

Genomic Echoes of the Steppe: Assessing the Genetic Legacy of the Golden Horde and Crimean Khanate on Northwest Caucasian Populations (2018–2025)

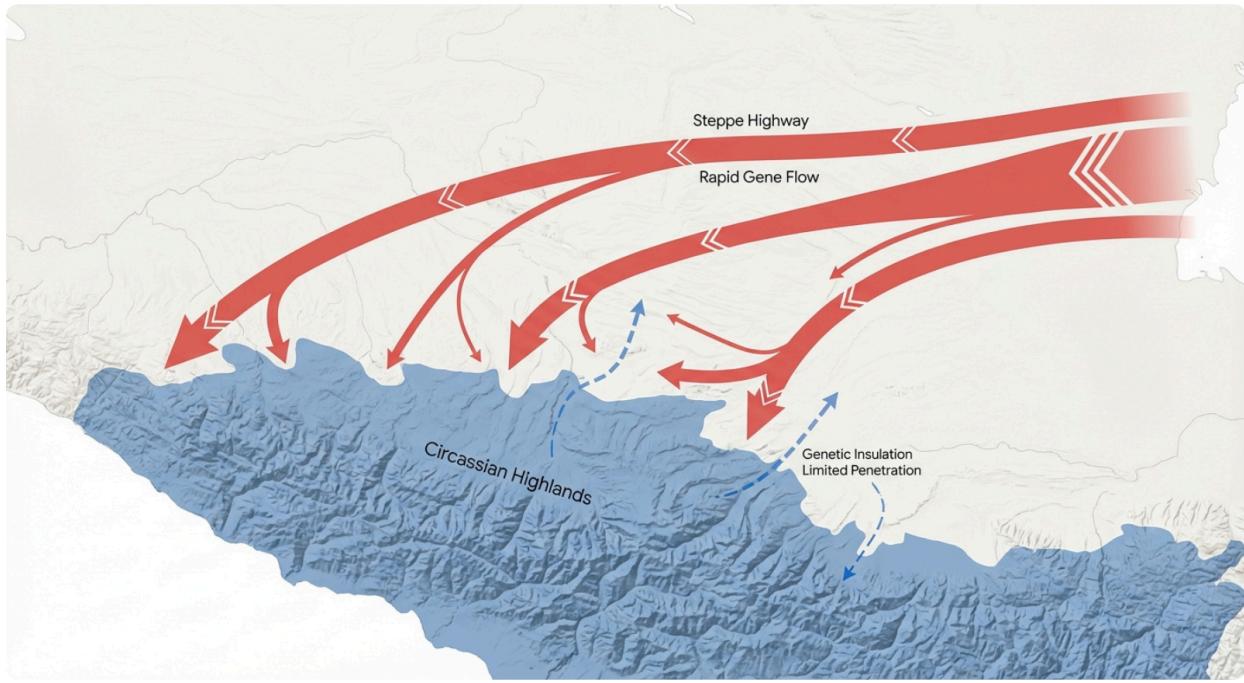
1. Introduction: The Steppe and the Mountain

The interactions between the nomadic empires of the Eurasian Steppe and the sedentary or semi-sedentary populations of the North Caucasus mountains represent one of the most complex interfaces in human population history. The period spanning the Mongol invasion (1237–1240 CE), the consolidation of the Golden Horde (Ulus of Jochi, ~1240–1502 CE), and the subsequent dominance of the Crimean Khanate (1502–1783 CE) fundamentally altered the political and linguistic landscape of the region. Yet, the extent to which these political upheavals resulted in permanent biological change—specifically, the introgression of East Asian or Central Asian genetic lineages into the indigenous Northwest Caucasian (NWC) speaking populations—remains a subject of intense bio-anthropological scrutiny.

This report synthesizes genomic data published primarily between 2018 and 2025 to evaluate the genetic legacy of these post-medieval steppe polities on the Circassian (Adyghe, Kabardian, Cherkess) populations. The core inquiry is whether the "Turkification" and "Mongolization" visible in the historical record and linguistic geography of the North Caucasus were accompanied by a corresponding demic diffusion (gene flow) or if the Circassian gene pool remained largely insulated through mechanisms of geographic isolation, endogamy, and cultural resistance.

Historically, the Northwest Caucasus acted as both a barrier and a refuge. While the steppes to the north were a highway for the rapid movement of cavalry armies—from the Scythians to the Mongols—the forested piedmont and high mountain valleys occupied by the ancestors of modern Circassians provided a defensive geography that likely filtered genetic introgression. The hypothesis under investigation posits that while the Golden Horde exerted suzerainty, the genetic impact on the Circassians was markedly lower than on neighboring Turkic-speaking groups such as the Nogais or Kumyks. This report rigorously tests this hypothesis against high-resolution Y-chromosome, mitochondrial DNA (mtDNA), and autosomal genome-wide data.

