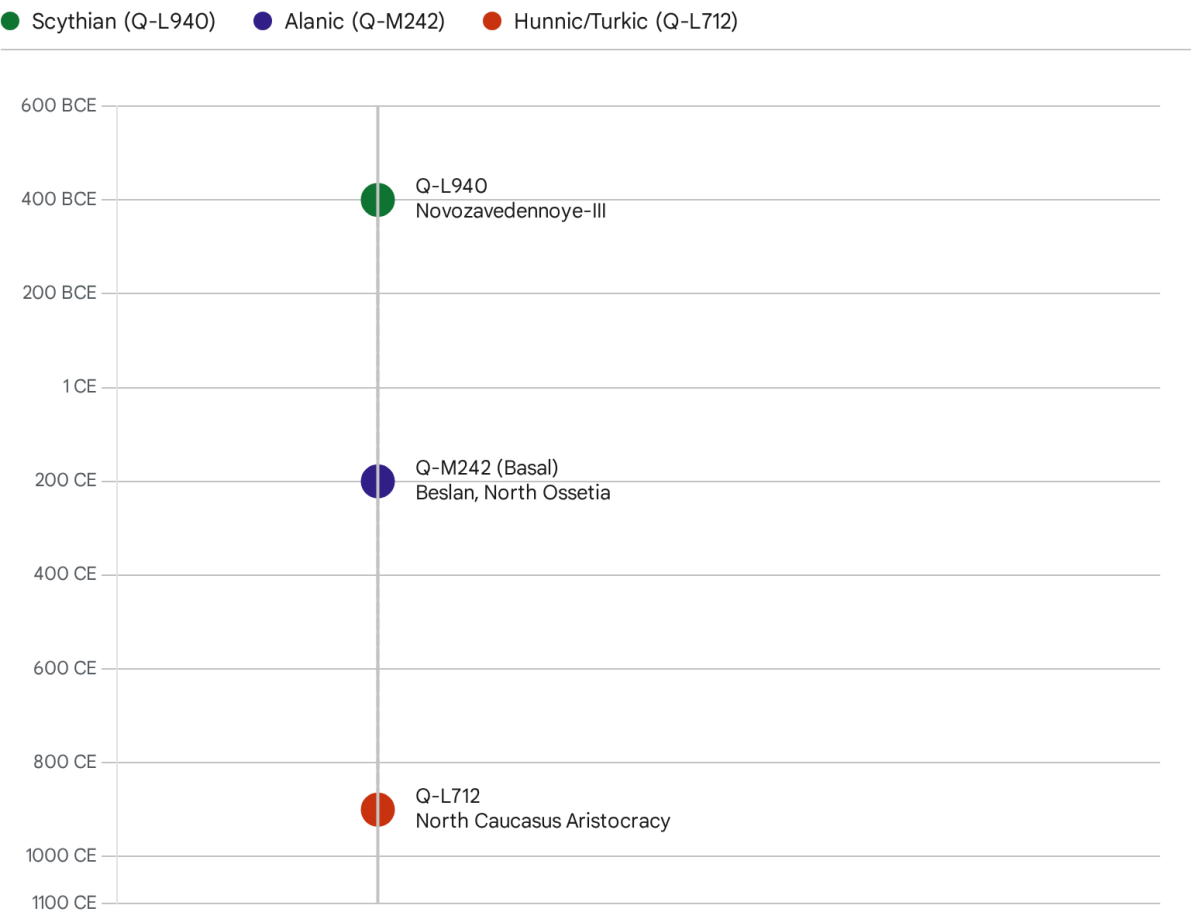
2.2. The Impact of Ancient DNA (aDNA)

The most critical development has been the publication of ancient genomes from the Pontic-Caspian steppe and the North Caucasus. Three pivotal datasets underpin the analysis in this report:

