

The North Wind and the Mountain Wall: A Genomic Reconstruction of Scythian and Sarmatian Legacies in the Circassian Gene Pool

1. Introduction: The Steppe-Caucasus Interface

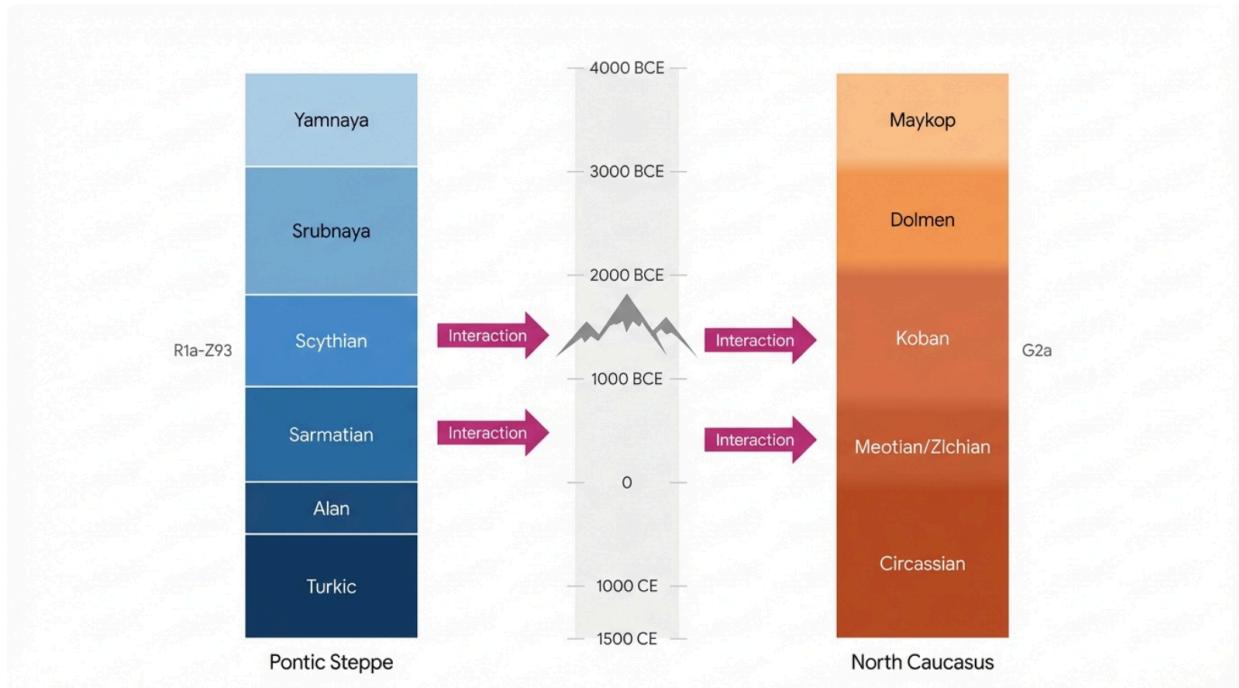
The genetic history of the Northwest Caucasus represents one of the most complex and enduring frontiers in Eurasian population genetics. For millennia, the Great Caucasus range has served not merely as a geological barrier but as a sophisticated bio-geographic filter, selectively permitting the flow of cultural innovations while strictly regulating demographic introgression. This dynamic is most critically observed in the relationship between the indigenous populations of the high valleys—the ancestors of the modern Circassian (Adyghe) peoples—and the successive waves of nomadic confederations that dominated the Pontic-Caspian steppe to the north. Among these nomads, the Scythians (7th–3rd century BCE) and the Sarmatians (4th century BCE–4th century CE) represent the "Iron Age Horizon," a period of intense militarization, mobility, and cultural exchange often referred to as the Scytho-Siberian world.