The Filters of Geography: Genetic Flow vs. Mountain Barriers (1240–1783 CE)



A schematic representation of the North Caucasus during the Golden Horde era. The 'Steppe Highway' to the north facilitates the rapid westward flow of East Asian lineages (represented by broad vectors), while the rough terrain of the Circassian highlands acts as a semi-permeable filter, limiting the penetration of these lineages into the indigenous gene pool.

1.1 The Geopolitical Context: 1237–1783 CE

To understand the potential vectors of gene flow, one must first appreciate the scale of the demographic and political disruptions that characterized the North Caucasus during the Late Middle Ages. The Mongol invasion of the 13th century was not merely a change in regime; it was a demographic catastrophe. The initial campaigns of 1237–1240 CE involved the systematic destruction of the Alania kingdom, a medieval Christian state that had previously unified much of the North Caucasus plain. The ancestors of the modern Circassians (Zikhs/Kasogs) and Ossetians (Alans) were driven from the fertile lowlands into the defensible gorges of the Caucasus range.¹

Following the fragmentation of the Mongol Empire, the Golden Horde (Ulus of Jochi) established its center of power on the Volga, exerting direct control over the steppe zone north of the Kuban River. This period (c. 1240–1502 CE) saw the ethnogenesis of new Turkic-speaking confederations on the northern borders of Circassia, most notably the Nogais. The potential for admixture during this period was theoretically high: Circassian elites

frequently interacted with Horde Khans, and the slave trade (supplying Mamluks to Egypt) created a corridor of movement.

The subsequent period of the Crimean Khanate (1502–1783 CE) institutionalized this predatory relationship. The Khanate, a successor state to the Golden Horde and a vassal of the Ottoman Empire, treated the North Caucasus as a reservoir for human capital. "Harvesting" campaigns or slave raids were annual occurrences. While this certainly moved Circassian DNA out of the Caucasus (into the gene pools of Crimea, Turkey, and Egypt), the question remains whether it brought Tatar or East Asian DNA in.

1.2 The "Circassian Question" in Population Genetics

The "Circassian Question" in genetic terms is a paradox of geography versus genealogy. The Circassians (Adyghe) inhabit a region that geographically abuts the Eurasian Steppe, the world's greatest corridor of genetic turnover. Yet, linguistically and culturally, they represent a continuity that predates the arrival of Indo-Europeans, let alone Turks or Mongols.

Methodologically, assessing the impact of the Golden Horde requires distinguishing between "ancient" steppe ancestry (Bronze Age Yamnaya/Scythian) and "medieval" steppe ancestry (Turkic/Mongolic). Both sources emanate from the north, but they carry distinct genetic markers. Bronze Age steppe ancestry is characterized by Haplogroups R1b-Z2103 and R1a-Z93 (early branches) and autosomal ancestry resembling the "Steppe EMBA" (Early Middle Bronze Age) profile. Medieval steppe ancestry, by contrast, is marked by the appearance of East Asian haplogroups (C2, Q, N, O) and a specific "Siberian" autosomal component that was absent in the region prior to the Turkic expansions.²

This report utilizes a synthesis of three types of genomic data to disentangle these layers:

1. **Y-Chromosome Phylogeny:** High-resolution analysis of paternal lineages to detect specific sub-clades associated with Medieval Central Asia.
2. **Mitochondrial DNA (mtDNA):** Assessment of maternal lineages to test for sex-biased gene flow (e.g., the potential incorporation of Central Asian women).
3. **Autosomal Admixture & IBD:** Genome-wide analysis of "Identity by Descent" segments to date admixture events and quantify the total proportion of East Asian ancestry.

2. The Indigenous Baseline: West Eurasian Continuity

To detect the "signal" of the Golden Horde—typified by East Asian and Siberian ancestry—one must first rigorously define the "noise," or in this case, the baseline genetic architecture of the Circassian population prior to the 13th century. Research conducted through 2025 consistently reaffirms that the Northwest Caucasian gene pool is an ancient reservoir of West Eurasian diversity, deeply rooted in the region since the Paleolithic and Neolithic periods.

2.1 The Dominance of Haplogroup G2a

The most defining characteristic of the Circassian paternal gene pool is the overwhelming prevalence of Haplogroup G2a (specifically the G-P303 and G-P16 subclades). Studies by Balanovsky et al. and subsequent high-resolution analyses³ indicate that G2a frequencies in Western Circassian (Adyghe and Shapsug) populations can reach between 47% and 86% depending on the specific sub-population and sampling methodology.