1. **Damgaard et al. (2018):** *"137 ancient human genomes from across the Eurasian steppes."* This foundational study provided the first genomic look at the Huns and Alans in the Caucasus, identifying the presence of Haplogroup Q in Alanic contexts.⁴
2. **Andreeva et al. (2025):** *"Genetic history of Scythia."* This recent, high-resolution study focused specifically on the Scythian period (7th–3rd c. BCE) in the North Caucasus (Stavropol Krai). It provided decisive evidence for the presence of Q-L940 in the "Great Scythia" population, challenging previous models of Scythian homogeneity.⁷
3. **Skourtanioti et al. (2024):** *"The Genetic History of the South Caucasus..."* While focused on the South Caucasus, this massive transect helps define the "autochthonous" baseline (G, J, L) against which the intrusive Q lineages in the North must be measured.¹⁴

These studies allow us to anchor modern genetic diversity in ancient bio-reality. We no longer have to guess if Q was present in the Alans; we have physical samples proving it was.

Chronostratigraphy of Haplogroup Q Lineages in the North Caucasus (Iron Age – Medieval)



Temporal mapping of Haplogroup Q subclade appearances in the North Caucasus based on ancient DNA samples dated between 2018 and 2025. The timeline highlights the distinct arrival phases of Q-L940 (Scythian period), Q-M242 basal lineages (Alanic period), and Q-L712 (Hunnic/Turkic period), correlating them with key archaeological sites like Novozavedennoye-III and Beslan.

Data sources: [Scientific Data \(Scythian\)](#), [Nature 2018 \(Alanic\)](#), [FamilyTreeDNA \(Q-L712\)](#)

3. The Iron Age Horizon: Scythians and the Arrival of Q-L940

The narrative of Haplogroup Q in the Caucasus begins properly in the Iron Age. While the

Bronze Age North Caucasus was dominated by the Maykop and Koban cultures—characterized genetically by Haplogroups G2a, J2, and L1b—the emergence of the Scythian confederation in the 7th century BCE marked a demographic turning point. The Scythians, an Iranian-speaking nomadic people, established hegemony over the Pontic-Caspian steppe and the North Caucasian piedmont, bringing with them genetic lineages from the east.

3.1. The Novozavedennoye-III Revelation (2025)

The most significant recent contribution to this era comes from the study "*Genetic history of Scythia*" by **Andreeva et al. (2025)**. This high-resolution genomic analysis focused on 131 individuals from "Great Scythia," covering the region from the northern Black Sea coast to the Middle Don.¹³ Crucially, the study included samples from the **Novozavedennoye-III** burial ground, located in the Georgievsk district of Stavropol Krai, in the central Pre-Caucasus.⁷

Novozavedennoye-III is a key archaeological site dating to the late 5th–4th centuries BCE. It represents a zone of intense interaction between the nomadic Scythian elite and the sedentary, autochthonous population of the Koban culture. The genomic analysis of individuals from this site yielded a groundbreaking result: the identification of **Haplogroup Q1b (specifically Q-L940)** among the Scythian males.⁷

3.2. Deconstructing the "Scythian" Genome

The identification of Q-L940 in a Scythian context challenges the monolithic view of Scythian genetics. Previously, the Scythians were strongly associated with Haplogroup R1a-Z93, a lineage linked to the Indo-Iranian expansion. The Andreeva et al. study reveals a much more heterogeneous picture:

- **Paternal Diversity:** Alongside the dominant R1a lineages (R-Y2631, R-Y934), the Scythians of the North Caucasus carried lineages belonging to G2a (G-S9409), J2a1 (J-Y26650), N1a (N-Z1934), and Q1b (Q-L940).⁷ This diversity suggests that the Scythian "confederation" was a multi-ethnic polity that absorbed various tribal groups as it expanded westward from Central Asia.
- **The Origins of Q-L940:** The subclade Q-L940 is phylogenetically distinct from the Q-M3 lineages found in the Americas or the Q-M25 lineages common in Central Asia. Today, Q-L940 is found at low frequencies in Western Eurasia, Scandinavia, and South Asia.⁸ Its presence in the North Caucasus during the Iron Age indicates that this lineage was part of the "Western Scythian" gene pool—a distinct population cluster formed by the admixture of incoming Andronovo-related nomads with local Srubnaya and Koban populations.¹⁵