The central inquiry of this report evaluates the extent to which these Iranic-speaking nomadic groups contributed to the biological ancestry of the modern Circassian people. Historically, the proximity of the Scythian domains in the Kuban steppe to the proto-Circassian Maeotian settlements in the piedmont has led to hypotheses of extensive admixture, population replacement, or elite dominance. However, the advent of high-resolution ancient DNA (aDNA) sequencing between 2018 and 2025 has provided the granular data necessary to test these hypotheses with unprecedented precision. By integrating paleogenomic data from key studies—including Krzewińska et al. (2018), Unterländer et al. (2017), Wang et al. (2019), and Damgaard et al. (2018)—we can now reconstruct the demographic history of this region not as a monolithic wave of conquest, but as a nuanced stratification of selective gene flow.

The emerging consensus supports a "Permeable Barrier Model." While the Circassian gene pool remains overwhelmingly indigenous, rooted in the deep ancestry of the Caucasus Hunter-Gatherers (CHG) and the Early Bronze Age Maykop culture, there exists a discernible, stratified signal of Steppe introgression. This report will demonstrate that the "Scythian" legacy in Circassians is not the result of a singular demographic inundation but rather a composite accumulation of genetic inputs, mediated primarily through the assimilation of the Alanic populations in the first millennium CE and the earlier, subtle interactions of the Bronze Age. We will rigorously dissect the Y-chromosomal evidence, particularly the interplay between the indigenous G2a lineages and the intrusive R1a-Z93 haplogroups, and quantify

the autosomal admixture that defines the modern Circassian genetic profile.

Parallel Histories: Genetic Continuity vs. Steppe Turnover (4000 BCE - 1500 CE)



Comparative chronology of the North Caucasus Piedmont (Mountain Zone) versus the Pontic-Caspian Steppe. Note the strong genetic continuity in the Circassian ancestral line (Koban/Meotian continuity) compared to the frequent population replacements in the Steppe (Scythian, Sarmatian, Hunnic transitions). Red arrows indicate periods of potential gene flow.

2. The Indigenous Substrate: The Genetic Fortress of the Northwest Caucasus

To accurately detect and quantify the genetic contribution of Scythians or Sarmatians, one must first rigorously define the "indigenous substrate"—the genetic baseline of the Northwest Caucasus populations prior to the Iron Age. The Circassian peoples (Adygehe, Kabardians, Cherkess, Shapsugs) possess a genetic profile that is remarkably distinct from the populations of the open steppe to their north, characterized by a profound continuity that dates back to the Upper Paleolithic and Neolithic periods. This continuity serves as the anchor against which all subsequent admixture events are measured.

2.1 The Dominance and Antiquity of Haplogroup G2a

The defining feature of the Western Caucasus paternal gene pool is the extreme prevalence of Y-chromosome haplogroup **G2a** (specifically subclades G-P15, G-P303, and G-U1). In various modern Circassian subpopulations, particularly the Shapsugs and Kabardians, this haplogroup reaches frequencies between 50% and 70%, establishing it as the foundational lineage of the region.¹ The ubiquity of G2a is not merely a modern phenomenon but a direct echo of the region's deep prehistory.

Paleogenomic analysis has confirmed that G2a lineages were already the dominant paternal marker in the Northwest Caucasus during the Eneolithic and Early Bronze Age. Genomic data from the **Darkvetsi-Meshoko** culture (Eneolithic) and the **Maykop** culture (ca. 3700–3000 BCE) reveal that individuals from these periods carried G2a lineages almost exclusively.³ This continuity is a critical finding; it establishes that the demographic core of the Circassian population formed *in situ* and successfully resisted total displacement despite millennia of pressure from the steppe. The molecular clock estimates for the diversification of G2a subclades in the Caucasus align with the expansion of these early agricultural and metal-working societies, suggesting that the "founder effect" for the modern Circassian population occurred well before the arrival of Indo-European nomads.

The survival of G2a at such high frequencies is anomalous in the broader context of West Eurasia. In Europe, the G2a lineages associated with Early European Farmers (EEF) were largely replaced by R1a and R1b lineages during the Late Neolithic and Bronze Age expansions of Steppe pastoralists. The preservation of G2a in the Northwest Caucasus indicates that the mountains acted as a "refugium" or a fortress, preventing the genetic turnover that characterized the rest of the continent.