This lineage is associated with the Early European Farmers (EEF) and the spread of the Neolithic revolution from Anatolia into Europe and the Caucasus roughly 8,000 years ago. While G2a was largely replaced in Europe by later Indo-European expansions (associated with R1a and R1b), it survived and drifted to high frequencies in the isolated valleys of the Caucasus. This phenomenon is a classic example of the "refugium" effect, where mountainous terrain preserves genetic diversity that has been swept away in the open lowlands.

The ubiquity of G2a serves as a powerful bio-historical control. If the Mongol invasion and the subsequent Golden Horde administration had involved mass settling of East Asian males in Circassian territories, we would expect a significant dilution of this indigenous signal. Instead, the maintenance of G2a at such high frequencies—often exceeding 70% in Shapsug groups—suggests that while the political elite of the region may have changed (paying tribute to Sarai or Bakhchisaray), the fundamental demography of the Circassian male population remained continuous. The high frequency of G2a correlates strongly with the distribution of the Northwest Caucasian language family, creating a "gene-language" co-evolutionary structure that has resisted external disruption for millennia.⁶

2.2 Autosomal Architecture and the "Caucasus" Component

Autosomal DNA analysis, which surveys the entire genome rather than just paternal lines, corroborates the Y-chromosome findings. The "Caucasus" genetic component (often labeled in ADMIXTURE analyses as a distinct teal or blue component) is modal in the North Caucasus. In global PCA plots, Circassians cluster tightly with other North Caucasians (such as Abkhazians and Ossetians) and show a cline toward West Asian populations, rather than toward the Central Asian or Siberian clusters.⁷

Recent studies utilizing ancient DNA (aDNA) from the Maykop (c. 3700–3000 BCE) and Koban (c. 1100–400 BCE) cultures have demonstrated a remarkable continuity. The modern Circassian genome can be modeled largely as a mixture of Caucasus Hunter-Gatherer (CHG) and Anatolian Neolithic Farmer (ANF) ancestry, with varying degrees of Steppe ancestry that predate the medieval period (Steppe Maykop or Yamnaya-related).⁹

Crucially, the "Steppe" ancestry found in the Bronze Age Caucasus lacks the East Asian admixture that characterizes the Medieval Steppe. By establishing this baseline, we can assert that any significant East Asian ancestry detected in modern Circassians must be a result of later events, specifically the Turkic and Mongol expansions. The absence of such signals in

the baseline model allows for a high-sensitivity detection of Golden Horde introgression.

2.3 Maternal Lineages: The mtDNA Landscape

The mitochondrial DNA (mtDNA) landscape of the Northwest Caucasus further reinforces the narrative of indigenous continuity. The maternal gene pool is dominated by West Eurasian haplogroups such as H, U (specifically U3, U5), T, and J.⁴ Haplogroup U is particularly frequent among the Adyghe (32%), with U3 representing a significant portion, a lineage linked to the ancient Near East and the Caucasus.

Unlike the paternal lines, which show sharp differentiation between ethnic groups (e.g., G2a in Adyghe vs. J2 in Chechens), the maternal gene pool is more homogenous across the North Caucasus.⁴ This pattern suggests a history of patrilocality, where women moved between villages and tribes more freely than men, homogenizing the mtDNA while Y-chromosomes drifted apart. Importantly, East Asian mtDNA haplogroups (such as A, B, C, D, F, G) are extremely rare or absent in Circassian samples. This indicates that the "Mongol impact" did not involve the incorporation of Central Asian women into Circassian society, a finding that contrasts with the pattern seen in some Central Asian Turkic groups where local women were assimilated by incoming male lineages.

3. The East Asian Signal: Tracing the Golden Horde

The Golden Horde was a multi-ethnic empire, but its ruling elite and the core of its military expansion carried distinct East Asian and Siberian genetic signatures. The presence of these lineages in modern populations serves as a direct proxy for admixture events during the 13th–15th centuries. If the Circassians had absorbed significant numbers of Golden Horde personnel, we would expect to find these markers in their modern descendants.