3.3. Implications for Caucasian Prehistory

The discovery of Q-L940 at Novozavedennoye-III provides the earliest direct evidence of

Haplogroup Q in the North Caucasus. It suggests that the introduction of this lineage was a **demographic event** mediated by the settlement of militarized nomadic groups. The genetic data shows that these Scythians intermarried with local women (carrying lineages such as U2 and U5), facilitating the introgression of Steppe Y-chromosomes into the sedentary gene pool.¹³ This admixture event laid the foundation for the complex genetic mosaic observed in later periods. Furthermore, the study notably linked these ancient Scythian populations to a specific mutation (p.Ala150Pro) causing fructose intolerance, tracing the dispersion of this trait through lineages including the Q carriers, which highlights the biomedical relevance of these ancient migrations.⁷

4. The Migration Period: Alans, Huns, and the Q-L712 Lineage

Following the decline of Scythian power, the North Caucasus was dominated by the Sarmatians and their subgroup, the Alans (1st–4th centuries CE). This was followed by the tumultuous "Great Migration Period," heralded by the arrival of the Huns in the late 4th century CE. The genetic data from this era reveals a shift in the specific subclades of Haplogroup Q present in the region, marking a second, distinct pulse of gene flow.

4.1. The Beslan Connection: Alans and Admixture

The Alans are traditionally viewed as an Iranian-speaking confederation ancestral to the modern Ossetians. However, genetic studies published between 2018 and 2022 have revealed that the Alans were far from genetically uniform. A pivotal study by **Damgaard et al. (2018)** and subsequent analyses examined DNA from the **Beslan** mound cemetery in North Ossetia (dated c. 200–600 CE).⁴

- **The Findings:** While many Alanic samples carried Haplogroups G2a and R1a (consistent with local and Sarmatian origins), the study identified an individual belonging to **Haplogroup Q-M242**.⁴
- **Interpretation:** The presence of Q in an Alanic context is a significant anomaly if one assumes a purely Iranian origin for the Alans. It likely reflects admixture with **Hunnic** or **Proto-Turkic** groups that were beginning to impinge on the Pontic-Caspian steppe during this period. The Alans incorporated various tribal remnants as they retreated into the Caucasian foothills, and the Q lineage in Beslan may represent one such assimilated element.
- **Modern Continuity:** Perhaps the most striking finding is the genealogical link between this ancient Beslan individual and modern populations. Genetic analysis suggests a kinship match between the ancient Q-M242 sample and members of the modern **Chechen Shoanoy Teip**.⁴ This provides rare, direct evidence of paternal continuity from the Late Antique period to the modern clan structures of the Northeast Caucasus, bridging a 1,500-year historical gap.

4.2. The Hunnic Signature: Q-L712

The arrival of the Huns (c. 370 CE) fundamentally altered the genetic landscape of the steppe. Recent phylogenetic analyses, particularly those by the "Q-L712 Focus Group" and researchers analyzing FTDNA databases, have zeroed in on the **Q-L712** subclade (a branch of Q-M25) as a primary candidate for a Hunnic genetic marker.¹⁰

- **Phylogeny and Timing:** TMRCA (Time to Most Recent Common Ancestor) estimates for the Q-L712 subclades align remarkably well with the timeline of the Hunnic expansion. For instance, the **Q-BZ640** branch is dated to approximately 4,900 years before present (ybp), while younger downstream branches coalesce around 1,700 ybp—the exact timeframe of the Hunnic storm.¹⁰
- **Geographic Distribution:** Q-L712 displays a disjointed distribution that mirrors the historical trajectory of the Huns. It is found at significant frequencies in two specific populations: the **Karachay-Balkars** of the North Caucasus and the **Székelys (Szeklers)** of Transylvania (Romania).¹⁰
- **The "Aristocratic" Founder Effect:** In the North Caucasus, Q-L712 is not randomly distributed. It correlates strongly with specific "Taib" (clan) structures, notably the **Badeliat and Basiat** dynasties—the traditional aristocracy of the Balkars and Digor Ossetians.¹⁰ This distribution pattern is consistent with an **Elite Dominance** model, where a small, militarized elite of Hunnic or Bulgar origin established dynastic rule over autochthonous mountain populations, leaving a disproportionate genetic legacy through social stratification and reproductive success.

