

The Phylogeography and Population Genetics of Haplogroup J2a-SK1313 (J-Y12379) in the Caucasus: A Comprehensive Analysis (2020–2025)

1. Introduction: The Caucasus as a Genetic Refugium and Evolutionary Laboratory

The Greater Caucasus mountain range, extending over 1,100 kilometers between the Black Sea and the Caspian Sea, represents one of the most biologically and anthropologically significant regions in Western Eurasia. It serves not merely as a geographic barrier dividing the Eurasian Steppe from the Near East but as a complex demographic filter and refugium that has preserved human genetic diversity for millennia. In the parlance of population genetics, the Caucasus is often described as a "sink" for lineages, where mountainous topography fosters high degrees of endogamy, genetic drift, and the preservation of ancient haplotypes that have been replaced or diluted in the surrounding lowlands.

This report focuses specifically on the Y-chromosome haplogroup **J2a-SK1313** (phylogenetically equivalent or intimately linked to **J-Y12379** and **J-Y12378**). While the broader J2a (J-M410) macro-haplogroup is ubiquitous across the Mediterranean, Near East, and Central Asia—often associated with the spread of Neolithic agriculture or later civilizations like the Greeks and Phoenicians—the J-SK1313 subclade tells a fundamentally different story. It is not a marker of recent migration but a signal of deep, autochthonous continuity. It represents the genetic legacy of the **Caucasus Hunter-Gatherers (CHG)**, a distinct human population that weathered the Last Glacial Maximum (LGM) in the Colchian refugium and contributed substantially to the genetic makeup of modern Europeans and South Asians.

The scope of this analysis covers the period from 2020 to 2025, synthesizing data from high-resolution Next Generation Sequencing (NGS) tests (such as the Big Y-700), academic population studies, and citizen science projects like the FTDNA J-SK1313 Project.¹ We aim to deconstruct the phylogeographic distribution of this lineage among the core populations of the Caucasus—Georgians (specifically Imeretians, Rachans, and Mingrelians), Ossetians, Circassians, and the Nakh peoples (Chechens and Ingush)—while delineating the precise subclade structures (SK1317, Y26654, Y26651, Z35859) that define these groups. Furthermore, we will critically evaluate Time to Most Recent Common Ancestor (TMRCA) estimates to correlate genetic bifurcation events with archaeological horizons, such as the Kura-Araxes and Colchian cultures, and contrast this indigenous Caucasus lineage with its distant cousins

found in Europe.

1.1 The Genomic Context: Haplogroup J2a in the Caucasus

Haplogroup J2a (J-M410) originated in West Asia approximately 31,000 to 43,000 years ago.³ In the context of the Caucasus, J2a is one of the dominant paternal lineages, but it is not monolithic. The genetic landscape of the region is characterized by sharp phylogenetic divides that mirror linguistic boundaries.

- The **Nakh peoples** (Chechens and Ingush) in the Northeast Caucasus are dominated by the **J2a-M67** clade (specifically J-Z1847), which represents a distinct founder effect separate from the Western Caucasus.⁴
- The **Kartvelian peoples** (Georgians), particularly in the west, and the **Northwest Caucasian peoples** (Abkhaz, Circassians) harbor the **J-SK1313** clade.