2.2 Autosomal Continuity: The CHG-Anatolian Cline

Beyond uniparental markers, the autosomal DNA of Circassians tells a story of deep persistence. Modern Circassians cluster tightly with other North Caucasian groups (such as the Abkhaz and Ossetians) in a genetic space defined by a dominant **Caucasus Hunter-Gatherer (CHG)** component mixed with **Anatolian Neolithic Farmer (ANF)** ancestry.³ This unique admixture profile, often termed the "Caucasus Cluster," is distinct from the "Steppe Cluster" found in the Yamnaya, Scythian, and Sarmatian populations.

The "Steppe" genetic profile is characterized by high levels of Eastern Hunter-Gatherer (EHG) ancestry and distinct ratios of CHG, typically lacking the high ANF component found in the Caucasus. The persistence of the CHG-ANF profile in modern Circassians—despite their geographic proximity to the steppe—demonstrates that the gene flow from north to south was highly selective. While material culture, such as the "Scythian Triad" of weapons, horse gear, and animal-style art, flowed across the range and heavily influenced local cultures like the **Koban** (Late Bronze/Early Iron Age), the demographic impact was asymmetric. The mountains filtered the incoming population, allowing trade and elite interaction while blocking

mass migration that would have swamped the local autosomal signature.

3. The Scythian Horizon (7th–3rd c. BCE): Contact without Replacement

The Scythians, an Iranic-speaking nomadic confederation, dominated the Pontic-Caspian steppe during the Iron Age. The historical record, rich with Greek accounts of Scythian raids and trade, prompts the question: *Did the Scythians penetrate the mountain valleys and leave a genetic legacy among the ancestors of the Circassians?* The genomic data suggests a relationship of contact and influence, but not of demographic replacement.

3.1 Genomic Structure of the Pontic Scythians

Recent high-coverage sequencing efforts, particularly by Krzewińska et al. (2018), have fundamentally clarified the genetic structure of the Scythian world. The term "Scythian" does not denote a monolithic ethnicity but rather a multi-ethnic confederation sharing a cultural horizon. However, the genetic core of the Western (Pontic) Scythians—those geographically nearest to the Circassians—displays a recognizable profile.

Genetic Component	Pontic Scythian Profile	Significance for Circassians
Y-Haplogroup	R1a-Z93 (Dominant), R1b-Z2103, Q1c	High frequency of R1a contrasts with indigenous G2a.
Autosomal DNA	Late Bronze Age Steppe (Srubnaya-like) + Southern (ANF/EEF) + Minor East Asian	High EHG ancestry distinguishes them from the high-CHG Circassians.
G2a Presence	Rare to Absent in core steppe samples	Absence suggests little gene flow <i>from</i> Caucasus to Steppe in this era.

The overwhelming majority of Scythian males carried haplogroup **R1a**, specifically the **Z93** branch and its downstream clades like Z2124 and Z2123.⁶ While R1b-Z2103 and Q1c lineages appear, they are secondary. Crucially, **haplogroup G2a is vanishingly rare** in core Scythian steppe contexts. Where G2a does appear in Scythian-era samples (e.g., sporadic finds in the Don or pre-Caucasian steppe), it is frequently interpreted as evidence of local assimilation—Scythians incorporating local Caucasian or settled European men into their

ranks—rather than G2a being a "Scythian" lineage itself.⁴ This distinction is vital: if Scythians had settled the mountains in large numbers, we would expect a dilution of G2a and a surge of R1a in the Iron Age layers of the Caucasus. The data does not show this.

3.2 The Meotian Interface: A Zone of Interaction

The primary theatre of interaction between the Scythian nomads and the sedentary ancestors of the Circassians (proto-Adyge) was the **Kuban River basin**. Here, the **Meotian culture** (Maeotians) flourished in the piedmonts and swampy deltas. The Meotians are widely regarded as the archaeological ancestors of the Adyge/Circassian people.