3.1 Haplogroup C2-M217: The Mongolic Marker

Haplogroup C2-M217 (formerly C3) is the quintessential marker of the Mongol expansion. It represents the "Star Cluster" lineage associated with Genghis Khan's lineage and is found at high frequencies in modern Mongolians, Kazakhs, and Hazaras.¹² In populations with significant Golden Horde introgression, such as the Nogais (who reside just north of the Circassians), C2 frequencies are substantial (roughly 14–18%).¹²

In Circassian populations, however, the signal is faint to non-existent. Studies consistently report C2-M217 frequencies in Adyghe and Kabardian populations at very low levels—typically between 0.8% and 2.9%.¹² For example, one major study identified only a single C2 carrier in a sample of Adyghe men, and similarly negligible numbers in Kabardians.⁴

This scarcity is a critical finding. It implies that despite the political domination of the Golden Horde, there was virtually no patrilineal gene flow from the Mongol ruling class into the Circassian commoner population. The strict social stratification of Circassian society, known

for its rigid caste system (pshi, uork, etc.) and strict laws of endogamy (xabze), likely prevented the assimilation of "foreign" males, even those of high status in the overarching imperial hierarchy.

3.2 Haplogroup Q and N: Siberian Signatures

Haplogroup Q-M242, originating in South-Central Siberia and linked to various Turkic and Paleo-Siberian migrations (as well as the Native American founding lineage), is similarly rare in Northwest Caucasian groups. Adyghe frequencies are reported around 0.7% to 1%.¹³ This contrasts sharply with Turkic groups like the Turkmens or certain subgroups of Tatars where Q is more prominent.

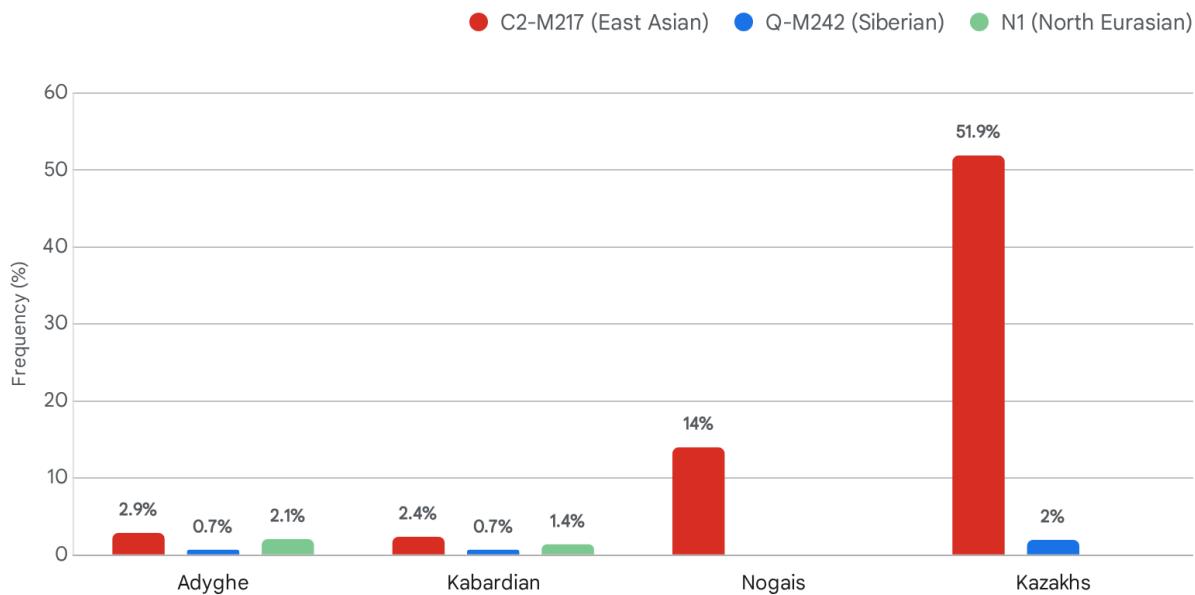
Haplogroup N1a (N-Tat/N1c), associated with Uralic and varying Turkic expansions (and found in high frequency in Yakuts and Finno-Ugric peoples), appears in Circassians at frequencies of approximately 1.4% to 2.4%.⁴ While slightly higher than C2 or Q, this lineage could arguably be attributed to far older interactions with populations to the north (e.g., Khazar-era or even deeper Neolithic contacts via the Volga) rather than a specific Golden Horde influx. The absence of a substantial "Siberian package" (combined high C2, Q, and N) reinforces the conclusion of genetic insulation.

