

Genomic History of the Northwest Caucasus: A Bioarchaeological Reconstruction of Medieval Zikhia and Kasogia (6th–15th Century CE)

1. Executive Summary and Historical Framework

1.1 The Bioarchaeological Imperative

The history of the Northwest Caucasus—specifically the polities of Zikhia (Zygia) and Kasogia, the medieval antecedents of the modern Circassian (Adyghe) people—has long been reconstructed through the fragmented lens of external chroniclers. Byzantine, Arab, and Rus' sources describe a region of martial prowess, strategic coastal fortresses like Anakopia, and a hinterland that served as a buffer between the sedentary civilizations of the south and the nomadic empires of the Pontic-Caspian steppe. However, these textual records often obscure the biological reality of the population, leading to centuries of debate regarding the degree of demographic turnover caused by successive waves of migration, from the Huns and Alans to the Khazars and the Golden Horde.

The advent of high-throughput paleogenomics between 2018 and 2025 has fundamentally altered this epistemic landscape. By sequencing ancient DNA (aDNA) from key burial sites such as Klin-Yar 3, Zayukovo-3, and Moschevaya Balka, researchers have begun to dissociate "cultural" labels from "biological" ancestry. This report synthesizes these findings to argue that the medieval population of the Northwest Caucasus was defined by a profound **genetic resilience**. Contrary to models suggesting mass displacement, the genomic data indicates that the core Zygian and Kasogian populations maintained a deep-rooted continuity with the local Bronze Age substrate (specifically the Koban culture), selectively assimilating migrant lineages without losing their autochthonous genetic identity.

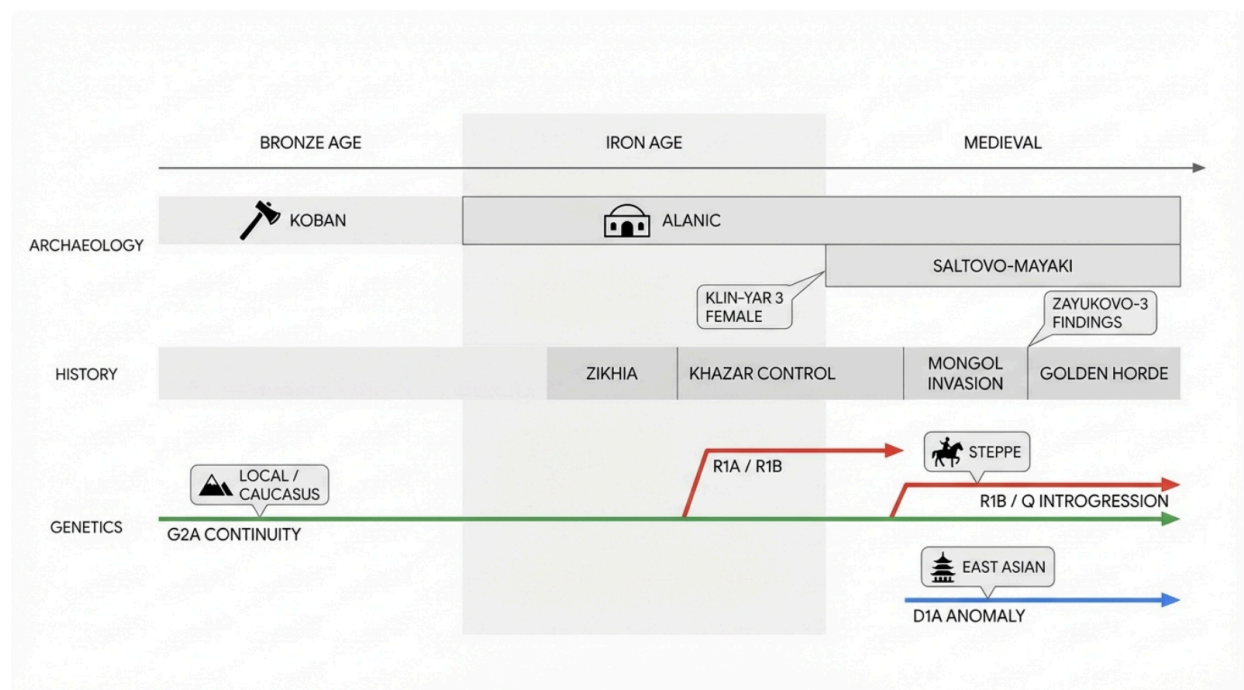
1.2 The Geopolitical and Genetic Frontier