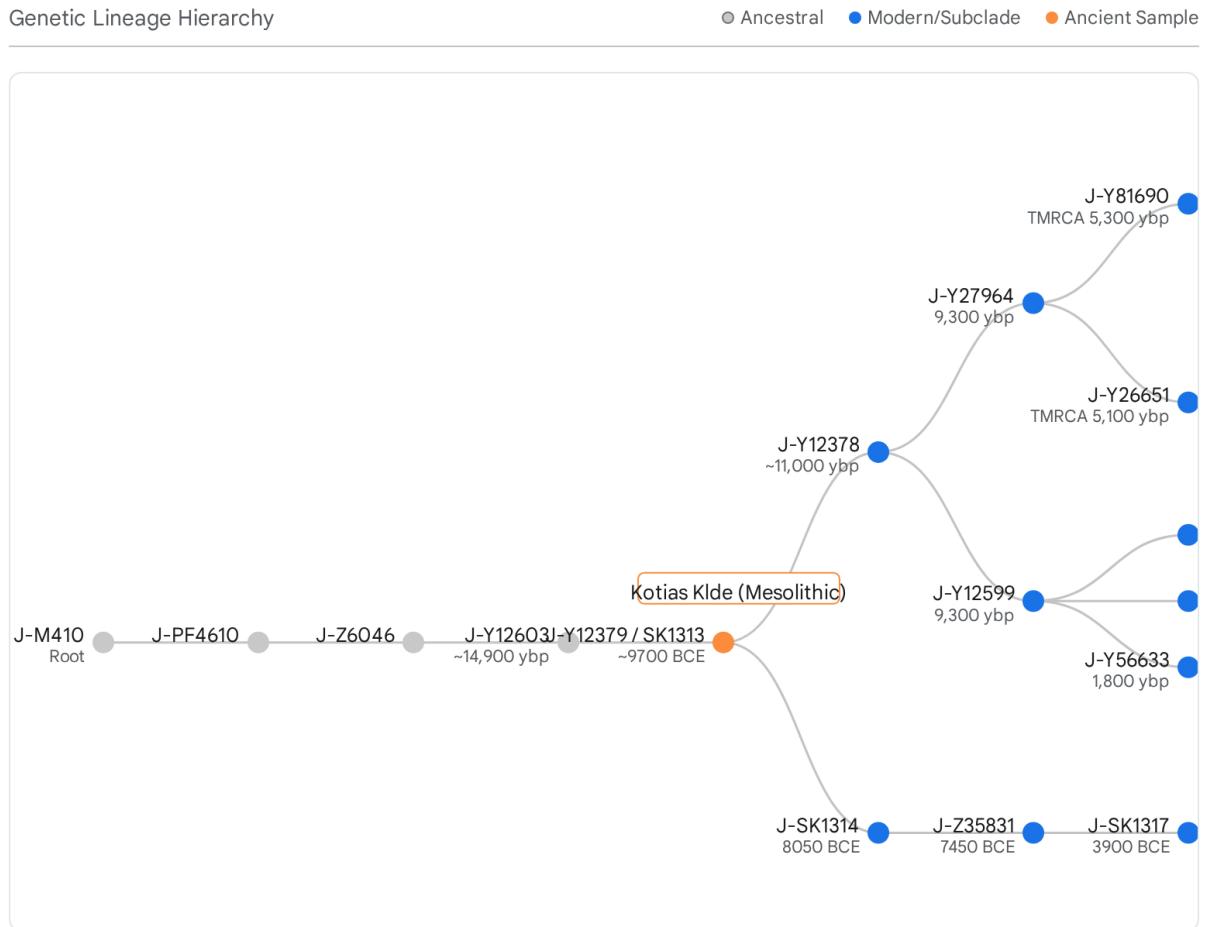
Understanding this dichotomy is essential. To lump all "J2a" together in the Caucasus is to obscure 15,000 years of distinct demographic history. J-SK1313 is the "Colchian" J2a, representing the western and central evolutionary trajectory, while J-M67 is the "Nakh" J2a, representing the eastern trajectory.

1.2 Methodology and Data Sources

The conclusions in this report are derived from a synthesis of:

1. **Ancient DNA (aDNA):** Direct comparison with the **Kotias Kide** Mesolithic genome¹, which anchors the J-SK1313 lineage to the Imereti region at 9,700 BCE.
2. **Modern Population Frequency Data:** Aggregated from the FamilyTreeDNA J-SK1313 Project (131+ members)², the Ossetian DNA Project⁶, the Chechen-Noahcho DNA Project⁷, and academic papers (e.g., Wang et al. 2019, various years).
3. **Phylogenetic Trees:** Utilization of the YFull and FTDNA Haplotrees⁸ to determine the precise branching order and age estimates of subclades like SK1317 and Z35859.

Phylogenetic Tree of J-SK1313 and Key Subclades



The lineage descends from J-M410 and J-PF4610. The 'Kotias Klde' ancient sample anchors the tree at the Y12379 level. Major branches formed during the Neolithic and Bronze Ages.