Archaeological distributions mirror the genetic findings. Scythian kurgans (burial mounds) are densely packed in the steppe north of the Kuban River but decrease rapidly in frequency as one moves south into the wooded foothills and mountain valleys.⁴ This distribution suggests a political and military boundary. The mountains acted as a "sovereignty shield," preserving the local Meotian demographic structure. While Scythian elites likely extracted tribute, engaged in trade, and perhaps formed marriage alliances with Meotian chieftains, they did not demographically swamp the population. The genetic barrier at the Kuban was maintained by the distinct ecological zones: the pastoralist economy of the Scythians was ill-suited for the densely forested mountain terrain of the Circassians.

3.3 Evaluating R1a-Z93 Transfer

The presence of **R1a-Z93** in modern Circassians at frequencies of roughly 10-20%² is often cited as the "smoking gun" of Scythian admixture. Did Scythians transfer this lineage to the Circassians? The answer is affirmative, but with significant caveats regarding timing and proportion.

Assigning all Circassian R1a to the Scythians is a simplification that ignores the stratified nature of steppe introgression.

- **Layer 1: The Bronze Age Signal:** Some R1a lineages in the North Caucasus may date back to the **Steppe Maykop** or **Catacomb** cultures (2800–2000 BCE).³ These groups infiltrated the piedmont steppe long before the Scythian ethnogenesis. The Wang et al. (2019) study identified "Steppe Maykop" individuals with a distinct genetic profile that included R1a, representing a deeper, pre-Scythian layer of admixture.
- **Layer 2: The Scythian-Sarmatian Signal:** High-resolution phylogenetics suggests that a significant portion of Circassian R1a does cluster with Iron Age variants (e.g., R-Z2124) found in Scythian and Sarmatian burials. This supports the hypothesis of gene flow during the Iron Age, likely mediated through the assimilation of Meotian groups who had mixed with nomads.
- **Layer 3: The Turkic Overlay:** Later incursions by Turkic speakers (Khazars, Kipchaks, Crimean Tatars) also carried R1a-Z93 subclades. Differentiating "Scythian" R1a from "Turkic" R1a requires extremely granular SNP testing, but the diversity of R1a in the

Caucasus suggests a cumulative legacy rather than a single event.

4. The Sarmatian and Alanic Impact (4th c. BCE – 13th c. CE)

If the Scythian impact can be characterized as a "surface wave" that broke against the foothills, the Sarmatian and subsequent Alanic impact was a "deep current" that permeated the North Caucasus more thoroughly. The Sarmatians, and their later subgroup the Alans, established a long-term presence in the region that fundamentally altered its demography.

4.1 Sarmatian Genetics: The Eastern Shift

Sarmatian genomes differ in subtle but important ways from their Scythian predecessors. Originating from the Southern Urals and the trans-Uralic steppe, Sarmatians typically harbor higher proportions of **East Asian** and **Siberian** ancestry.⁴ This "eastern shift" serves as a genetic marker for distinguishing Sarmatian admixture from earlier Scythian or Yamnaya ancestry.

- **Paternal Lineages:** Like the Scythians, Sarmatians were dominantly **R1a-Z93**. However, their gene pool appears more diverse, incorporating **J2** and **Q** lineages reflecting their interactions with Central Asian and potentially southern populations.¹⁰
- **Mitochondrial Exchange (mtDNA):** A distinguishing feature of the Sarmatian period is the potential for distinct maternal gene flow. Sarmatian society is noted in classical sources for the high status of its women (the historical basis for Amazon myths). Ancient DNA from Sarmatian burials has yielded mtDNA haplogroups such as **U5a**, **H**, and **T**.¹⁰ These lineages overlap significantly with those found in modern Circassians. The presence of **U5a** in Circassians (approx. 8%)¹¹ is a strong candidate for a maternal lineage introduced from the steppe during this period, as U5 is comparatively rare in the ancient, pre-Iron Age indigenous Caucasus, which was dominated by other haplogroups.¹²

4.2 The Alanic Bridge: From Neighbors to Ancestors

The Alans (Alani), a constituent tribe of the Sarmatian confederation, established a powerful kingdom in the Central and North Caucasus (Alania) that endured until the Mongol invasions of the 13th century. While the Alans are the direct linguistic ancestors of the **Ossetians**, their genetic legacy extends broadly to the **Circassians** and other North Caucasian groups.