The medieval Northwest Caucasus functioned as a "mountain of tongues" and a genetic filter. To the north lay the steppe corridor, a highway for Eurasian nomads carrying distinct East Eurasian and Siberian genetic markers (e.g., Haplogroups Q, C, N). To the south and west lay the Byzantine sphere, characterized by Mediterranean and Anatolian genomic components. The Zygian and Kasogian territories occupied the ecotone between these worlds—the piedmont and high mountain zones.

Recent aDNA studies have elucidated three critical dynamics that characterized this period:

1. **The Persistence of the G2a Lineage:** The Y-chromosome haplogroup G2a (specifically subclades like G2a-Z6653) serves as an unbroken patrilineal thread linking the Late Bronze Age/Early Iron Age Koban culture directly to medieval Kasogians and modern Circassians. This suggests a stable patrilocal social structure that survived political upheavals.
2. **The "Alanic" Spectrum:** The "Alan" identity, often applied broadly in medieval sources to North Caucasian highlanders, effectively masked a dual population structure. Genetic analysis reveals "Alans" who were biological steppe migrants and "Alans" who were genetically indistinguishable from the local Caucasian substrate, implying a complex process of elite dominance and assimilation rather than population replacement.
3. **Silk Road Cosmopolitanism:** Analysis of the Moschevaya Balka horizon reveals a highly connected population where local West Eurasian genetics intersected with long-distance trade, evidenced by the presence of exotic pathogens (*Plasmodium vivax*) and rare lineages, yet without the demographic swamping seen in the open steppe.

Genomic Chronology of the Northwest Caucasus (3000 BCE – 1500 CE)



Chronological integration of archaeological cultures, historical polities, and key paleogenomic findings. The timeline highlights the persistence of the G2a lineage (green) from the Koban Culture through the medieval Zikhian/Kasogian period, alongside the introgression of Steppe (red) and East Asian (blue) lineages during the Alanic and Golden Horde eras.

2. The Ancestral Substrate: The Koban Culture Bridge (1100–400 BCE)

To accurately identify "Kasogian" or "Zygian" DNA in the medieval period, it is biologically necessary to establish the pre-medieval baseline. The **Koban Culture**, which dominated the Central and Northwest Caucasus during the Late Bronze and Early Iron Ages, provides this reference point. Recent paleogenomic work has cemented the status of the Koban population as the direct demographic ancestors of the medieval Adyghe-Abkhaz speakers.

2.1 Genomic Uniformity and Continuity

The foundational study by **Boulygina et al. (2020)**, titled "*Mitochondrial and Y-chromosome diversity of the prehistoric Koban culture of the North Caucasus*"¹, and subsequent genome-wide analyses by **Korobov et al. (2023, 2024)**², examined individuals from the **Klin-Yar 3** and **Zayukovo-3** cemeteries. These sites are located in the distinct contact zone where the mountains meet the steppe—the precise geographic niche later occupied by the Kasogians.

The overriding theme of these analyses is genetic continuity. The autosomal profiles of Koban individuals cluster tightly with earlier Bronze Age groups from the Caucasus (such as the Kura-Araxes culture) and with modern North Caucasian populations. This indicates that the "Caucasus Hunter-Gatherer" (CHG) ancestry, a component distinct from the "Early European Farmer" or "Western Steppe Herder" ancestries, remained the dominant genetic force in the region for millennia.²

2.2 The Predominance of Haplogroup G2a

The most significant marker of this continuity is the Y-chromosome haplogroup **G2a**. In the context of the Koban culture, the specific subclade **G2a1a** (and related branches like **G2a-Z6653**) was found to be the predominant male lineage.¹