Data sources: [FTDNA J2-SK1313](#), [FTDNA Discover](#), [FTDNA Path](#), [FTDNA Project Results](#)

2. The Ancient Anchor: Kotias Klde and the Mesolithic Roots

The scientific narrative of Haplogroup J-SK1313 was revolutionized in 2015 with the sequencing of an ancient individual known as **KK1**, discovered in the **Kotias Klde** cave in Western Georgia (Imereti region). This discovery transformed J-SK1313 from an obscure cluster of modern DNA results into a pivotal lineage for understanding the peopling of Eurasia.

2.1 The Kotias Klde Individual (KK1)

The remains found in Kotias Klde date to approximately **9,700 BCE** (Mesolithic period).¹ This timeframe corresponds to the pre-agricultural hunter-gatherer societies that inhabited the Caucasus following the retreat of the Pleistocene glaciers.

- **Genetic Assignment:** The individual was assigned to Y-haplogroup **J2a-Y12379***.¹ In the current phylogenetic nomenclature, J-Y12379 is the direct parent or equivalent level to J-SK1313. This indicates that the modern men carrying J-SK1313 are direct patrilineal descendants (or extremely close collateral relatives) of this specific hunter-gatherer population.
- **Autosomal Profile (CHG):** KK1 is the type specimen for the **Caucasus Hunter-Gatherer (CHG)** autosomal component.² The CHG genome is a major ancestral component of the **Yamnaya** steppe pastoralists (who formed from the admixture of CHG and Eastern Hunter-Gatherers) and, by extension, a significant ancestor of modern Europeans. However, while the *autosomal* CHG ancestry spread west into Europe via the Steppe, the *Y-chromosomal* lineage J-SK1313 largely remained in the Caucasus.

2.2 Implications of Continuity

The discovery of KK1 in Imereti, combined with the high frequency of J-SK1313 in modern Imeretians and Mingrelians¹, provides indisputable evidence of **genetic continuity spanning nearly 12,000 years**.

- **Refugia Dynamics:** During the Last Glacial Maximum (LGM), the Colchian lowland (modern Western Georgia) acted as a warm refugium for flora, fauna, and humans.¹³ As the climate warmed in the Holocene, these populations expanded into the highlands (Svaneti, Racha) and the North Caucasus.
- **Resistance to Replacement:** Despite millennia of invasions—by Scythians, Greeks, Romans, Persians, Mongols, and Ottomans—the paternal lineage of the original Mesolithic inhabitants was never replaced. It remains the dominant signal in the West Georgian gene pool. This suggests a high degree of social resilience and demographic stability in the Colchian populations.

3. Phylogenetic Architecture of J-SK1313

To fully grasp the history of this lineage, we must dissect its internal structure. The J-SK1313 tree is not a straight line but a complex bush of branches that formed during critical periods of Caucasus prehistory.

3.1 The Basal Structure (J-M410 to J-Y12379)

The path from the root of J2a to our specific clade defines its deep history:

- **J-M410 (J2a):** The macro-haplogroup, formed ~31,000+ ybp in West Asia.³
- **J-PF4610:** A major bifurcation. While sibling clades like J-L26 moved toward the Fertile Crescent, PF4610 became established in the highland zone between Anatolia and the Caucasus.¹⁴
- **J-Z6046 > J-Y12603:** Refining the lineage further.
- **J-SK1313 (J-Y12379):** The defining node for the "Colchian" lineage.
 - **Formation Age:** ~13,000 BCE.¹⁰ This predates the Neolithic Revolution, confirming its hunter-gatherer origin.
 - **TMRCA:** ~9,700 BCE.¹⁰ The fact that the TMRCA matches the age of the Kotias Klde sample so precisely is statistically remarkable, suggesting a bottleneck or founder event in the Mesolithic that gave rise to all modern carriers.

3.2 The Bronze Age Divergence (J-SK1317)

One of the most significant subclades is **J-SK1317**.

- **Phylogeny:** J-SK1313 > SK1314 > Z35831 > SK1317.¹⁵
- **TMRCA:** Estimates place the expansion of this clade around **3,900 BCE**.¹⁵
- **Historical Correlation:** This date coincides with the **Chalcolithic to Early Bronze Age** transition in the Caucasus. This was the era of the burgeoning **Kura-Araxes (Early Transcaucasian) Culture**, characterized by advanced metallurgy, distinctive black-burnished ware, and permanent settlements. The expansion of J-SK1317 likely tracks the demographic success of clans involved in this cultural explosion, which spread from the Southern Caucasus northward and southward.