4.3. The Khazar (Saltovo-Mayaki) Interlude

The Khazar Khaganate (c. 650–965 CE) represents the final major phase of Steppe domination before the Mongol era. The Saltovo-Mayaki archaeological culture is the material manifestation of the Khazar state.

- **Genetic Heterogeneity:** Studies by **Afanasiev et al. (2015)** and subsequent re-analyses have sequenced individuals from Saltovo-Mayaki burials. The results depict a cosmopolitan society. Elite burials have yielded Haplogroups G, J2a, R1a, and, crucially, **Q**.²⁰
- **Sample A80410/A80411:** While some Khazar samples carried West Asian lineages (G, J2a), the presence of Q (alongside Central Asian C2b and N1a) confirms the persistence of Turkic paternal lineages within the Khazar ruling class.²¹ This period likely facilitated the secondary expansion of Q-M25 and Q-M346 lineages into the ancestral populations of the Karachays, Balkars, and Kumyks.

5. Modern Phylogeography: The Karachay-Balkar Core

The interplay of these ancient migrations has resulted in a highly structured distribution of Haplogroup Q in the modern North Caucasus. The lineage is not ubiquitous; rather, it is

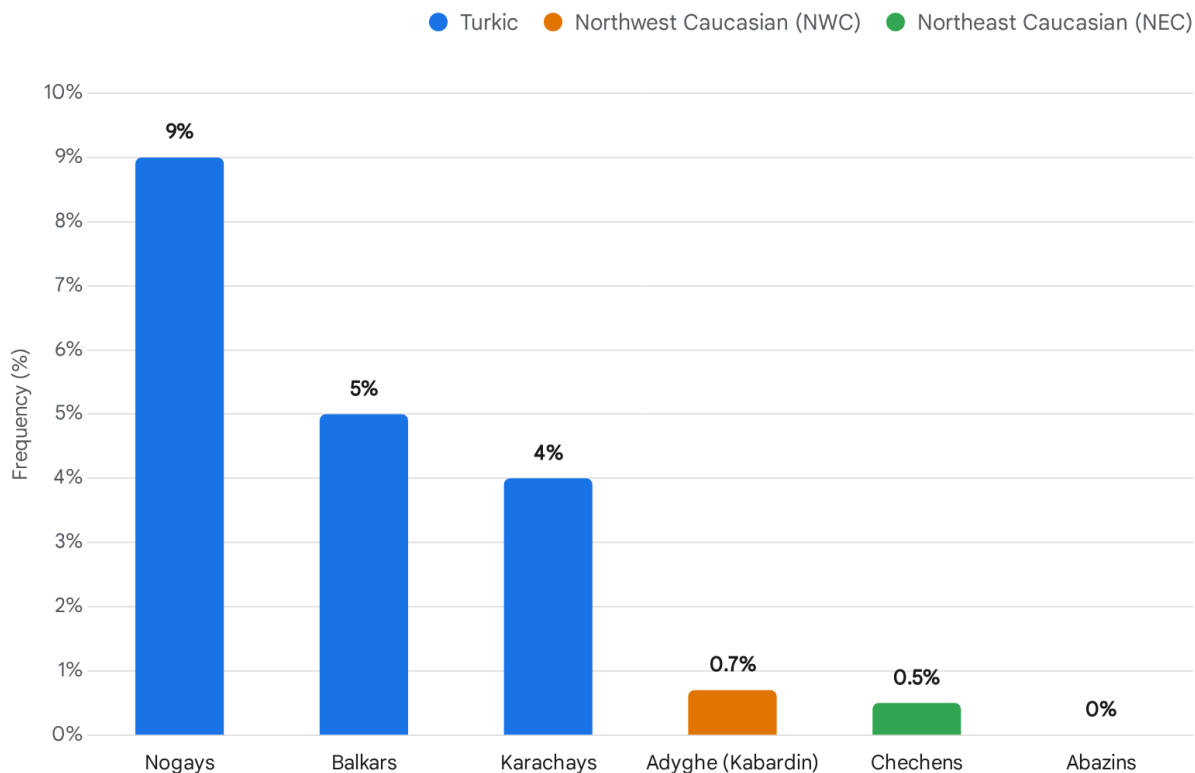
concentrated in specific ethnic enclaves, most notably among the Turkic-speaking Karachays and Balkars.