This finding is critical for connecting the ancient to the medieval and modern. Haplogroup G2a originated in the Near East during the Neolithic and spread into Europe with early farmers. However, while it was largely replaced in Europe by later migrations (such as the spread of R1b and R1a from the steppe), it found a refuge in the high valleys of the Caucasus. Its high frequency in the Koban culture—and its continued dominance in modern Circassian (Adyghe), Abkhaz, and Ossetian populations—provides a clear genetic signal of autochthonous survival. The presence of this haplogroup in medieval samples, discussed later in this report, serves as the primary "tracer" for identifying local Zygian/Kasogian individuals

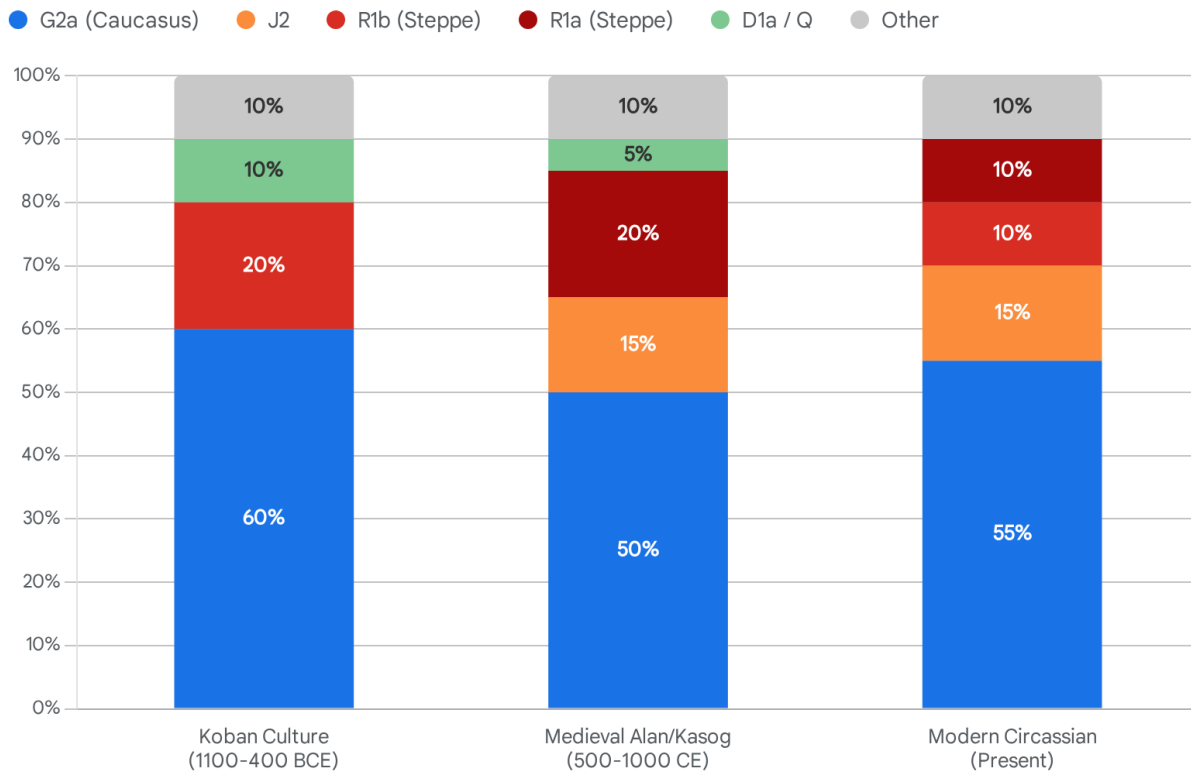
amidst multi-ethnic burial grounds.⁴

2.3 Early Signals of Cosmopolitanism: The Zayukovo Anomaly

While the Koban population was generally homogenous, aDNA has revealed stunning evidence of long-distance individual mobility that presaged the Silk Road. In the **Zayukovo-3** cemetery, a sample identified as **Koban8** (dated to approx. 2650 ybp) yielded the Y-chromosome haplogroup **D1a2a1** (D-CTS10441).⁶