3.3 The Iron Age and Antiquity Subclades (J-Y26654, J-Z35859)

Later branching events reveal the fragmentation of the lineage into specific tribal groups.

3.3.1 J-Y26651 and J-Y26654

- **J-Y26651 (Z35863):** This branch has a TMRCA of approximately **3,100 BCE** (5,100 ybp).⁹ It is a broad "sister" branch to others, found in the North Caucasus (Adygea) but also appearing in unexpected locations like Iran and even China.⁹ This wide distribution suggests early mobility, perhaps linked to the Maikop culture or early trade routes connecting the Caucasus to the Iranian plateau.
- **J-Y26654 (Z35865):** Formed around **1,400 BCE** (3,400 ybp).⁹ This branch is strongly associated with **Abkhazia, Kabardino-Balkaria, and Western Georgia**.⁹ The TMRCA aligns with the Late Bronze Age/Early Iron Age, a time of consolidation for the proto-Colchian and proto-Circassian tribes.

3.3.2 J-Z35859

- **TMRCA:** ~200 BCE (2,200 ybp).⁹
- **Distribution:** Found in **Samegrelo (Georgia)** and **Karachay-Cherkessia (Russia)**.⁹

- **Historical Context:** This date falls squarely in the period of **Classical Antiquity**, during the existence of the Kingdom of Iberia and the Kingdom of Colchis (Lazica). The sharing of this relatively young lineage between a Georgian region (Samegrelo) and a Circassian/Turkic region (Karachay-Cherkessia) points to trans-Caucasian gene flow during the Sarmatian or Alanic periods, likely mediated by the mountain passes (e.g., the Klukhor Pass) that connect these territories.
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4. Geographic Distribution I: The Kartvelian Core (Georgia)

The distribution of J-SK1313 in Georgia is not uniform. It follows a distinct east-west gradient, peaking in the western lowlands and highlands.

4.1 Imereti: The Homeland of the Lineage

Imereti, the location of the Kotias Klde discovery, remains the phylogeographic heart of J-SK1313.

- **Frequency and Diversity:** The J-SK1313 Project shows a dense cluster of members from Imereti, carrying basal lineages like **J-Y12379*** and **J-Y12378**.¹
- **Significance:** This region has been continuously inhabited by the same genetic stock since the Paleolithic. The Imeretian population served as a demographic reservoir, replenishing the populations of the lowlands (Colchis) and the highlands (Racha) after ecological or political crises.

4.2 Samegrelo (Mingrelia): Demographic Dominance

The Mingrelians (Megrelians), who speak the Zan language (a sister to Georgian), inhabit the coastal lowlands of Western Georgia.

