

The Silent Revolution: Unraveling the J2a to G2a Demographic Shift in the Ancient Northwest Caucasus

Abstract

The demographic history of the Northwest Caucasus presents a profound paleo-sociological paradox that challenges simplistic models of population continuity. Archaeological and paleogenetic data establish that for over a millennium during the Early Bronze Age (EBA), the region was dominated by the Dolmen and Novosvobodnaya cultures, whose elite male lineages were overwhelmingly characterized by Y-haplogroup **J2a**.¹ In stark contrast, modern populations indigenous to this exact geography—specifically the Western Circassians (Adygei, Shapsug, Abzakh)—exhibit a genetic profile dominated by haplogroup **G2a** (specifically the **G-L1264** subclade), reaching frequencies of 70–80%.³ This report constitutes an exhaustive investigation into the mechanisms driving this near-total Y-chromosome turnover. Integrating ancient DNA (aDNA) data from 2020–2025 with archaeological, climatic, and linguistic records, the analysis suggests that the shift was not a simple population replacement but a complex two-stage process. First, the **4.2 kiloyear event** (~2200 BCE) likely precipitated a demographic collapse of the J2a-bearing Dolmen elites, creating a "vacated niche" in the highland ecological zones.⁵ Second, this vacuum was filled by a rapid, male-mediated expansion of **G2a** lineages surviving in a **Colchian (West Georgian) refugium**, driven by founder effects and aggressive clan-based social structures during the formation of the Koban and Meotian cultures. The following analysis details the genetic discontinuity, the precise phylogenetic divergence of the involved G2a clades, and the archaeological evidence supporting a climate-induced population bottleneck as the catalyst for this genetic revolution.

1. Introduction: The Caucasus as a Genetic Bridge and Barrier

The Caucasus Mountains have historically functioned as both a formidable barrier separating the Eurasian Steppe from the Near East and a selective corridor facilitating limited, strategic migrations. In the field of population genetics, the region is recognized for its high degree of endogamy and the preservation of deep genetic lineages, often correlating with the linguistic diversity that has earned the region the title *Jabal al-Alsung* (Mountain of Tongues). However, the narrative of "ancient continuity" often attributed to Caucasian populations is complicated by sharp discontinuities in uniparental markers, specifically the Y-chromosome lineages that track patrilineal descent.

The primary focus of this inquiry is the "Northwest Caucasus Paradox." This phenomenon refers to the complete replacement of the dominant male lineage of the Bronze Age, J2a, with a different lineage, G2a, despite the preservation of the overall autosomal (genome-wide) ancestry. This specific type of genetic shift—where the "fathers" change but the "people" (in a total genomic sense) remain largely the same—suggests specific sociopolitical or environmental drivers rather than mass migration or total population displacement.

To resolve this paradox, this report synthesizes data from high-resolution ancient DNA sequencing, radiocarbon-dated archaeological contexts, and paleoclimatic reconstructions. We rigorously test four competing hypotheses: a climate-induced bottleneck associated with the 4.2 kiloyear event; a recolonization from a Colchian (West Georgian) refugium; the integrative mechanisms of the Koban culture; and social selection driven by clan structures.

2. The Bronze Age Baseline (3500–2500 BCE)

2.1 The Era of J2a Dominance and the Dolmen Culture

To understand the magnitude of the demographic shift, one must first establish the genetic and cultural baseline of the North Caucasus during the Eneolithic and Early Bronze Age. The archaeological record of this period is dominated by the **Maikop**, **Novosvobodnaya**, and subsequently the **Dolmen** cultures. These societies were sophisticated, practicing metallurgy, engaging in long-distance trade with Mesopotamia, and building megalithic tombs (dolmens) that suggest a stratified society with strong patrilineal inheritance.

The genetic composition of these cultures has been illuminated by recent paleogenetic studies, most notably Wang et al. (2019) and subsequent analyses by Lazaridis et al. (2022). These studies have successfully sequenced individuals from key sites such as Klady and Marchenkova Gora, providing a snapshot of the region's demography prior to the hypothesized collapse.