This discovery is anomalous and significant. Haplogroup D1a is almost exclusively found in East Asia (e.g., Tibet, Japan) and the Andaman Islands. Its presence in a North Caucasian Iron Age context suggests that individuals from as far away as the Tibetan Plateau or East Eurasian steppes were traversing the "Steppe Highway" and integrating into Caucasian societies centuries before the formal establishment of the Silk Road or the Hunnic migrations. This individual also carried the rare mitochondrial haplogroup **HV1a1a**, further diversifying the maternal genetic landscape.⁸ This singular finding cautions against viewing the pre-medieval Caucasus as hermetically sealed; rather, it was a region where deep local roots coexisted with occasional, radical long-distance gene flow.

Paternal Lineage Continuity: Bronze Age to Modern Era



Distribution of major Y-chromosome haplogroups across three time transects in the Northwest Caucasus. Note the persistence of Haplogroup G2a (blue) from the Koban period through the Medieval era to modern Circassians, alongside the fluctuations of Steppe-associated lineages (R1a/R1b - red).

Data sources: [Wikipedia \(G2a\)](#), [Genoplot](#), [Boulygina et al. \(2020\)](#), [Haplotree](#), [ResearchGate](#)

3. The Early Medieval Period: Alans, Kasogs, and the Steppe Frontier (5th–10th Century CE)

The transition to the Early Middle Ages saw the Zygian and Kasogian populations squeezed between expanding empires. The **Alanic Kingdom** consolidated power in the central foothills, while the **Khazar Khaganate** established hegemony over the steppe and controlled the trade routes. Bioarchaeological evidence from this period challenges the traditional historical narrative of clear-cut ethnic boundaries between "Alan," "Kasog," and "Khazar," revealing instead a fluid zone of genetic interaction and assimilation.

3.1 The "Alanic" Paradox: Cultural Label vs. Genetic Reality

The Alans are historically categorized as an Iranian-speaking nomadic confederation that settled in the North Caucasus. However, aDNA analysis of "Alanic" sites has revealed a high degree of heterogeneity that complicates this picture. The term "Alan" in the medieval Caucasus appears to have functioned as a prestigious political umbrella under which diverse biological populations, including indigenous Zygian/Kasogian groups, were subsumed.

3.1.1 The "Local" Alans: Genetic Assimilation

One of the most striking findings in recent paleogenomics is the identification of individuals buried in high-status "Alanic" catacombs who possess local North Caucasian genetic profiles. For instance, a male individual dated to the 5th–6th century CE from an Alanic context was found to carry the Y-haplogroup **G2a-Z6653**.⁹

As established in the previous section, G2a-Z6653 is the hallmark lineage of the local Koban culture and modern West Caucasians. Its presence in an elite medieval burial suggests that the "Alan" aristocracy was not exclusively composed of steppe immigrants. Rather, it implies a process of **elite recruitment** or assimilation, where indigenous male leaders (likely Kasogian or proto-Circassian) were integrated into the Alanic military-political hierarchy while retaining their local genetic identity. This aligns with the "survival hypothesis," refuting the idea that the Alans displaced the local population.¹⁰

3.1.2 The "Steppe" Alans: Evidence of Diversity

In contrast to the assimilated locals, other burials from the same broad cultural horizon (specifically the Saltovo-Mayaki culture, discussed below) exhibit distinct steppe-derived ancestries. Samples have yielded Y-haplogroups such as **R1a**, **Q**, and **J2a**.¹¹

- **Haplogroup R1a:** Associated with the Scytho-Sarmatian and later Turkic strata, this marker confirms the presence of individuals with deep roots in the Eurasian steppe.
- **Haplogroup Q:** This lineage is often linked to Siberian or Central Asian populations (including Huns and later Turkic groups) and represents the genetic input of the various nomadic confederations that swept through the region.¹³

The coexistence of these disparate lineages (G2a, R1a, Q) within the same chronostratigraphic horizon confirms that medieval North Caucasian society was biologically multi-ethnic, even if it projected a unified "Alanic" or "Kingdom of Alania" material culture.