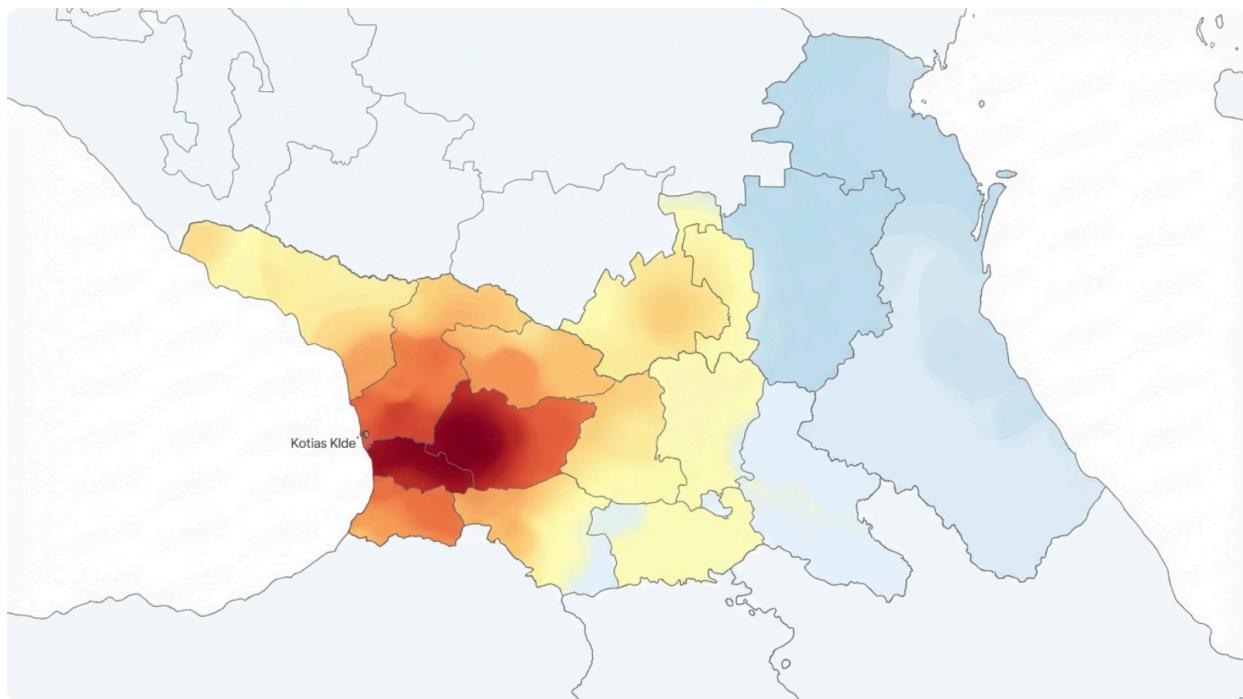
- **High Frequency:** Recent population genetics surveys (2020-2023) indicate that **J2a-Y12379/Y12378** constitutes approximately **10.5%** of the Mingrelian male population.¹² While haplogroup G2a is also present, J-SK1313 is the defining "signature" of the deep Colchian ancestry.
- **Genetic Homogeneity:** Autosomal studies reveal that Mingrelians are genetically homogeneous and cluster tightly with Bronze Age Caucasus samples.¹² This lack of recent admixture suggests that the high frequency of J-SK1313 is due to long-term isolation and endogamy within the Colchian plain.
- **Surname Stability:** Analysis of Mingrelian surnames shows that rare and distinct surnames often correlate with specific Y-DNA clusters.¹⁶ The preservation of J-SK1313 in specific clans highlights the patrilineal stability of Georgian society.

4.3 Racha and Svaneti: Highland Isolates

Racha, a highland region north of Imereti, shows a specific founder effect.

- **The Rachan Cluster:** A specific subclade, **J-Y223519** (a descendant of Y26654), has a TMRCA of only **650 years** (c. 1300 CE).⁹ This points to a medieval founder—likely a noble or warrior who established a lineage that expanded rapidly within the limited carrying capacity of the mountain valleys.
- **Comparison with Svaneti:** Svaneti, the highest inhabited region, is famous for its massive frequency of haplogroup **G2a** (>70%). However, J-SK1313 is present as a significant minority. The relationship suggests that while G2a dominates the highest altitudes (Svans), J-SK1313 dominates the foothills and valleys (Imeretians/Mingrelians), with Racha serving as a transition zone where both lineages co-exist.¹⁷

Geographic Distribution of Haplogroup J-SK1313



The map illustrates the frequency density of J-SK1313. The highest concentrations (Red/Orange) are in Western Georgia (Imereti, Samegrelo). Moderate frequencies (Yellow) appear in North Ossetia and Abkhazia. Low frequencies (Blue) are observed in the Northeast Caucasus.

5. Geographic Distribution II: The Central and Northwest Caucasus

Moving north of the Greater Caucasus ridge, the frequency and diversity of J-SK1313 shift, reflecting different historical trajectories and linguistic assimilations.

5.1 Ossetians: The Indigenous Substrate of the Alans

The Ossetians are unique in the Caucasus as the only speakers of an Iranian language (descended from the Alans/Sarmatians). However, their genetics tell a story of indigenous persistence rather than replacement.