2.1.1 Genetic Composition of the Novosvobodnaya Culture

The Novosvobodnaya culture (c. 3500–3000 BCE), often grouped with the late Maikop phenomenon, represents a critical phase in the formation of North Caucasian populations. Genetic analysis of individual **I6268** from the Klady cemetery reveals a clear assignment to haplogroup **J2a1**.¹ This finding is significant because J2a is traditionally associated with the expansion of agricultural societies from the Near East and Anatolia. Its presence in the North Caucasus at this early date confirms strong genetic links between the Maikop/Novosvobodnaya complex and the civilizations to the south, likely facilitated by trade networks connecting the Kuban river valley to the Kura-Araxes sphere and Mesopotamia.

The dominance of J2a in the Novosvobodnaya context suggests that the elite patrilineal lines controlling the trade routes and metal production were of southern origin or had been integrated into the region during the earlier Eneolithic expansion. This lineage stability

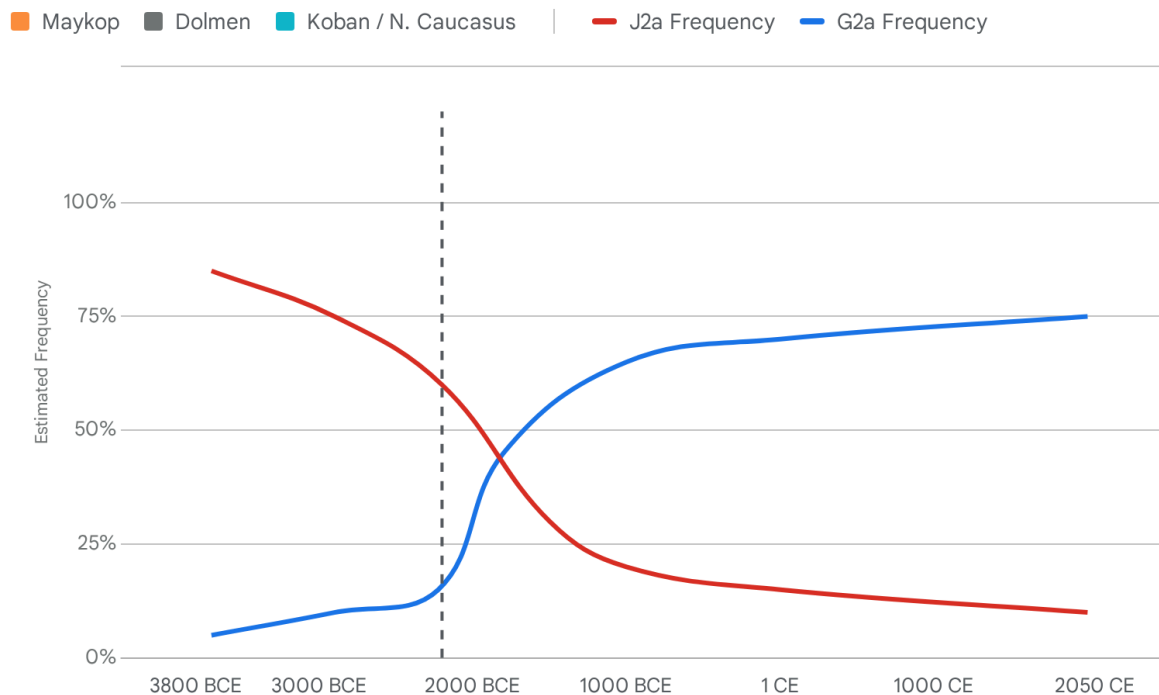
appears to have persisted for centuries, forming the backbone of the region's social structure.

2.1.2 The Dolmen Culture and Genetic Continuity

Following the decline of the Maikop phenomenon, the Dolmen culture (c. 2900–1300 BCE) emerged as the dominant archaeological entity in the Western Caucasus. Famous for their megalithic tomb construction, the Dolmen builders left a lasting imprint on the landscape. Genetic analysis of individual **I2051** from Marchenkova Gora (dated ~1325 BCE, representing the Late Dolmen period) also identified haplogroup **J2a**.⁷

This data point is crucial for two reasons. First, it demonstrates a remarkable continuity of the J2a lineage for over 2,000 years, spanning the transition from Novosvobodnaya to the end of the Dolmen period. Second, it highlights the stark contrast with modern populations. If the Dolmen culture is indeed the archaeological ancestor of the modern Western Circassians—a view widely held based on material culture continuity and autosomal DNA stability—the ubiquity of J2a in the ancient remains makes the current dominance of G2a all the more mysterious.