5.1. The Karachay-Balkar Enclave

The Karachays and Balkars, titular nations of the North Caucasus speaking closely related Turkic languages of the Kipchak branch, harbor the highest frequencies of Haplogroup Q in the region. Recent high-resolution analyses, such as those by **Dzhaubermmezov et al. (2017/2018)** and subsequent meta-analyses¹, have refined the classification of these lineages.

- **Frequency and Substructure:** While Haplogroup G2a (specifically G2a1a) and R1a-Z2123 are the dominant lineages (accounting for ~60-70% of the gene pool), Haplogroup Q persists as a significant minor lineage, reaching frequencies of **5–6%** in the general population but spiking much higher in specific subpopulations and clans.¹
- **Subclade Specificity:** The primary lineage is **Q-M25 (Q1a1b)**, specifically the **Q-L712** branch discussed above. This lineage is distinct from the Q-M242 basal lineages found elsewhere. Its presence supports the hypothesis of a **Bulgar-Hunnic substrate** in the Karachay-Balkar ethnogenesis.²
- **Comparison with Hungarians:** A recurring theme in the literature from 2018–2025 is the genetic affinity between Karachay-Balkar Q lineages and those found in the **Székelys** and ancient **Hungarian Conquerors**.²³ Studies by Neparáczi et al. have shown that Hungarian Conqueror elites shared specific haplotypes with North Caucasian populations. This confirms the historical narrative of the "Magyar" presence in the North Caucasus (near the city of Majar) before their migration to the Carpathian Basin. The shared Q-L712 lineage is the molecular smoking gun of this connection.¹⁰

Frequency of Haplogroup Q in North Caucasian Populations



Comparative frequencies of Y-chromosome Haplogroup Q among key North Caucasian ethnic groups. Note the elevated presence in Turkic-speaking populations (Karachay, Balkar, Nogay) compared to Northwest (Adyghe) and Northeast (Chechen) Caucasian speakers, reflecting differential steppe ancestry inputs.

Data sources: [ResearchGate \(Balkars & Karachays\)](#), [Wikipedia \(Caucasus DNA\)](#), [Khazaria.com](#), [Wikipedia \(Haplogroup Q\)](#)

5.2. The Circassian (Adyghe) and Northeast Caucasian Context

In stark contrast to the Turkic groups, the Northwest Caucasian (Adyghe, Kabardian) and Northeast Caucasian (Chechen, Dagestani) populations show a marked dominance of autochthonous haplogroups (G2a and J2/J1, respectively). However, Haplogroup Q is not entirely absent; its distribution here tells a different story—one of assimilation rather than dominance.

- **Adyghe and Kabardians:** Among the Circassian tribes, Haplogroup Q is detected at low frequencies, typically ranging from **0.7% to 1.4%**.²⁵ Unlike the "founder" signal in Balkars, the Q lineages here (often Q-M242*) appear as trace signals of "steppe admixture." They likely represent the genetic residue of individual Scythian or Sarmatian males who were

assimilated into the Adyghe tribal structure over millennia.³ The low diversity of subclades suggests sporadic gene flow rather than a mass migration event.