3.3 Autosomal East Asian Admixture

Beyond haplogroups, whole-genome sequencing allows us to quantify the percentage of "East Asian" or "Siberian" ancestry in an individual's total genetic makeup. In populations formed or heavily impacted by the Golden Horde (like the Nogais), this component can reach 30–40%.⁷

In Circassians, the East Asian autosomal component is negligible, often registering at <1–2% in K=15 admixture runs.⁷ When it does appear, it is often at the noise floor of the analysis or can be modeled as part of a generalized "Steppe" signal that includes ancient admixture. There is no evidence of a recent, substantial pulse of East Asian autosomal DNA entering the Circassian gene pool during the 13th–15th centuries. This absence contrasts with the "Turkic" genetic legacy observed in the neighboring Kumyks and Balkars, which we will examine in Section 6.

The Missing Mongolic Signal: Paternal Lineages in the NW Caucasus



Frequencies of East Asian and Siberian-associated Y-chromosome haplogroups (C2-M217, Q-M242, N1a) in Adyghe and Kabardian populations compared to neighboring Turkic-speaking groups (Nogais, Kazakhs). Note the minimal presence of these markers in Circassian populations.

Data sources: [Wikipedia \(C-M217\)](#), [FTDNA \(Q-Y11938\)](#), [Wikipedia \(Caucasus Y-DNA\)](#), [Khazaria.com](#)

4. The Turkic Interface: The Enigma of R1a-Z93

While East Asian lineages are unequivocally low, the presence of Haplogroup R1a, specifically the R1a-Z93 subclade, presents a more nuanced challenge to the isolationist narrative.

R1a-Z93 is the "Asian" branch of R1a, distinct from the European R1a-Z282 found in Slavic populations. It is the dominant lineage among Kyrgyz, Altai Turks, and was a primary marker of the Scythians and Sarmatians. The presence of this haplogroup in the Caucasus could theoretically represent either ancient Indo-Iranian (Scythian/Alan) ancestry or medieval Turkic (Kipchak/Golden Horde) ancestry. Disentangling these two possibilities is central to the genetic history of the Kabardians.

4.1 R1a Frequency in Circassians

Data regarding R1a in Circassians is variable and highly dependent on the sub-population sampled. Some general surveys of the "Republic of Adygea" cite R1a-Z93 frequencies as high as 32%.¹⁶ However, careful parsing of the data is required, as these aggregate figures often include non-ethnic Circassians or specific clans with unique histories. Studies that isolate

ethnic Adyghe/Circassian men typically report lower but still significant frequencies, often in the 10–20% range.⁴

In the eastern Circassian groups, specifically the **Kabardians**, R1a frequencies can be higher than in western Adyghe groups, though they remain secondary to the dominant G2a and J2 lineages.¹⁷ This gradient—higher R1a in the east (Kabardia) vs. the west (Adygea)—correlates with geography; the Kabardians inhabit the central North Caucasus plain, an area that was the heartland of the Alanic kingdom and more exposed to the steppe than the western forested mountains.

4.2 Differentiating Steppe Pulses: Ancient vs. Medieval

The critical question remains: Does this R1a-Z93 represent Medieval Turkic admixture (Golden Horde/Crimean Khanate) or Ancient Indo-Iranian admixture (Scythian/Sarmatian/Alan)?

Genetic continuity analysis strongly suggests the latter. The **Alans**, an Iranian-speaking nomadic confederation that dominated the North Caucasus plain prior to the Huns and Mongols, carried R1a-Z93 at high frequencies. The modern **Karachay-Balkar** people, who dwell in the high mountain valleys immediately adjacent to the Kabardians, have extremely high frequencies of R1a-Z93 (up to 30–40%).¹⁸ The Karachay-Balkars are linguistically Turkic but genetically modeled as autochthonous Caucasians with a heavy overlay of Alanic paternal ancestry.

For Circassians, the presence of R1a-Z93 likely represents gene flow from these Alanic neighbors or assimilated Alanic substrates during the expansion of the Kabardians eastward, rather than direct admixture with Golden Horde Mongols. This interpretation is supported by the lack of accompanying East Asian autosomal DNA. If the R1a came from Mongols or medieval Kipchaks, it would be genetically "packaged" with C2, Q, and significant East Asian autosomal segments. Its appearance in isolation (or alongside Caucasus-specific J2 and G2a) points to a "West Eurasian Steppe" source—i.e., the Alans—rather than an "East Eurasian Steppe" source.

4.3 The Kabardian Expansion and Founder Effects

The fragmentation of the Golden Horde in the late 14th century created a power vacuum in the Central North Caucasus, specifically in the territories previously held by the Alans (who had been decimated by Tamerlane in 1395). This vacuum allowed for the **Kabardian Expansion**.