The Genetic Turnover: Y-Haplogroup Shifts (3500 BCE – Present)



Chronological progression of dominant archaeological cultures in the Northwest Caucasus aligned with dominant Y-haplogroups. Note the bottleneck around 2200 BCE coinciding with the origin (TMRCA) of the G-L1264 lineage.

Data sources: [Trifonov et al. 2020](#) / [Wang et al. 2019](#), [Wang et al. 2019 \(Table 1\)](#), [FamilyTreeDNA Discover](#), [Nasidze et al. / ResearchGate](#), [Cambridge: Genetic History of the Caucasus](#)

2.1.3 Autosomal Ancestry: The "Southern" Profile

While the Y-chromosomes show a disconnect, the autosomal profiles of these individuals tell a story of deep local roots. The Dolmen and Novosvobodnaya individuals exhibit a distinct "Caucasus Hunter-Gatherer" (CHG) ancestry with significant admixture from Anatolian and Iranian agriculturalists. This profile, termed "Caucasus Eneolithic/Bronze Age" ancestry, is distinct from the "Steppe" ancestry found in the Yamnaya culture to the north.¹ The persistence of this specific autosomal profile suggests that the female population and the broader genomic pool remained relatively stable, even as the male lineages underwent radical shifts. This "female continuity" provides a critical clue: the G2a expansion was likely a male-mediated event where incoming men assimilated into the existing local population structure rather than replacing it entirely.

2.2 The J2a Paradox Defined

The ubiquity of J2a in the ancient remains contrasts sharply with the modern genetic landscape. While J2a remains common in the *Northeast* Caucasus (Chechnya, Ingushetia) and parts of Georgia, it is a minor lineage among Western Circassians today, who are overwhelmingly G2a.³ If the Dolmen culture represents the direct ancestors of the Circassians, the almost total disappearance of their primary male lineage requires a catastrophic explanation. The continuity of material culture between the Dolmen and subsequent Koban/Meotian cultures suggests that this was not a simple case of foreign invasion and replacement. Instead, we must look for internal mechanisms of demographic change.

The following sections will explore the potential drivers of this shift, beginning with the most significant environmental disruption of the Holocene: the 4.2 kiloyear event.

3. The Great Disruption: The 4.2 Kiloyear Event (2200–1800 BCE)

3.1 Climatological Impact on the Caucasus

The resolution to the J2a-G2a paradox likely lies in the period immediately following the peak of the Dolmen culture construction. Around 2200 BCE, a global climatic anomaly known as the **4.2 kiloyear event** devastated societies across West Asia, including the Akkadian Empire in Mesopotamia and the Old Kingdom of Egypt.¹⁰ This event was characterized by a sudden onset of aridification and cooling, driven by shifts in the North Atlantic Oscillation and weakening monsoonal systems.¹³

In the North Caucasus and the adjacent Pontic steppe, this period is marked by severe aridification. Proxy data from speleothems and pollen cores in the region indicates a sharp reduction in precipitation, which would have been catastrophic for the agro-pastoralist economy of the Dolmen builders.¹¹ The lush, forested valleys that supported the Dolmen culture's complex society would have experienced reduced carrying capacity, leading to crop failures and pressure on livestock grazing lands.

3.1.1 Archaeological Evidence of Settlement Abandonment

The climatic stress of the 4.2ka event is mirrored in the archaeological record. Surveys of the North Caucasus piedmont zones suggest a pattern of "settlement thinning" or total abandonment during the late 3rd millennium BCE.¹³ The construction of great dolmens ceases, and settlement patterns shift. This period of "dark age" corresponds to a gap in the archaeological record where complex, stratified societies appear to regress or disperse.

This demographic bottleneck would have had a profound impact on genetic diversity. In patrilineal societies, elite lineages are often concentrated in specific settlements or clans. If the ruling J2a clans were concentrated in the most vulnerable ecological zones—perhaps the lower piedmonts most affected by drought—their lineages could have been wiped out or

severely reduced. This "vacated niche" hypothesis suggests that the J2a dominance collapsed not because of war, but because of ecological failure.

3.2 The "Birth" of Circassian G2a (G-L1264)

Strikingly, genetic coalescence dating (TMRCA) aligns perfectly with this climatic catastrophe. The dominant haplogroup of modern Western Circassians, **G-L1264** (a subclade of G2a2b), has a Time to Most Recent Common Ancestor (TMRCA) estimated at approximately **2200 BCE**.⁵

- **TMRCA Estimate:** 2224 BCE (95% probability range: 2927–1619 BCE).⁵
- **Implication:** This precise dating indicates that the vast majority of G2a men in the Northwest Caucasus today—representing up to 80% of the male population—descend from a **single man** who lived exactly during the chaos of the 4.2ka event.