- **Chechens and Dagestanis:** In the Northeast Caucasus, Q is even more sporadic. However, the connection between the ancient Beslan Q sample and the modern **Shoanoy Teip** in Chechnya is a critical finding.⁴ It demonstrates that while Q is rare, specific lineages have been preserved within the strict clan endogamy of the region for over 1,500 years. In Dagestan, Q appears primarily in the steppe-dwelling Kumyks and Karanogais, consistent with their Turkic origins and recent (Golden Horde era) steppe ancestry.²⁶

6. Phylogenetic Deep Dive: The Subclade Architecture

To fully understand the history of Haplogroup Q in the Caucasus, one must look beyond the macro-haplogroup level. The specific subclades present function as molecular timestamps, dating the arrival of different waves of migrants.

6.1. The Q-M25 > Q-L712 Branch

This is the "Hunnic/Turkic" signature. **Q-M25** originated in Central Asia. Its downstream branch, **Q-L712**, separates the North Caucasian lineages from the Siberian Q-M3 lineages (Indigenous Americans) and the Chinese Q-M120 lineages.⁵

- **TMRC:** The Time to Most Recent Common Ancestor for Q-L712 fits the Migration Period (c. 300–500 CE).¹⁹
- **Distribution:** Its exclusive high-frequency appearance in the Balkar aristocracy and the Székelys creates a distinct "Steppe-Mountain" axis, linking the Caucasus directly to the Pannonian basin migrations.¹⁰

6.2. The Q-L940 (Q1b) Branch

This is the "Scythian" signature. As confirmed by Andreeva et al. (2025), this lineage was present in the North Caucasus by the 5th century BCE.⁷

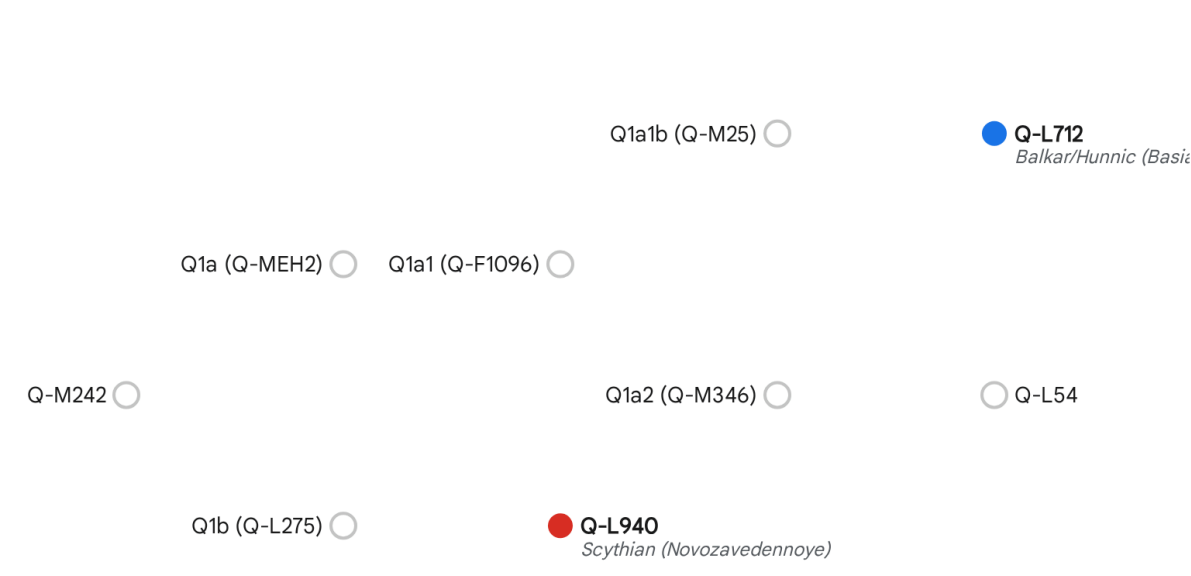
- **Geography:** Today, Q-L940 is found in Western Eurasia, Scandinavia, and parts of South Asia, but is rare in Central Asia. This distribution supports the idea of a distinct "Western Scythian" genetic cluster that evolved in the Pontic-Caspian steppe, separate from the Eastern Saka populations.⁸

6.3. The Q-M346 (Q1a2) Branch

This lineage represents a broader, "generalist" Central Asian signal. It is found at lower frequencies across the Caucasus and likely represents background gene flow from various Turkic migrations, including the later Cuman and Nogay expansions.²³ It lacks the specific "aristocratic" founder signal of Q-L712.