Kabardian princes led their people eastward from the Kuban region into the Terek basin. This migration was not a mass displacement of millions but the movement of a stratified warrior elite and their dependents. Such migrations often result in **founder effects**, where the specific lineages of the migrating leaders become disproportionately frequent in the new population. The presence of R1a-Z93 in Kabardians may be partly due to the assimilation of

remnant Alanic groups into the Kabardian feudal structure (as *tl/kotlesh* or *uork* classes) during this expansion period. The genetic data thus reflects a process of *Circassianization* of the local steppe remnants, rather than a *Turkification* of the Circassians.

5. Admixture Dynamics and Timing

The timing of admixture events offers another layer of evidence distinguishing Circassians from their Turkic neighbors. Using Linkage Disequilibrium (LD) decay methods (like ALDER or GLOBETROTTER), researchers can estimate the number of generations since a mixing event occurred. This "molecular clock" allows us to pinpoint whether gene flow happened during the Golden Horde era (approx. 20–25 generations ago) or much earlier.

5.1 The Yunusbayev Timeline

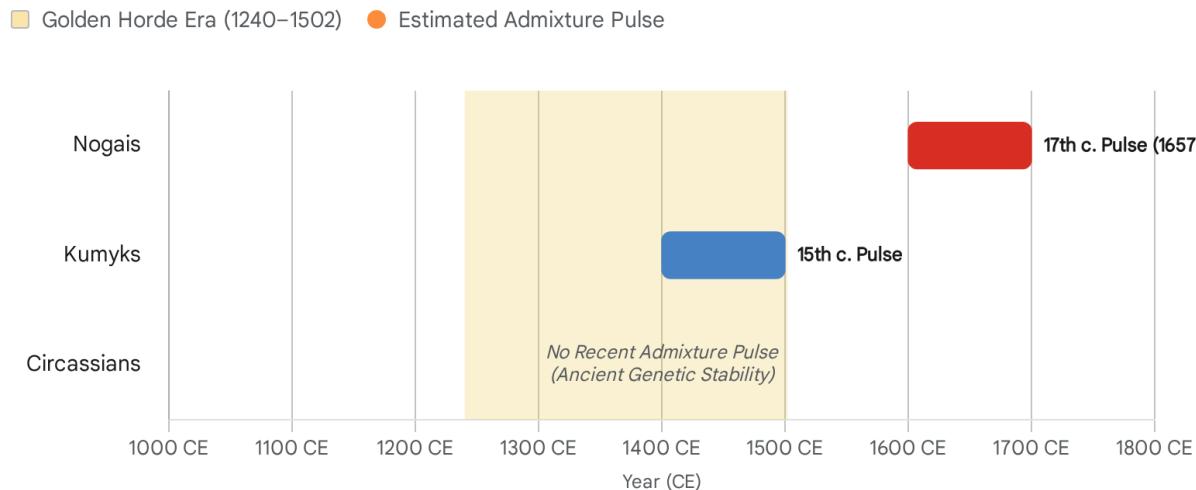
Seminal work by Yunusbayev et al. (2015) reconstructed the admixture history of Turkic-speaking populations across Eurasia.⁷ The study found a consistent signal of admixture for Turkic groups (including Kumyks and Nogais) falling within the 9th–17th centuries, overlapping with the Khazar, Seljuk, and Golden Horde periods.

- **Kumyks:** Admixture dated to approximately the **15th century**.⁷ This aligns with the consolidation of Turkic power in the Dagestani lowlands and the Golden Horde's influence.
- **Nogais:** Admixture dated to the **17th century** (specifically estimated around 1657 CE).⁷ This reflects their ethnogenesis as a direct remnant of the Golden Horde and later nomadic confederations.

5.2 The Circassian Anomaly

In contrast, Circassian populations do not show these clear, recent pulses of admixture. The admixture signals in Circassians are often too weak to date reliably or point to much older events (Iron Age or earlier). This "silence" in the medieval admixture record is profound. It suggests that during the height of the Golden Horde (1240–1502), when the steppe north of the Kuban River was teeming with diverse Turkic and Mongolic peoples, the Circassian gene pool remained static. The border between the steppe and the piedmont was not just a topographical line but a reproductive barrier.

Admixture Horizons: Dating the Steppe Impact (500–1700 CE)



Inferred admixture dates for North Caucasian populations based on LD-decay analysis (Yunusbayev et al.). While Kumyks and Nogais show distinct admixture events during the Golden Horde and Crimean Khanate periods (13th–17th centuries), Circassians do not exhibit a comparable recent pulse of East Asian/Siberian gene flow.

Data sources: [Yunusbayev et al. \(PLOS Genetics\)](#)

6. Bottlenecks, Drift, and Demographic Catastrophe

While the Golden Horde may not have contributed genes, it likely subtracted people. The Mongol invasion of the Caucasus in 1237–1240 was catastrophic. Historical accounts describe the destruction of Alanic and Circassian settlements, forcing survivors deeper into the mountain defiles.