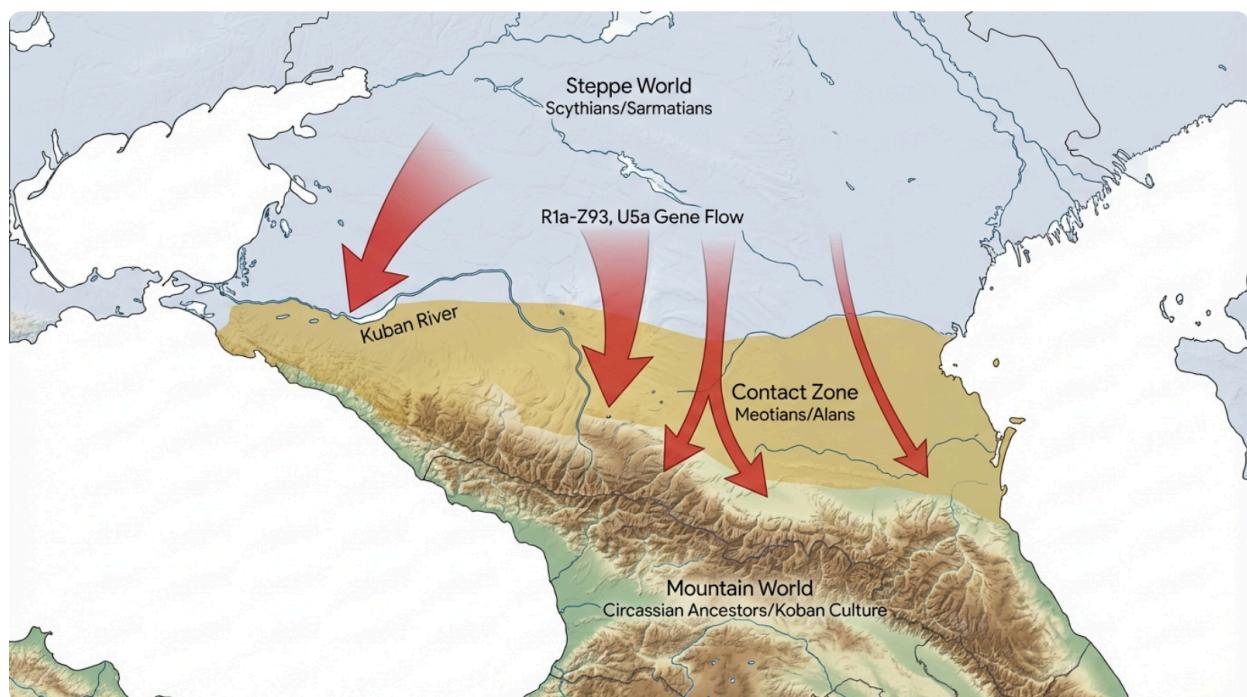
The Alans represent the crucial "bridge" between the steppe and the mountains.

- **Admixture in Alania:** Genetic analysis of Alanic burials (e.g., from the Don River and North Ossetia contexts) reveals a population that was already admixed. These individuals carried a combination of **R1a-Z94** (Steppe paternal origin) and **G2a** (Local/Caucasian paternal origin).¹³ This indicates that by the first millennium CE, the "Steppe" population

had thoroughly intermarried with the "Mountain" population.