Phylogenetic Structure of Haplogroup Q Lineages in the North Caucasus

Lineage Divergence (Click nodes to expand/collapse)



Phylogenetic tree of Haplogroup Q-M242, detailing the subclades identified in North Caucasian ancient and modern populations. The divergence of the 'Scythian' Q-L940 branch and the 'Hunnic/Turkic' Q-M25>Q-L712 branch highlights the distinct origins of these lineages.

Data sources: [Wikipedia \(Q-M25\)](#), [FamilyTreeDNA](#), [Wikipedia \(Q-M242\)](#)

7. Synthesis: Mechanisms of Gene Flow and Historical Implications

The data accumulated between 2018 and 2025 supports a **Stratified Integration Model** for Haplogroup Q in the North Caucasus. The lineage did not arrive in a single wave, nor did it simply "diffuse" from neighbors. Instead, specific historical events injected specific Q lineages into the region, which were then processed differently by the social structures of the host populations.

7.1. Stratum 1: The Scythian Interface (Iron Age)

The first stratum involves **Q-L940**. Its presence in the Novozavedennoye-III burials (c. 400 BCE) indicates that Q was part of the Scythian "package." However, the persistence of local mtDNA lineages (U2, U5) suggests that these Scythian males married into the local Koban population. This admixture event likely occurred in the piedmont zone, creating a mixed population that would later be absorbed by the Alans.

7.2. Stratum 2: Elite Dominance (Migration Period)

The second stratum involves **Q-L712**. This lineage appears to have established itself via **Elite Dominance**. The arrival of the Huns and Bulgars (c. 370–650 CE) brought a new, distinct Q lineage. The strong correlation between Q-L712 and the Balkar/Digor aristocracy (Badeliats/Basiats) suggests that a small, Q-carrying elite stratum imposed its language (Turkic) and social structure on a larger, indigenous G2a/R1a population. This explains why Q is found in "founder clusters" (high frequency in specific clans) rather than being evenly distributed across the population. This model perfectly fits the "Majar" origin legends found in North Caucasian folklore.

7.3. Stratum 3: Background Admixture (Medieval - Modern)

The final stratum involves **Q-M346** and other minor clades. These likely entered the gene pool through continuous, low-level interaction with the Golden Horde, the Nogay Horde, and other steppe polities from the 13th to 18th centuries. In this phase, Q was just one component of a larger "Steppe Ancestry" package (along with C, N, and O) that influenced the ethnogenesis of the Nogays and Kumyks.

8. Conclusion

The research period of 2018–2025 has been transformative for our understanding of Haplogroup Q in the North Caucasus. We have moved from viewing Q as a generic "Siberian" marker to recognizing it as a highly specific archive of steppe history. The identification of **Q-L940** in Scythians and **Q-L712** in the ancestral Karachay-Balkar populations resolves long-standing debates about the biological legacy of the region's nomadic conquerors.

The data confirms that the North Caucasus was not merely a barrier to migration but a selective filter and refuge. While the deep autochthonous lineages (G, J) remained dominant in the highlands, the mountain valleys and piedmonts absorbed and preserved distinct lineages from the Great Steppe. Haplogroup Q, in its specific Caucasian subclades, serves as the genetic footprint of the Scythian archers and Hunnic warlords who shaped the history of this crossroads of civilizations.

Future research must focus on higher-resolution sequencing of the "missing links"—specifically, samples from the enigmatic Saltovo-Mayaki culture and the early medieval Alania—to fully reconstruct the genealogical bridges connecting the ancient nomads to the

modern peoples of the Caucasus.

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