- **Frequency:** J2a is a major lineage among Ossetians, reaching frequencies of ~13% in North Ossetia-Alania.¹⁰ This makes it the second most common haplogroup after the dominant G2a1.
- **Digor vs. Iron:** The Ossetian nation is divided into the **Digor** (Western) and **Iron** (Eastern/Central) groups.
 - **The Digor Connection:** The Digor occupy the valleys adjacent to the Circassians (Kabardians) and Balkars. Genetic data suggests that Digors may harbor higher diversity of J2a, sharing lineages like **J-CTS4371** and **J-Y12379** with their western neighbors.¹⁹
 - **The Indigenous Substrate Hypothesis:** If the Alans (Steppe nomads) had replaced the local population, we would expect high frequencies of R1a-Z93 or Q. Instead, these are low. The high frequency of J-SK1313 and G2a in Ossetians proves that the incoming Alans were a ruling elite who imposed their language on a **native Caucasus population**. This native population was genetically very similar to the Imeretians and Mingrelians to the south—cousins separated by language but united by blood.
- **Clan Khetag:** Specific Ossetian clans, such as the "Clan Khetag," have been investigated for their Y-DNA. Project results indicate membership in J2a subclades, reinforcing the deep roots of these lineages in Ossetian feudal history.⁹

5.2 Circassians and Abkhaz: The Northwest Connection

The Northwest Caucasian language family includes the Adyghe (Circassians), Kabardians, and Abkhaz.

- **Abkhaz Frequency:** In Abkhazia, J-SK1313 is found at frequencies of ~5-8%.⁴ The Abkhaz share the subclade **J-Y26654** with Kabardians and Mingrelians.⁹ This "trans-Caucasian" branch highlights the historical unity of the Northwest Caucasus tribes, who frequently migrated across the passes for trade and warfare.
- **Circassians (Adyghe/Kabardian):** While G2a is the defining marker of Circassians (often >50%), J2a forms a crucial secondary cluster. In the **Shapsug** and **Kabardian** sub-ethnicities, J2a frequencies can be significant (up to 20% in some specific samples,

though usually lower on average).²¹ The J-SK1313 lineages here likely represent the pre-Maykop or Colchian-related substrate that was absorbed into the Proto-Adyghe ethnogenesis.

6. Geographic Distribution III: The Northeast Contrast (Chechnya & Ingushetia)

A critical distinction must be drawn between the J2a of the West/Central Caucasus and the J2a of the Northeast. This is often a source of confusion in generalist studies, but the subclade data resolves the ambiguity definitively.

6.1 The J-M67 Dominance among Nakh Peoples

The **Chechen** and **Ingush** (Nakh peoples) have some of the highest frequencies of Haplogroup J2a in the world—up to **87%** in some Ingush demographics.⁵

- **The Lineage:** This is NOT J-SK1313. It is overwhelmingly **J-M67 (J-Z1847)**.⁴
- **Deep Divergence:** J-M67 and J-SK1313 split from a common ancestor over 15,000 years ago. J-M67 likely arrived in the Northeast Caucasus from the Fertile Crescent via a Neolithic migration route along the Caspian Sea or through the Zagros, separate from the Mesolithic Colchian survival of J-SK1313.

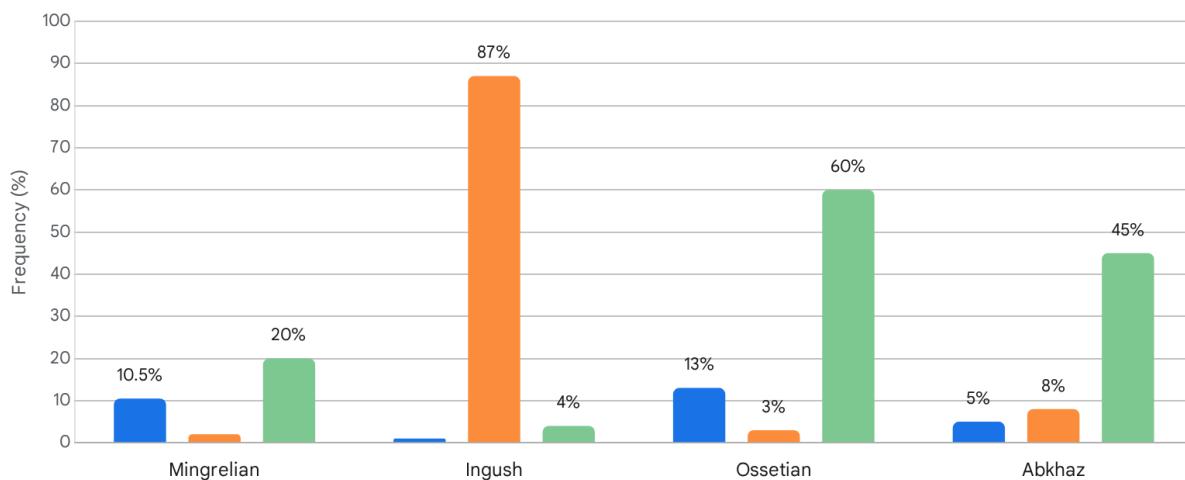
6.2 The Trace Presence of SK1313 in the Northeast