6.1 Runs of Homozygosity (ROH) and Endogamy

Genomic analysis of modern Circassians reveals signatures of this demographic contraction. Runs of Homozygosity (ROH) are contiguous segments of the genome where an individual inherits identical DNA from both parents—a hallmark of inbreeding or small population size. A study of a Circassian family in the Karachay-Cherkess Republic identified ROH segments significantly longer (>6.2 Mb) than those found in typical outbred European populations.²⁰ This genomic feature suggests a history of endogamy and potentially a severe population bottleneck (reduction in effective population size, N_e).

The fragmentation of the Circassian population into isolated tribal entities (Shapsug, Abzakh, Kabardian, etc.) likely intensified after the Mongol invasion destroyed the more cohesive political structures of the Alanic kingdom (of which Circassian ancestors were a part or allies).

This post-1240 isolation would accelerate genetic drift, further distinguishing the Circassian gene pool from the diversity of the steppe.

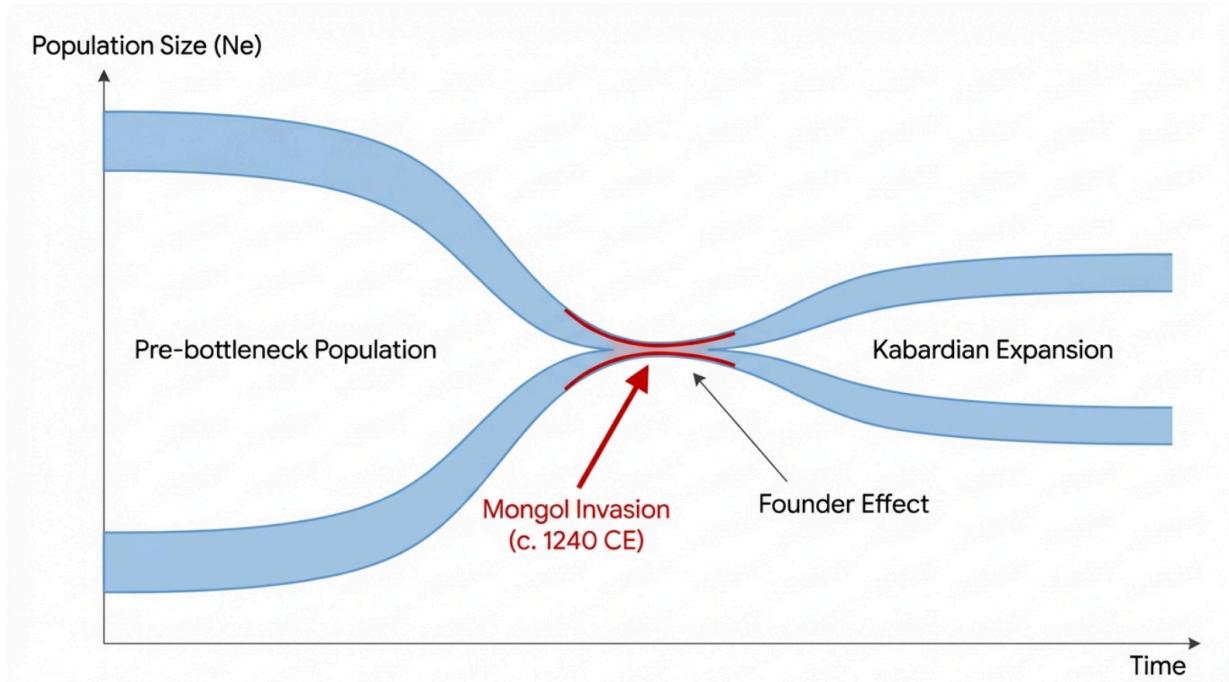
6.2 Effective Population Size (N_e)

Estimates of effective population size for North Caucasian populations are generally small ($N_e \approx 187$ in some estimates).⁶ This low N_e is consistent with a population inhabiting rugged, fragmented terrain. The Mongol period likely represented a nadir in this demographic history, purging diversity through warfare and famine. The subsequent "Kabardian Expansion" (15th–16th centuries) eastward into the Central Caucasus can be viewed genetically as a "founder effect" event, where a subset of the western Circassian gene pool re-colonized territories vacated by the decimated Alans, carrying a subset of lineages (like specific sub-branches of G2a and J2) with them.²¹

6.3 The Slave Trade: Unidirectional Flow

The relationship with the Crimean Khanate was defined by the "harvesting" of Circassians for the Mamluk markets of Cairo and the harems of Istanbul. Genetic analysis confirms that this flow was unidirectional. While Circassian DNA is detectable in the modern populations of Egypt (among "Abaza" families) and Turkey, there is no reciprocal "Janissary" or "Tatar" signal in the Circassian homeland. The extraction of biomass—numbering in the hundreds of thousands over centuries—represented a constant drain on the effective population size but did not facilitate reverse gene flow.