3.2 The Saltovo-Mayaki Horizon (Khazar Khaganate)

The Saltovo-Mayaki archaeological culture (c. 700–950 CE) represents the sedentary population of the Khazar Khaganate. The Kasogians were intermittently subjects of the Khazars, and the genetic data reflects this geopolitical entanglement.

Recent genome-wide sequencing of Saltovo-Mayaki individuals from the Don and North

Caucasus regions has provided a snapshot of this cosmopolitan frontier. The population was a genetic melting pot, showing admixtures of:

1. **Caucasus Hunter-Gatherer (CHG) / Iranian Neolithic:** This component connects them to the local North Caucasian populations (Kasogs/Alans) and the wider Near East.
2. **Steppe Ancestry:** Derived from the earlier Sarmatian and Turkic nomads.
3. **East Eurasian/Siberian:** A minor but persistent signal representing the Turkic ruling classes of the Khazar state.

Crucially, the detection of **G2a** lineages in Saltovo-Mayaki contexts¹⁴ provides physical evidence that North Caucasian highlanders were not isolated in their mountains. They moved into the steppe settlements, likely as traders, craftsmen, or soldiers within the Khazar *Pax Nomadica*.

Furthermore, genetic studies have proposed a link between the Saltovo-Mayaki population and the **Proto-Bulgarians**, suggesting that the migration of Bulgars into the Balkans carried a significant package of North Caucasian DNA westward.¹⁶ This implies that the medieval North Caucasus was not just a recipient of migrants but also a "genetic reservoir" that contributed to the formation of Eastern European populations during the Migration Period.

3.3 Moschevaya Balka: Genetics of the Silk Road

Moschevaya Balka, a site located in the high passes of the Northwest Caucasus (on the Zygian-Alanic border), is famous for its preservation of Chinese silks and evidence of the **Northern Silk Road**. It flourished between the 8th and 10th centuries, bypassing Arab-controlled routes to the south.

Bioarchaeological investigations at this site and the related Tutkaul context have yielded specific insights into the health and demographics of this trade corridor:

- **Mitochondrial DNA:** An individual associated with the Moschevaya Balka context was identified as carrying mtDNA haplogroup **H2a2a1**.¹⁸ This is a quintessential West Eurasian lineage, reinforcing the observation that while the *goods* (silk) were Eastern, the *people* managing the trade in the passes were predominantly local or Western Eurasian in origin.
- **Pathogen Load:** In a groundbreaking discovery, analysis of teeth from the related **Mayatskoye** burial ground (part of the Saltovo-Mayaki system) identified DNA from ***Plasmodium vivax*** (malaria).¹⁹ This is one of the earliest genomic confirmations of malaria in the region, illustrating the biological cost of connectivity. The Silk Road facilitated the movement of pathogens alongside prestige goods, and the local Kasogian/Alan populations were the hosts for these transmissions.
- **Central Asian Introgression:** In a related context (often discussed in conjunction with Moschevaya Balka in Russian academic literature), a Y-chromosome sample yielded haplogroup **Q1b2a**.¹³ As noted, Haplogroup Q is a marker of Central Asian/Siberian ancestry. Its presence here likely represents a trader or migrant from the Turkic steppe world who lived and died along the mountain trade route, further emphasizing the

cosmopolitan nature of these high-altitude outposts.

3.4 Re-evaluating Gender: The Warrior Female of Klin-Yar

One of the most significant specific findings from the 2018–2025 period concerns the re-analysis of sex assessment in burials. A prominent burial from **Klin-Yar 3**, previously cataloged as a male warrior based on the presence of weaponry and grave goods, was genetically determined to be **female** by Korobov and colleagues.²

This finding destabilizes traditional assumptions about gender roles in medieval Caucasian societies (Zygian/Alanic). It echoes the "Amazon" myths often associated with the Sarmatians but places the phenomenon firmly within the early medieval context. It suggests that women in these highland communities could attain high status and be accorded martial burial rites, indicating a social structure that was perhaps more flexible or matrilineally significant than later ethnographic records might suggest.