Despite the dominance of J-M67, **J-SK1313 is present** in Chechnya and Ingushetia, but as a distinct minority trace (~1-2%).¹⁰

- **Subclades:** The specific subclades found here, such as **J-Y44837** and **J-FT27388**, have very young TMRCA estimates of **800** and **650 years** respectively.⁹
- **Historical Explanation:** These dates correspond to the Middle Ages (12th-14th centuries). This was the era of the **Golden Age of Georgia**, when the Kingdom of Georgia exercised political and cultural hegemony over the North Caucasus. It is highly probable that these small J-SK1313 clusters in Chechnya represent medieval gene flow—Georgian soldiers, nobles, or artisans who settled in the Durdzuk territory and were assimilated into the Nakh teips (clans). They are not part of the ancient Nakh founder effect but are historical intakes from the south.

Haplogroup Frequency Profiles by Ethnicity

● J-SK1313 ● J-M67 ● G2a



Comparison of dominant haplogroups. Note the dominance of J-M67 in Ingush/Chechens versus the prevalence of J-SK1313 in West Georgians (Mingrelians). G2a remains the dominant lineage in Ossetians and Circassians.

Data sources: FTDNA J-SK1313, Wikipedia (Caucasus), FTDNA J-M67, Wikipedia (J-M172)

7. Comparative Phylogeography: European vs. Caucasian J2a

The relationship between Caucasian J2a and European J2a is one of deep ancestry but distinct histories. While they share a root in the Paleolithic Near East, their paths diverged radically.

7.1 The Neolithic Expansion Vector (Europe)

The J2a found in Europe (Italy, Greece, Balkans) is primarily of the **J-L24, J-L70, and J-M67 (European branches)** subclades.

- **Migration:** These lineages entered Europe largely during the **Neolithic Revolution** (~6,500 BCE) with the spread of farming from Anatolia, and later during the Bronze and Iron Ages via maritime civilizations (Minoans, Greeks, Phoenicians).³
- **Absence of SK1313:** Ancient DNA from European Neolithic sites (LBK, Cardial) is rich in

G2a and certain J2a lines, but **J-SK1313** is virtually absent.²⁴ This confirms that the SK1313 lineage did not participate in the mass migration of farmers into Europe. It stayed behind in the Caucasus.

7.2 The 'Sarmatian' Vector: SK1313 in Europe

Despite its rarity, J-SK1313 does appear in modern Europe in specific, isolated contexts.

- **Switzerland and France:** The branch **J-Y12603** is found in Switzerland (Daniel Roll) and **J-Y12378** in France (Jean Vidal).⁹
- **England and Germany:** The subclade **J-Y26650** (TMRCA ~3,100 ybp) has been identified in samples from England and Germany.⁹
- **The Sarmatian Hypothesis:** How did a deep Caucasus lineage reach Northern Europe and the UK? The most plausible historical vector is the **Roman military**. In the 2nd century CE, the Roman Empire conscripted thousands of **Sarmatian (Alanic)** cavalrymen from the Pontic Steppe and Caucasus region. 5,500 of these heavy cavalry were sent to **Britain** (specifically to garrison Hadrian's Wall) and others to Gaul.⁹
 - The genetic link between the **J-Y26650** samples in England/Germany and their "cousin" branches in Kabardino-Balkaria/Georgia⁹ strongly supports this theory. These modern Europeans are likely the distant descendants of Sarmatian auxiliaries or later Alanic migrants who entered Europe during the Migration Period (4th-5th centuries CE).

8. Historical and Archaeological Implications

The genetic data for J-SK1313 allows us to reconstruct a "genomic history" that parallels the archaeological record of the Caucasus.