- **The Alanic Assimilation:** Following the Mongol devastation of the Alanic kingdom in the 13th and 14th centuries, surviving Alanic populations were pushed into the mountains or assimilated by expanding neighbors. The Circassians, particularly the **Kabardian** subdivision which expanded eastward into former Alanic territories, likely absorbed significant numbers of Alanic refugees. This event—the "Alanic Assimilation"—is the most plausible vector for the infusion of "Steppe" autosomal DNA and R1a lineages into the Circassian gene pool. It explains how steppe ancestry could penetrate the Circassian population without a violent conquest or total replacement: it was absorbed through the integration of a neighbor who was already a hybrid of the two worlds.

The Kuban Frontier: Genetic Interactions at the Steppe-Mountain Interface



Schematic representation of the North Caucasus contact zone (c. 500 BCE - 200 CE). The Kuban River and the Caucasian foothills acted as a semi-permeable barrier. While Scythian and Sarmatian material culture permeated the region, substantial gene flow (red arrows) was likely filtered through the sedentary Meotian and Alanic populations before reaching the high mountain valleys.

5. The Autosomal "Barrier Effect": Quantifying Steppe

Ancestry

The user poses a critical question: *Did mountains block steppe gene flow?* The genomic data from 2018–2025 provides a nuanced answer: The mountains did not fully block gene flow, but they acted as a highly effective filter, creating a sharp genetic discontinuity that persisted for millennia.

5.1 The Steppe vs. Caucasus Divide

The landmark study by **Wang et al. (2019)** demonstrated a profound genetic boundary in the North Caucasus during the Eneolithic and Bronze Age.

- **North of the Kuban/Terek:** Populations identified as **Steppe Maykop** carried a distinct ancestry profile characterized by Steppe ancestry admixed with a unique Siberian component.³ This profile is largely absent in the populations south of the Kuban river. This finding is revolutionary because it proves that simply living *near* the Caucasus did not ensure genetic contribution to the mountaineers; the "Steppe Maykop" people lived in the piedmont steppe but remained genetically distinct from their contemporaries in the mountains.
- **South of the Kuban:** The **Maykop** and **Koban** cultures were genetically continuous with the South Caucasus, dominated by CHG and ANF ancestry with minimal EHG admixture.¹⁴ This confirms that the cultural barrier of the Kuban River was also a formidable genetic barrier.

5.2 Iron Age Permeability and Modern Admixture Levels

In the Iron Age (Scythian/Sarmatian period), this barrier became permeable. While the core population structure of the Caucasus was maintained, Steppe ancestry began to trickle in. Modern Circassians are modeled as harboring approximately **10–20% Steppe ancestry** (modeled as Yamnaya-like or Steppe_MLBA).¹⁶

This percentage is instructive when compared to neighboring regions:

- **Pontic Scythians:** ~50%+ Steppe ancestry.
- **Modern Eastern Europeans:** ~30–50% Steppe ancestry.
- **Modern Circassians:** ~15% Steppe ancestry.

Table 1 illustrates the comparative admixture profiles, highlighting the "dilution" of Steppe ancestry as one moves from the open steppe into the Caucasus mountains.

Population Group	Primary Ancestry Component	Secondary Component	Approx. Steppe Ancestry %
Pontic Scythians	Steppe (EHG +	Anatolian Neolithic	~50%

	CHG)		
Sarmatians	Steppe (EHG + CHG)	East Asian / Siberian	~45–55%
Medieval Alans	Steppe + Caucasus Mixed	-	~30–40%
Modern Circassians	Caucasus (CHG + ANF)	Steppe / Anatolian	~10–20%
Bronze Age Maykop	Caucasus (CHG + ANF)	-	< 5%

Table 1: Comparative Autosomal Ancestry Quantification. Note the significant drop in Steppe ancestry in Circassians compared to the nomadic groups, confirming the 'Barrier Effect' of the Caucasus Mountains.⁴

The ~15% Steppe admixture in modern Circassians represents the cumulative legacy of all steppe interactions—the faint echo of Bronze Age Yamnaya/Catacomb introgression, the focused pulses of Scythian/Sarmatian intermarriage, and the assimilation of Alanic clans. It confirms that the mountains were a filter, not a wall. The Circassians are not genetic isolates, but they remain fundamentally "people of the mountains" who absorbed elements of the "people of the steppe," rather than being replaced by them.