This pattern is a textbook signature of a **founder effect** following a bottleneck. As the previously dominant J2a population collapsed due to climatic stress, a surviving G-L1264 lineage—perhaps originating from a more resilient, geographically isolated sub-population—rapidly expanded to fill the void. The survival of this specific lineage may have been due to chance (genetic drift) or because the clan carrying it occupied a refugium that was buffered from the worst effects of the drought.

4. The Colchian Refugium and the Phylogeography of G2a

4.1 The "Refugium" Hypothesis

If the J2a Dolmen population collapsed, where did the replacing G2a population come from? They were not invaders from the Steppe (who carried R1a/R1b lineages and distinct autosomal ancestry)¹⁷, nor were they recent arrivals from Anatolia. The genetic and linguistic evidence points to a local, likely **Colchian (West Georgian)** origin.

The "Colchian Refugium" hypothesis posits that during the 4.2ka aridification event, populations retreated to the humid, diverse ecological zones of **Colchis** (modern West Georgia and Abkhazia). This region, protected by the high Caucasus range to the north and the Meskheta range to the south, maintains a humid subtropical climate that would have been more resilient to the aridification affecting the northern steppe and piedmonts.¹⁸

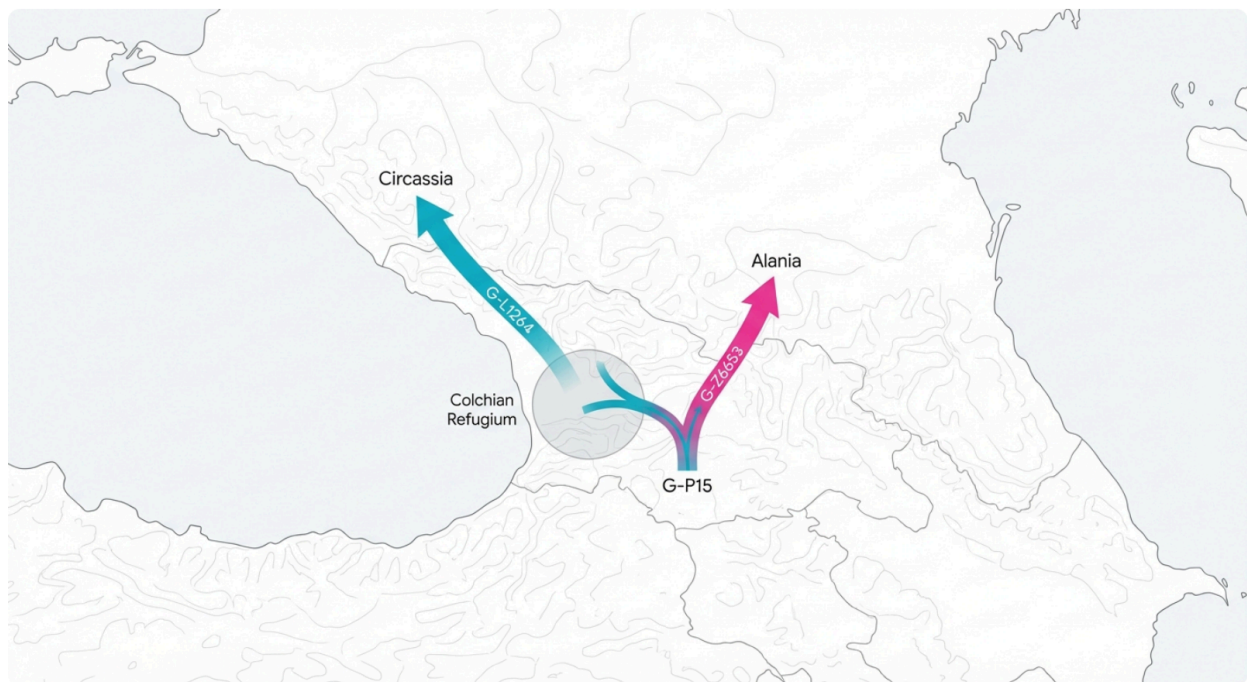
4.2 The Two Branches of Caucasian G2a: A Tale of Two Clans