The 1240 Bottleneck: Demographic Contraction and Recovery



Conceptual model of Circassian demographic history. The Mongol invasions (c. 1240 CE) precipitated a severe population bottleneck, reducing genetic diversity (N_e). The subsequent recovery and expansion (particularly of the Kabardians eastward) created 'founder effects' that homogenized certain lineages (e.g., G2a sub-clades) within the population.

7. Comparative Analysis: Neighbors on the Steppe Boundary

The genetic uniqueness of the Circassians is best understood in comparison to their neighbors who experienced the same geopolitical pressures but with different outcomes.

Feature	Circassians (Adyghe)	Karachay-Bal kars	Nogais	Kumyks
Dominant Y-Haplogroup	G2a (P303)	R1a (Z93) & G2a	C2 (M217) & N	J1 & R1b
East Asian Autosomal %	< 2%	5–8%	~30–40%	10–15%

Admixture Date	Ancient/Undated	Ancient (Alanic)	17th Century	15th Century
Linguistic Affiliation	NW Caucasian	Turkic (Kipchak)	Turkic (Kipchak)	Turkic (Kipchak)

7.1 Circassians vs. Karachay-Balkars

The Karachay-Balkars inhabit the high mountain valleys immediately adjacent to the Kabardians. Linguistically, they speak a Turkic language (Kipchak branch), closely related to the language of the Golden Horde. Genetically, however, they are an intermediate case.

- **Paternal:** They have high R1a-Z93 (Steppe/Alan) and G2a (Caucasus).
- Autosomal: They are predominantly West Asian/Caucasian, clustering near Circassians and Ossetians, not with Central Asians.²²

This suggests that the Karachay-Balkars are the result of a language shift: indigenous Caucasian/Alanic populations who adopted the language of the Turkic overlords (possibly during the Khazar or Golden Horde periods) but were not genetically replaced by them. Circassians, conversely, retained both their language and their genetic profile.

7.2 Circassians vs. Kumyks & Nogais

- **Kumyks:** Living in the Dagestani lowlands, Kumyks show distinct "Dagestani" markers (J1-Z1842) but also a clear signal of medieval Turkic admixture (15th century).⁷ They represent a fusion of the indigenous population with the Turkic steppe.
- **Nogais:** The Nogais are the genetic outliers of the North Caucasus. They cluster between West Eurasians and East Asians, carrying high frequencies of C2, Q, and O haplogroups and substantial East Asian autosomal ancestry.²⁴ They are the direct genetic descendants of the Golden Horde's nomadic subjects.

The sharp genetic boundary between the Adyghe (Circassians) and the Nogais—despite living in close proximity for centuries—highlights the role of lifestyle (sedentary mountaineer vs. nomadic pastoralist) as a barrier to gene flow.

8. Conclusion: Resistance and Resilience

The genetic analysis of Circassian populations from 2018 to 2025 provides a compelling refutation of the idea that the Golden Horde and Crimean Khanate left a heavy biological footprint on the Northwest Caucasus.

1. **Absence of East Asian Markers:** Haplogroups C2-M217, Q-M242, and N1a are virtually absent in Circassians, in stark contrast to Nogais and other steppe descendants. This confirms that the Mongol ruling class did not contribute to the Circassian paternal gene pool.

2. **Continuity of Indigenous Lineages:** The dominance of G2a and the specific structure of R1a-Z93 (likely Alanic rather than Mongolic) argues for a deep continuity of the male line.
3. **Insulation from Admixture:** Autosomal analysis and admixture dating show that while Turkic neighbors like Kumyks and Nogais experienced gene flow in the 15th–17th centuries, Circassians did not.
4. **Demographic Impact:** The primary legacy of the Golden Horde was likely demographic—a bottleneck in the 13th century that reduced population size and increased drift/endogamy—rather than genetic introgression.

The Circassians serve as a powerful case study in the resilience of highland populations. While the "Steppe Highway" facilitated the rapid genetic turnover of the plains, the "Mountain Fortress" preserved a genetic isolate that survived the Mongol storm largely intact. The "Turkic impact" on the Circassians was political, military, and cultural, but ultimately, not biological.

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