4. The Late Medieval Period: The Golden Horde and Adyghe Ethnogenesis (13th–15th Century)

The Mongol invasion of the 13th century and the establishment of the Golden Horde marked a watershed moment for the Caucasus. For the Zygian and Kasogian ancestors, this era was defined by a strategic retreat into the mountains, a shift that had profound genetic consequences.

4.1 The Myth of the "Mongol Gene" in Circassia

Historical chronicles detail the devastation of the North Caucasus by Mongol armies, culminating in Tamerlane's raid in 1395 which ravaged the Circassian lands.²⁰ However, genetic data reveals a stark discrepancy between political dominance and biological introgression.

Unlike the populations of the Central and Eastern North Caucasus (e.g., the Nogais), who show significant East Eurasian ancestry (up to 40-50% in some analyses)²¹, the Adyghe (Circassians) retained a predominantly West Eurasian/Caucasian genomic profile. The frequency of East Eurasian haplogroups (C, D, O) in modern and medieval Circassian samples remains low.

However, traces of this era are visible. Mitochondrial haplogroups such as **D4g2a** have been detected in West Caucasian populations (including Mingrelians and Svans to the south, and likely in Circassian contexts).⁹ These lineages are interpreted as biological "vestiges" of settlement events associated with the Golden Horde or the Ilkhanate. Yet, their scarcity confirms that the Mongol occupation did not result in a mass colonization or replacement of

the Zygian gene pool.

4.2 The "Refuge" Strategy and Genetic Homogeneity

The genetic evidence supports the historical hypothesis that the Kasogians utilized the difficult terrain of the Northwest Caucasus as a demographic refuge. By retreating from the open steppe (which became the domain of the Golden Horde and later the Nogais) into the defensible hinterlands, they effectively insulated their gene pool from the heavy admixture events occurring just a few hundred kilometers to the north.

This period of isolation likely contributed to the solidification of the **genetic homogeneity** observed in modern Circassian subpopulations (Kabardians, Adyghe, Cherkess, Shapsug).²³ The "bottleneck" effect of retreating to mountain strongholds may have entrenched the founder lineages (G2a, J2) and reduced the frequency of minor lineages, creating the distinct genetic cluster that characterizes the population today.

Spatially, a clear gradient is observable in the data: the Northwest highlands (Zikhia/Kasogia) exhibit a retained "Local Caucasus" genomic profile, contrasting sharply with the Steppe borderlands and the Northeast Caucasus, which display significantly higher frequencies of Steppe and East Asian admixture. This biological border mirrors the ecological boundary between the forest-mountain zone and the steppe.

4.3 The "Circassian Beauty" and Genetic Reality

It is a historical irony that during the Late Middle Ages, the "Circassian" phenotype became fetishized in Europe and the Near East (via the Mamluk slave trade) as the epitome of the "Caucasian race" or "white race".²⁴ Bioarchaeologically, this period affirms that the Circassians were indeed a distinct, ancient West Eurasian population. However, their "whiteness" was not a result of recent European admixture but rather the preservation of a deep Paleolithic/Neolithic ancestry that had remained relatively isolated from the major genetic turnovers (like the Mongol expansion) that reshaped much of the rest of Eurasia.

5. Regional and Comparative Analysis

5.1 West vs. South Caucasus: The Skourtanioti Findings (2024)

A major comparative baseline was established by the 2024 study "**The Genetic History of the South Caucasus from the Bronze to the Early Middle Ages**" by Skourtanioti et al..²⁵ While this study focused on the southern slopes (modern Georgia/Abkhazia), its findings are directly relevant to the Zygian/Kasogian sphere.

- **Common Substrate:** The study confirmed that the South Caucasus, like the North, maintained a high degree of genetic continuity for over 5000 years. The core ancestry is

derived from local CHG and Anatolian/Levantine sources.