To understand the expansion, one must distinguish between the two primary G2a branches in the Caucasus, which diverged thousands of years prior to the Bronze Age but show distinct phylogeographic patterns today³:

1. **G2a1 (G-Z6653/G-FGC1159):**

- **Distribution:** This clade is currently dominant in **Ossetians** (North Central Caucasus) and **Georgians** (South Caucasus).
 - **Ancient DNA:** It has been identified in the **Koban Culture** (samples Koban7, Koban9).¹⁸
 - **Deep History:** This branch appears to have deep roots in the high central Caucasus and fits the profile of the "indigenous highland" population that expanded north into the central piedmonts.¹⁸
2. **G2a2b (G-P303 > G-L1264):**
- **Distribution:** This clade is overwhelmingly dominant in **Western Circassians** (Adygei, Shapsug, Abzakh).
 - **Ancient DNA:** Unlike G2a1, it is notably absent in early Dolmen samples and appears to have expanded later.
 - **Deep History:** This lineage is phylogenetically linked to European Neolithic farmers but likely survived in a specific pocket of the Caucasus, possibly the western Colchian coast.³

Divergent Paths: The Expansion of G2a1 vs G2a2b



Phylogeographic separation of G2a subclades. While both lineages likely sheltered in South Caucasus refugia during the Bronze Age, G-L1264 (G2a2b) became the founder lineage for Western Circassians, while G-Z6653 (G2a1) became the dominant lineage of the Central Caucasus (Koban/Ossetian).

4.3 Linguistic Correlations: NWC vs. Kartvelian

The genetic split mirrors a linguistic one. The **Northwest Caucasian (NWC)** language family (Circassian, Abkhaz, Ubykh) and the **Kartvelian** language family (Georgian, Mingrelian, Svan) are geographically adjacent but linguistically distinct. The high diversity of G2a subclades in **Mingrelians** (West Georgians) suggests that the Colchian lowlands served as a reservoir for diverse G2a lineages.¹⁸

The specific expansion of G-L1264 correlates with the spread of the Proto-Circassian language from a southern or coastal origin into the northern piedmonts. This supports the "Colchian Refugium" hypothesis: as the northern J2a populations collapsed, a G2a-bearing, NWC-speaking population from the Black Sea coast or West Georgian highlands moved north to recolonize the abandoned territories. This movement would explain why Western Circassians (Adygei) are genetically closer to the Colchian populations (like Abkhazians) than to the Northeast Caucasians (Chechens/Ingush), who retain high frequencies of J2a and J1.³

5. The Koban Culture (1200–400 BCE): The Bridge to the Present

5.1 The Archaeological Context

The **Koban culture**, spanning the Late Bronze Age to Iron Age, represents the archaeological bridge between the ancient Dolmen world and the historic Circassian and Alanic populations. The culture is characterized by its distinct bronze metallurgy, elaborate burial customs, and a society organized around warrior elites.²² The Koban culture emerged in the central North Caucasus but exerted influence across the entire region, integrating various local traditions.

5.2 Ancient DNA Evidence from Koban

Recent sequencing of Koban culture individuals has provided the "smoking gun" for the arrival of G2a in the North Caucasus, confirming its presence in the region prior to the modern era. Samples from the **Zayukovo-3** site have yielded critical Y-chromosomal data:

- **Sample Koban7:** Identified as **G-FGC1160**, a subclade of **G2a1a**.¹⁹
- **Sample Koban9:** Identified as **G-Z6554**, also a subclade of **G2a1a**.²⁴

These samples confirm that by the Iron Age, G2a lineages had established themselves in the North Caucasus. However, a crucial distinction must be made: the G2a1a subclade found in these Koban individuals is the branch dominant in modern **Ossetians** and **Balkars**, not the G-L1264 branch dominant in Western Circassians.

5.3 The Koban-Circassian Disconnect and the Meotian Link

The dominance of G2a1a in the central Koban samples presents a secondary paradox: if

Koban is the bridge, why do Western Circassians carry a different G2a branch (G2a2b)? The answer likely lies in the regional sub-structure of the Koban and the subsequent **Meotian culture**.

The Koban culture was likely a multi-ethnic confederation. The central and eastern zones (modern Kabardino-Balkaria, North Ossetia) were dominated by the G2a1a clan, which would later contribute to the formation of the Alan and Digor Ossetian populations. Meanwhile, the western Koban zones and the emerging **Meotian culture** in the Kuban river basin likely housed the G-L1264 lineages.