6. R1a-Z93: Tracing the Paternal Lineages

The Y-chromosome haplogroup **R1a-Z93** is the most tangible genetic link between the Steppe and the Caucasus. Its presence in 10-20% of Circassian men requires a detailed forensic accounting to distinguish between potential sources.

6.1 Differentiating the Sources

- **Scenario A: The Bronze Age (Early Steppe):** Could this R1a come from the Yamnaya or Catacomb cultures (3000–2000 BCE)? While possible, it is less likely to be the *primary* source. Bronze Age North Caucasus groups like Maykop were predominantly G2a and J2. The "Steppe Maykop" population had R1a, but they appear to have been a dead-end lineage or one that did not mix heavily with the mountain Maykop groups.³
- **Scenario B: The Iron Age (Scythian/Sarmatian):** This is the most robustly supported hypothesis for the bulk of Circassian R1a. The **Z2123** subclade of R1a is a specific downstream branch of Z93. It has been frequently identified in Sarmatian remains.¹⁰ The

presence of this specific subclade in the modern North Caucasus strongly points to the Sarmatian/Alanic period as the main vector of introgression.

- **Scenario C: The Turkic Overlay (Late Medieval):** Some Z93 subclades are associated with later Turkic expansions (e.g., the Golden Horde, Crimean Tatars). However, deep phylogenetic sequencing often distinguishes "Scythian" Z93 lineages from distinct "Turkic" branches. While Turkic admixture contributed to other groups like the Karachay and Balkars, the Circassian R1a profile retains a strong signal consistent with earlier Indo-Iranian (Sarmatian/Alan) sources.

Conclusion on R1a: The Circassian R1a-Z93 is likely a **composite legacy**, but the foundational introgression event aligns best with the **Sarmatian-Alanic period**. This suggests that as the Alans settled and mixed with indigenous groups, their paternal lineages were incorporated into the Adyghe tribal structure, eventually becoming established clans within the Circassian nobility and commoner classes.

7. Conclusion: A Legacy of Interaction, Not Replacement

The genetic relationship between the Scythian/Sarmatian nomads and the Circassian people is defined by **selective introgression into a resilient indigenous substrate**. The paleogenomic evidence from 2018–2025 supports the following nuanced conclusions:

1. **Scythian Penetration:** Genetically, the Scythians did **not** penetrate the mountain valleys in a way that caused population replacement. The core Scythian profile (high EHG, R1a dominance) did not displace the indigenous profile (high CHG, G2a dominance). Interaction was likely limited to the piedmont interface (Meotians) and was mediated by trade and tribute rather than settlement.
2. **Sarmatian and Alanic Influence:** The Sarmatian impact was deeper and more lasting. The Alans, emerging from the Sarmatian milieu, settled in the North Caucasus and fundamentally intermixed with local populations. This **Alanic Assimilation** is the primary historical mechanism that introduced **R1a-Z93** and **U5a** lineages into the Circassian gene pool.
3. **The Mountain Barrier:** The Caucasus range was highly effective at preserving the deep population structure formed in the Early Bronze Age. The "Steppe Maykop" distinction proves that even in the Bronze Age, the steppe and mountain populations were distinct. Modern Circassians are genetically "people of the mountains" who absorbed "people of the steppe," maintaining their ancestral continuity while integrating specific steppe lineages.
4. **Steppe Ancestry Quantification:** Present but minor. The ~15% Steppe ancestry in Circassians is a genetic echo of the millennia-long interaction on the frontier where the vast Eurasian steppe crashes into the fortress of the Caucasus. It is a testament to the region's role as both a barrier and a bridge—a place where cultures collide, but where the mountains ultimately hold their ground.

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