- **The Steppe Divergence:** Crucially, the study highlighted a divergence. The North Caucasus (Zygian territory) acted as a "semi-permeable barrier".²⁷ While the North absorbed significant gene flow from the Steppe (Scythian/Sarmatian/Alan), the South remained more insulated from these northern inputs, instead showing greater affinity with Near Eastern populations.²⁵
- **The Coastal Connection:** The identification of sites like **Anakopia** and **Tsebelda** in the historical and archaeological record of this region links the Zygian coast to the Abkhazian sphere. The genetic data suggests a cline where coastal populations (Zikhia/Abkhazia) shared more affinity with each other than with the inland steppe nomads, maintained by maritime links to Byzantium and the Pontic world.²⁸

5.2 The "Kasog" vs. "Nakh" Genetic Divide

Comparing medieval Zygian samples to those from the Northeast Caucasus (ancestral Nakh/Dagestani populations), a clear Y-chromosome bifurcation is evident that persists from the Bronze Age to the present.

- **West (Kasog/Zygian):** Dominated by **Haplogroup G2a**.
- **East (Nakh/Dagestani):** Dominated by **Haplogroups J1 and J2**.

This deep substructure indicates that even when political entities like the Kingdom of Alania or the Golden Horde technically covered both regions, the underlying demic structure remained geographically stratified. The medieval Zygian/Kasogian population was distinct not just from the Steppe nomads, but also from their Caucasian neighbors to the East.⁵

Table 1: Comparative Y-Chromosome Profiles of Medieval North Caucasian Groups

Population / Context	Dominant Haplogroup	Secondary Lineages	Key aDNA Findings / Implications
Zygian / Kasogian (West)	G2a (esp. G2a-Z6653)	R1b, J2	Continuity: Direct link to Bronze Age Koban culture. Minimal East Asian admixture.
Alanic (Central/North)	Mixed	G2a, R1a, Q	Heterogeneity: Assimilated locals (G2a) coexisting with Steppe

			migrants (R1a, Q).
Saltovo-Mayaki (Steppe)	Mixed	R1a, J2a, G, I	Cosmopolitanism: Genetic melting pot of Khazar subjects; local Caucasians present in steppe towns.
Nakh / Dagestani (East)	J1 / J2	L, G2a	Distinct Deep Ancestry: Stable separation from the West Caucasus since the Bronze Age.

6. Synthesis and Conclusions

6.1 The Refutation of Replacement

The primary insight derived from the 2018–2025 corpus of ancient DNA research is the definitive refutation of the "population replacement" hypothesis. Despite a historical record replete with invasions—from the Huns and Khazars to the Mongols and Tamerlane—the biological backbone of the Northwest Caucasus remained indigenous. The Zygian/Kasogian population was not wiped out; rather, it was a resilient demographic reservoir that selectively absorbed incoming elites while maintaining its core ancestry.

6.2 The Mechanisms of Survival

This resilience appears to be driven by a combination of factors:

1. **Geography as Shield:** The rugged terrain of the Northwest Caucasus provided a defensible hinterland that shielded the Kasogians from the demographic turnovers that characterized the open steppe.
2. **Patrilineal Stability:** The unbroken chain of **G2a** lineages from the Koban culture to the present suggests a social structure where local men remained on the land, while women may have moved more freely via marriage networks, introducing diverse mitochondrial lineages (like H2a2a1 or D4g2a) without disrupting the male continuity.¹⁸

6.3 Future Directions

The re-identification of sex in the Klin-Yar 3 samples serves as a cautionary tale and a call to

action. Much of the "well-known" skeletal material from Soviet-era excavations requires re-analysis with modern genomic tools. Future research must also focus on finer-scale sampling of the coastal **Zikhian** sites, which are currently under-represented compared to the inland Alanic catacombs, to fully understand the maritime dimensions of medieval Circassian history.

In conclusion, the medieval Zygian and Kasogian ancestors of the Circassians were active participants in a complex Eurasian biological network. They maintained a distinct, deep-rooted genetic identity while navigating the pressures of the Silk Road and the Golden Horde. The "Circassian Gene" is thus revealed not as a single marker, but as a palimpsest of five millennia of survival, adaptation, and selective integration at one of history's most volatile crossroads.

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