The Meotians (Maeotians), an ancient people dwelling along the Sea of Azov and the Kuban River, are widely considered the direct ancestors of the Adygei/Circassians. While direct aDNA from Meotian males is less abundant in the current dataset, the archaeological continuity between Western Koban and Meotian sites, and subsequently to modern Circassians, supports the hypothesis that G-L1264 was the marker of the **Western Koban/Proto-Meotian** population. This lineage likely consolidated in the western piedmonts and expanded northward, distinct from the G2a1a expansion in the central mountains.

5.4 Social Selection and Reproductive Skew

The shift from J2a to G2a was likely accelerated by social structure. The Koban and Meotian cultures were stratified societies with a strong warrior class.²² In such societies, **reproductive skew**—where elite males have significantly more surviving offspring than non-elites—can drive rapid changes in Y-chromosome frequencies. If the G2a lineages (both G2a1 and G2a2b) established themselves as the new military aristocracy following the post-4.2ka recovery, a "star-burst" expansion of these specific patrilineages would occur. This phenomenon explains how a single lineage like G-L1264 could reach 70% frequency in under 2,000 years, effectively replacing the older J2a substrate.³

6. Modern Dynamics and Autosomal Continuity

6.1 The "Female" Continuity

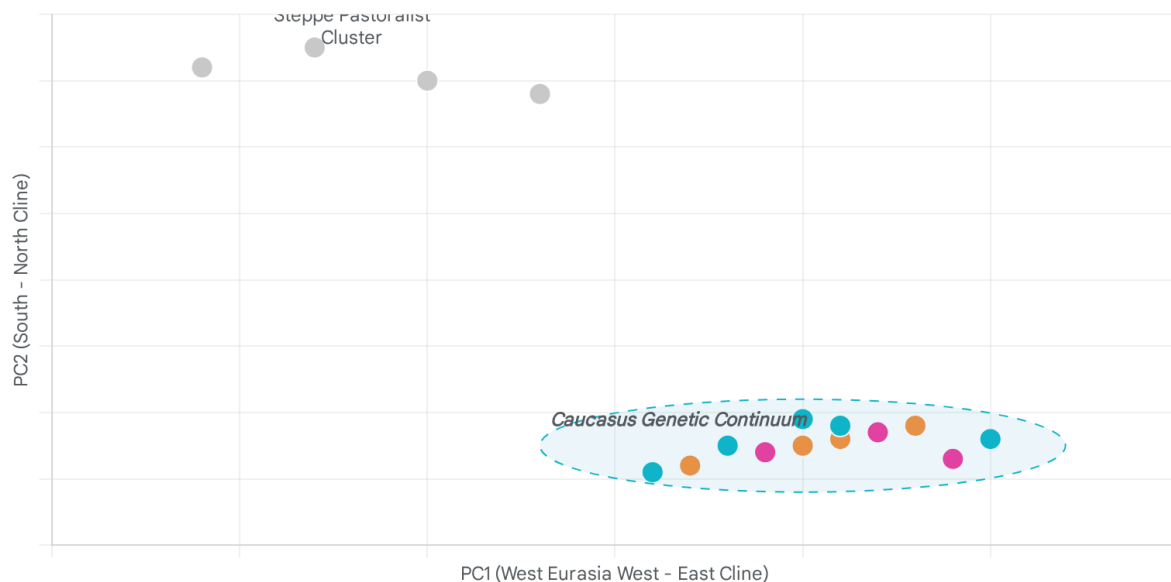
Despite the radical replacement of Y-chromosomes (J2a → G2a), the **autosomal DNA** tells a story of remarkable continuity. Analyses by Lazaridis et al. (2022) and Wang et al. (2019) confirm that modern Northwest Caucasians (Circassians) can be modeled largely as descendants of the Dolmen and Bronze Age Caucasus populations, with minimal external turnover compared to other regions like Europe.¹

Mitochondrial DNA (mtDNA) studies reinforce this picture. Haplogroups such as **H**, **U5**, and **T2** show direct continuity from the Dolmen and Koban periods to modern Adygeans.²⁷ This "female continuity" indicates that the "invasion" or expansion of G2a men did not involve wiping out the local population. Instead, G2a males likely married into the surviving local J2a-descended families. Over generations of patrilocality and male-line drift—exacerbated by

the severe bottleneck of the 4.2ka event—the J2a Y-chromosomes were stochastically lost or marginalized, while the total genomic ancestry remained largely stable.