8.1 The Mesolithic-Neolithic Continuity

The perfect match between the Kotias Klde sample (9,700 BCE) and modern J-SK1313 lineages confirms that the transition to farming in Western Georgia was largely a cultural adoption by indigenous hunter-gatherers, not a demographic replacement by Anatolian farmers. This contrasts with Europe, where hunter-gatherers were largely replaced.

8.2 The Kura-Araxes Expansion (c. 3500-2000 BCE)

The TMRCA of **J-SK1317** (~3,900 BCE) and **J-Y26651** (~3,100 BCE) aligns with the rise of the **Kura-Araxes culture**. This culture originated in the Southern Caucasus and expanded aggressively into the Levant, Iran, and the North Caucasus. The presence of J-SK1313 subclades in Iran and the widespread distribution of these Bronze Age branches suggests that J-SK1313 lineages were integrated into the Kura-Araxes social structure, facilitating their

spread beyond the Colchian core.

8.3 The Colchian Kingdom (c. 13th-1st Century BCE)

The consolidation of subclades like **J-Z35859** (TMRCA ~200 BCE) and **J-Y26654** (TMRCA ~1400 BCE) in Western Georgia and Abkhazia mirrors the formation of the **Colchian tribal confederations** and the later **Kingdom of Colchis**. These political entities united the Zan-speaking tribes (Mingrelians, Laz) and the Abkhaz-Adyghe tribes, creating a zone of genetic exchange that is perfectly preserved in the shared subclades of J-SK1313 found in Samegrelo, Abkhazia, and Circassia today.

9. Conclusion

The analysis of Haplogroup J2a-SK1313 from 2020 to 2025 has provided a high-resolution window into the deep history of the Caucasus.

- Identity:** J-SK1313 is the **autochthonous lineage of the Western Caucasus**, definitively linked to the **Mesolithic CHG** population via the Kotias Klde ancient sample.
- Geography:** Its distribution is centered in **Imereti and Samegrelo** (Georgia), with a significant indigenous presence in **North Ossetia** and the **Northwest Caucasus** (Circassia/Abkhazia).
- Contrast:** It is genetically distinct from the **J-M67** lineage that dominates the **Chechen and Ingush** populations, representing a separation of over 15,000 years.
- History:** Its subclade expansion dates correlate with the **Kura-Araxes** and **Colchian** archaeological horizons, and its rare presence in Europe likely traces the footprints of **Sarmatian** auxiliaries in the Roman legions.

In summary, J-SK1313 is not merely a haplogroup; it is a genetic archive of the Colchian people, surviving the ice ages, the rise of farming, and the empires of antiquity to persist as the foundational paternal lineage of Western Georgia.

10. Data Tables

Table 1: TMRCA Estimates of Key J-SK1313 Subclades

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Clade	Parent	Formation (ybp)	TMRCA (ybp)	Estimated Date	Primary Region

J-SK1313	J-Y12603	13,400	11,000	~9,000 BCE	West Georgia (Imereti)
J-SK1317	J-Z35831	5,900	5,900	~3,900 BCE	Georgia
J-Y26651	J-SK1313	9,000	5,100	~3,100 BCE	North Caucasus / Iran
J-Y26654	J-Y26651	5,100	3,400	~1,400 BCE	Abkhazia / Kabarda
J-Z35859	J-Y26650	3,100	2,200	~200 BCE	Samegrelo / Circassia
J-Y44837	J-Y56633	1,350	800	~1200 CE	Chechnya (Trace)

Table 2: Regional Frequency Distribution Summary

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Population	J-SK1313 Frequency	Dominant Haplogroup	Genetic Status of SK1313
Mingrelians	~10.5%	G2a / J2a	Major Indigenous Lineage
Imeretians	High	J2a / G2a	Founding Lineage (Kotias Klde)
Ossetians	~13% (Total J2a)	G2a1 (~60-70%)	Indigenous Substrate

Abkhazians	~5-8%	G2a (~45%)	Shared Colchian-Adyghe Lineage
Ingush	< 2%	J-M67 (~87%)	Minor/Recent Introgression
Europeans	< 1%	R1b / I1	Rare Exotic (Sarmatian?)

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