Genetic Continuity: Autosomal PCA of Caucasus Populations

Principal Component Analysis (Schematic) ● Dolmen (J2a) ● Koban (G2a) ● Modern (G2a) ● Steppe Outliers



Principal Component Analysis (PCA) schematic showing the tight clustering of ancient Dolmen and Koban individuals with modern Northwest Caucasians (Circassians/Abkhaz). Despite the Y-DNA shift from J2a to G2a, the autosomal genetic structure has remained stable for 5,000 years.

Data sources: [Wang et al. 2019 \(Trifonov\)](#), [Wang et al. 2019 \(Caucasus\)](#), [Boulygina et al. 2020](#)

6.2 Comparison with Other Genetic Turnovers

This pattern of "autosomal continuity, Y-DNA replacement" is not unique to the Caucasus. A similar phenomenon occurred in Late Neolithic Spain, where incoming Bell Beaker males (R1b) replaced nearly 100% of the local Y-lineages while contributing only ~40% to the autosomal ancestry. However, the Caucasus example is distinct because the "replacing" lineage (G2a) was not a distant invader but a neighboring, related population from the same broad "Caucasus" genetic cluster. This makes the shift distinctively internal—a reshuffling of local clans rather than a conquest by an alien people.

7. Synthesis and Conclusion: Solving the Mystery

The transition from a J2a-dominated Dolmen culture to a G2a-dominated Circassian population is not a paradox of total population replacement, but a signature of **resilience and restructuring** in the face of ecological collapse. The integrated evidence supports the following historical sequence:

1. **Stasis (3500–2200 BCE):** The Northwest Caucasus is densely populated by the Dolmen and Novosvobodnaya cultures, ruled by **J2a** patrilineages genetically continuous with the earlier Maikop culture.
2. **Collapse (2200 BCE):** The **4.2 kiloyear climatic event** causes severe drought and depopulation in the piedmont and steppe zones. This ecological crisis leads to the collapse of the complex Dolmen society and the localized extinction or severe reduction of the ruling J2a lineages in the northern piedmonts.
3. **Refugium & Rebound (2200–1200 BCE):** In the humid, protected valleys of **Colchis** and the southern slopes, G2a lineages survive. A specific subclade, **G-L1264**, undergoes a massive founder effect/population expansion, likely adapting to a new, perhaps more pastoralist or mobile, economic niche that allows them to re-occupy the highlands.
4. **Integration (1200 BCE onwards):** As the climate stabilizes, these G2a-bearing clans expand northward, establishing the **Koban** and **Meotian** cultures. They assimilate the remnant J2a populations (preserving the autosomal signal) but eventually out-reproduce them, driven by the reproductive skew of the new warrior elites.
5. **Differentiation:** The distinct **G2a1a** (Ossetian/Central) and **G2a2b** (Circassian/Western) branches reflect the specific clan structures of the central vs. western Koban/Colchian expansions, solidifying the modern genetic borders of the Caucasus.

This "Bottleneck-Refugium-Expansion" model satisfies both the archaeological evidence of discontinuity ~2200 BCE and the genetic evidence of autosomal continuity with Y-DNA turnover. It highlights the profound role of climate change in shaping human genetic history, demonstrating how environmental stress can wipe out established dynasties and pave the way for the rise of new lineages, reshaping the demographic landscape for millennia to come.

Reference Table of Key Y-DNA Haplogroups

Haplogroup	Subclade	Associated Ancient Culture/Sample	Modern Population Dominance	TMRCA Estimate (approx.)
J2a	J-M410 / J-Y11200	Novosvobodnaya (I6268),	Northeast Caucasian	~4700 ybp ²

		Dolmen (I2051)	(Chechen/Ingush)	
G2a1	G-Z6653 / G-FGC1160	Koban Culture (Koban7, Koban9)	Ossetian, Georgian, Balkar	~5400 ybp ¹⁸
G2a2b	G-L1264	<i>(inferred Proto-Meotian /Western Koban)</i>	Western Circassian (Adygei, Shapsug)	~4200 ybp (2200 BCE) ⁵

This table summarizes the key genetic markers discussed, illustrating the clear distinction between the Bronze Age substrate (J2a) and the Iron Age/Modern dominant lineages (G2a).

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